



## SEQUENCE LISTING

<110> Gish, Kurt C.  
Mack, David H.  
Wilson, Keith E.  
Afar, Daniel  
Peter, Hevezzi

<120> Methods of Diagnosis of Prostate Cancer, Compositions and Methods  
of Screening for Modulators of Prostate Cancer

<130> 05882.0183.NPUS00

<140> 09/976,858  
<141> 2001-10-12

<150> 60/276,791  
<151> 2001-03-16

<150> 60/288,589  
<151> 2001-05-04

<150> 60/276,888  
<151> 2001-03-16

<150> 60/286,214  
<151> 2001-04-24

<150> 60/281,922  
<151> 2001-04-06

<150> 60/263,957  
<151> 2001-01-24

<160> 294

<170> PatentIn version 3.2

<210> 1  
<211> 4793  
<212> DNA  
<213> human organism

<400> 1  
atggatcaa acatgtcaca agagtcggac aataataaaa gactagtggc ctttagtgccc 60  
atgcccagtg accctccatt caatacccgaa agaggcttaca ccagtggat tgaaggctgg 120  
aagtctact tggagaatcc cctgacagca gccaccaagg ccatgtatgtat cattaatgg 180  
gatgaggaca gtgctgtgc cctcggcctg ctctatgtact actacaagg tcctcgagac 240  
aagaggctgc tgtctgtaa caaagcaagt gacagccaag aagaccaggaa gaaaagaaaac 300  
tgccttggca ccagtgaagc ccagagtaat ttgagtggag gagaaaaaccg agtgcaagtc 360  
ctaaagactg ttccagtgaa cctttcccta aatcaagatc acctggagaa ttccaagcgg 420

gaacagtaca gcatcagctt ccccgagagc tctgccatca tcccgggtgc gggaaatcacg 480  
gtggtaaaag ctgaagattt cacaccagtt ttcatggccc cacctgtgca ctatccccgg 540  
ggagatgggg aagagcaacg agtggttatac tttgaacaga ctcagtatga cgtgccctcg 600  
ctggccaccc acagcgcccta tctcaaagac gaccagcgca gcactccgga cagcacatac 660  
agcgagagct tcaaggacgc agccacagag aaatttcgga gtgcttcagt tggggctgag 720  
gagtagatgt atgatcagac atcaagtggc acatttcagt acaccctgga agccacaaa 780  
tctctccgtc agaagcaggg ggagggccccc atgacacctacc tcaacaaagg acagttctat 840  
gccataacac tcagcgagac cgagacaac aaatgcttcc gacaccccat cagcaaagtc 900  
aggagtgtgg tgatggtggt cttagtgaa gacaaaaaca gagatgaaca gctcaaatac 960  
tggaaatact ggcactctcg gcagcatacg gcgaagcaga gggccttga cattgccat 1020  
tacaaggaga gcttaatac gattggaaac attgaagaga ttgcataataa tgctgttcc 1080  
tttacctggg acgtgaatga agaggcgaag atttcatca ccgtgaattt cttgagcaca 1140  
gatttctcct cccaaaaagg ggtgaaagga ctcccttga tgattcagat tgacacatac 1200  
agttataaca atcgttagcaa taaaccatt catagagtt attgccagat caaggttttc 1260  
tgtgacaaag gacgacaaag aaaaatccga gatgaagagc agaagcagaa caggaagaac 1320  
gggaaaggcc aggcctccca aactcaatgc aacagctcct ctgatggaa gttggctgcc 1380  
atacccttac agaagaagag tgacatcacc tacttcaaaa ccatgcctga tctccactca 1440  
cagccagttc tcttcatacc tgatgttcac tttgcaaacc tgcagaggac cggacaggtg 1500  
tattacaaca cggatgatga acgagaaggt ggcagtgtcc ttgttaaacg gatgtccgg 1560  
cccatggaag aggagttgg tccgggtgcct tcaaagcaga tggaaagaaga agggacaaag 1620  
cgagtgtct tgcgttgag gaaggagact gacgatgtgt tcgatgcatt gatgttgaa 1680  
tctcccacag tgatgggcct gatggaagcg atatctgaga aatatggct gcccgtggag 1740  
aagatagcaa agcttacaa gaaaagcaaa aaaggcatct tggtaacat gatgacaac 1800  
atcatcgagc actactcgaa cgaggacacc ttcatcctca acatggagag catggtgag 1860  
ggcttcaagg tcacgctcat gggaaatctag ccctgggttt ggcatccgct ttggctggag 1920  
ctctcagtgc gttcctccct gagagagaca gaagccccag ccccaagaacc tggagaccca 1980  
tctccccat ctcacaactg ctgttacaag accgtgctgg ggagtggggc aaggacagg 2040  
ccccacagtc ggtgtgcttg gcccacccac tggcacctac cacggagccg aagcctgagc 2100

ccctcaggaa ggtgccttag gcctgttgg a ttcctattta ttgcccac ct tttcctggag 2160  
cccaggtcca ggcccgcag gactctgcag gtcactgcta gctccagatg agaccgtcca 2220  
gcgttcccc ttcaagagaa acactcatcc cgaacagcct aaaaaattcc catcccttct 2280  
ttctcacccc tccatatcta tatctcccga gtggctggac aaaatgagct acgtctgggt 2340  
gcagtagtta taggtggggc aagaggtgga tgcccactt ctggtcagac accttttaggt 2400  
tgctctgggg aaggctgtct tgctaaatac ctccagggtt cccagcaagt ggccaccagg 2460  
ccttgtacag gaagacattc agtcaccgtg taatttagtaa cacagaaagt ctgcctgtct 2520  
gcattgtaca tagtgtttat aatattgtaa taatataatt tacctgtgg atgtggcat 2580  
gttactgcc actggcctag aggagacaca gacctggaga ccgtttaat gggggtttt 2640  
gcotctgtgc ctgttcaaga gacttgcagg gctaggtaga gggccttgg gatgttaagg 2700  
tgactgcagc ttagtgcctaa atggactctg caatggcat acctggggc tcgttccctg 2760  
tccccagagg aagccccctc tccttctcca tgggcatgac tctccttcga ggccaccacg 2820  
tttatctcac aatgatgtgt tttgcctgac tttccctttg cgctgtctcg tggaaaggt 2880  
cattctgtct gagaccctcag ctccctctcc agctttggct gcgggcatgg cctgagctt 2940  
ctggagagcc tctgcagggg gttgccatc agggccctgt ggctgggtct gctgcagagc 3000  
tccttggcta tcaggagaat cctggacact gtacttgcc tcccagttta caaacacgcc 3060  
cttcatctca agtggccctt taaaaggcct gctgccatgt gagagctgt aacagctcag 3120  
ctctgagtcg gcagactggg gcttcctcct gggccaccag atggaaaggg ggtattgtt 3180  
gcctcactcc tggatgctgc gtttaagga agtgagtgag aaagaatgtg ccaagatacc 3240  
tggctcctgt gaaaccagcc tcaggaggg aactggaga gagaagctgt ggtctcctgc 3300  
tacatgccct gggagctgga agagaaaaac actccctaa acaatcgcaa aatgatgaac 3360  
catcatgggc cactgttctc tttgagggg caggtttagg gtttgcgtt cgcccttgc 3420  
ggctgaagca ctatgtttt gtagctaga cacatcctgc acccaaagg tctctacaaa 3480  
ggcccagatt tgttttaaaa gcactttgac tcttacctgg aggcccgctc tctaagggt 3540  
tcctgcgctc ccacccatc tgtccctgag atgcagagca ggatggaggg tctgcttcta 3600  
gctcagctgt ttctccttga gttgcggag gaattgaatt gaatgggaca gagggcaggt 3660  
gctgtggcca agaagatctc cgagcagcag tgacggggca cttgctgtg tgtccctgg 3720  
gcatgttaac cttctgtgg ggccaaagg ttgcattgtg gatccagctg tgctccagtc 3780  
tgtccctcc tcctccatc tgactgccac gccccggacc agcagcttgg ggaccctcca 3840

gggtactaat ggggctctgt tctgagatgg acaaattcag tgttggaaat acatgttgta	3900
ctatgcacctt cccatgctcc tagggtagg aatagttca aacatgattg gcagacataa	3960
caacggcaaa tactcgact ggggcataagg actccagagt aggaaaaaga caaaagattt	4020
ggcagcctga cacaggcaac ctaccctct ctctccagcc tctttatgaa actgtttgtt	4080
tgcgcagtcct gccctaaggc agaagatgaa ttgaagatgc tgtgcattt tcctaagtcc	4140
ttgagcaatc atggtgtgtga caattgccac aagggatatg aggccagtgc caccagaggg	4200
tggtgccaag tgccacatcc cttccgatcc attccccctct gtatcctcgg agcacccccag	4260
tttgcctttg atgtgtccgc tgtgtatgtt agctgaactt tgatgagcaa aatttcctga	4320
gcgaaacact ccaaagagat aggaaaaactt gccgcctctt ctttttgc ccttaatcaa	4380
actcaaataa gctaaaaaaaaa aatccatgga agatcatgga catgtgaaat gagcattttt	4440
ttctttctt tttttttttt ttttttaac aaagtctgaa ctgaacagaa caagactttt	4500
tcctcataaca tctccaaatt gtttaaactt actttatgag tgtttgc gaaatcgaa	4560
ccaaacagaaa aatgcagtca gatgtcatct tggaaattgggt ttctaaaaga gtaaggcatg	4620
tccctgccccaa gaaacttagg aagcatgaaa taaatcaaattt gtttattttc cttcttattt	4680
aaaatcatgc taatgcaaca gaaatagagg gtttgc gaaatcgaa aatgcatttgc acggcccttt	4740
cttaaaqaca aqcaaggqag attgatatat gtacaatttgc ctctcatgtt ttt	4793

<210> 2

<211> 625

<212> PRT

<213> human organism

<400> 2

Met	Ser	Gln	Glu	Ser	Asp	Asn	Asn	Lys	Arg	Leu	Val	Ala	Leu	Val	Pro
1				5					10					15	

Met	Pro	Ser	Asp	Pro	Pro	Phe	Asn	Thr	Arg	Arg	Ala	Tyr	Thr	Ser	Gl
20								25						30	

Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr  
 35 40 45

Lys Ala Met Met Ile Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu  
50 55 60

Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg Leu Leu  
65 70 75 80

Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Glu Lys Arg Asn  
85 90 95

Cys Leu Gly Thr Ser Glu Ala Gln Ser Asn Leu Ser Gly Gly Glu Asn  
100 105 110

Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Ser Leu Asn Gln  
115 120 125

Asp His Leu Glu Asn Ser Lys Arg Glu Gln Tyr Ser Ile Ser Phe Pro  
130 135 140

Glu Ser Ser Ala Ile Ile Pro Val Ser Gly Ile Thr Val Val Lys Ala  
145 150 155 160

Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr Pro Arg  
165 170 175

Gly Asp Gly Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr Gln Tyr  
180 185 190

Asp Val Pro Ser Leu Ala Thr His Ser Ala Tyr Leu Lys Asp Asp Gln  
195 200 205

Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp Ala Ala  
210 215 220

Thr Glu Lys Phe Arg Ser Ala Ser Val Gly Ala Glu Glu Tyr Met Tyr  
225 230 235 240

Asp Gln Thr Ser Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala Thr Lys  
245 250 255

Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu Asn Lys  
260 265 270

Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn Lys Cys  
275 280 285

Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val Val Phe

290

295

300

Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys Tyr Trp  
 305 310 315 320

His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile Ala Asp  
325 330 335

Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile Ala Tyr  
                  340                   345                   350

Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys Ile Phe  
355 360 365

```
Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
      370          375          380
```

Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr Asn Asn  
 385                   390                   395                   400

Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys Val Phe  
405 410 415

Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Gln Lys Gln  
420 425 430

Ser Ser Asp Gly Lys Leu Ala Ala Ile Pro Leu Gln Lys Lys Ser Asp  
450 455 460

Ile	Thr	Tyr	Phe	Lys	Thr	Met	Pro	Asp	Leu	His	Ser	Gln	Pro	Val	Leu
465					470					475					480

Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly Gln Val  
485 490 495

Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Gly Ser Val Leu Val Lys  
           500                 505                 510

Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Val Pro Ser Lys  
515 520 525

Gln Met Lys Glu Glu Gly Thr Lys Arg Val Leu Leu Tyr Val Arg Lys  
530 535 540

Glu Thr Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro Thr Val  
545 550 555 560

Met Gly Leu Met Glu Ala Ile Ser Glu Lys Tyr Gly Leu Pro Val Glu  
565 570 575

Lys Ile Ala Lys Leu Tyr Lys Ser Lys Lys Gly Ile Leu Val Asn  
580 585 590

Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr Phe Ile  
595 600 605

Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Val Thr Leu Met Glu  
610 615 620

Ile  
625

<210> 3  
<211> 777  
<212> DNA  
<213> human organism

<400> 3	
atgatagcaa tctctgccgt cagcagtgc a ctcctgttct cccttctctg tgaagcaagt	60
accgtcgcc tactcaattc cactgactca tccccgcca a ccaataattt cactgatatt	120
gaaggcagctc tgaaagcaca attagattca gcggatatcc ccaaagccag gcggaagcgc	180
tacatttcgc agaatgacat gatgccatt cttgattatc ataatcaagt tcggggcaaa	240
gtgttcccac cgccagcaaa tatggaatat atggttggg atgaaaatct tgcaaaatcg	300
gcagaggctt gggcggtac ttgcatttg gaccatggac cttcttactt actgagattt	360
ttggggcaaa atctatctgt acgcactgga agatatcgct ctattctcca gttggtcaag	420
ccatggatcg atgaagtgaa agattatgct tttccatatc cccaggattt caaccccaaga	480
tgtccttatga gatgtttgg tcccatgtgc acacattata cgcagatggt ttggggccact	540
tccaatcgga taggatgcgc aattcatgct tgccaaaaca tgaatgttg gggatctgtg	600
tggcgacgtg cagtttactt ggtatgcaac tatgccccaa agggcaattt gattggagaa	660

gcaccatata aagttaggggt accatgttca tcttgcctc caagttatgg gggatcttgt 720  
actgacaatc tgtgtttcc aggagttacg tcaaactacc tgtactggtt taaataa 777

<210> 4  
<211> 777  
<212> DNA  
<213> human organism

<400> 4  
atgatagcaa tctctgccgt cagcagtgc ctccgttct cccttcctg tgaagcaagt 60  
accgtcgcc tactcaattc cactgactca tccccccaa ccaataattt cactgatatt 120  
gaagcagctc tgaaagcaca attagattca gcggatatcc ccaaagccag gcggaaagcgc 180  
tacatttcgc agaatgacat gatgccatt cttgatttac ataatcaagt tcggggcaaa 240  
gtgttcccac cggcagcaaa tatggaatat atggtttggg ataaaaatct tgcaaaatcg 300  
gcagaggctt gggcggtac ttgcatttgg gaccatggac ctcttactt actgagattt 360  
ttggggccaaa atctatctgt acgcactgga agatatcgct ctattctcca gttggtaag 420  
ccatggtatg atgaagtgaa agattatgct tttccatatac cccaggattt caacccaga 480  
tgtcctatga gatgtttgg tcccatgtgc acacattata cgcatgggt ttggccact 540  
tccaatcgg taggatgcgc aattcatact tgccaaaaca tgaatgtttg gggatctgtg 600  
tggcgacgtg cagttactt ggtatgcaac tatgccccaa agggcaattt gattggagaa 660  
gcaccatata aagttaggggt accatgttca tcttgcctc caagttatgg gggatcttgt 720  
actgacaatc tgtgtttcc aggagttacg tcaaactacc tgtactggtt taaataa 777

<210> 5  
<211> 258  
<212> PRT  
<213> human organism

<400> 5  
Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu  
1 5 10 15

Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro  
20 25 30

Pro Thr Asn Asn Phe Thr Asp Ile Glu Ala Ala Leu Lys Ala Gln Leu  
35 40 45

Asp Ser Ala Asp Ile Pro Lys Ala Arg Arg Lys Arg Tyr Ile Ser Gln  
50 55 60

Asn Asp Met Ile Ala Ile Leu Asp Tyr His Asn Gln Val Arg Gly Lys  
65 70 75 80

Val Phe Pro Pro Ala Ala Asn Met Glu Tyr Met Val Trp Asp Glu Asn  
85 90 95

Leu Ala Lys Ser Ala Glu Ala Trp Ala Ala Thr Cys Ile Trp Asp His  
100 105 110

Gly Pro Ser Tyr Leu Leu Arg Phe Leu Gly Gln Asn Leu Ser Val Arg  
115 120 125

Thr Gly Arg Tyr Arg Ser Ile Leu Gln Leu Val Lys Pro Trp Tyr Asp  
130 135 140

Glu Val Lys Asp Tyr Ala Phe Pro Tyr Pro Gln Asp Cys Asn Pro Arg  
145 150 155 160

Cys Pro Met Arg Cys Phe Gly Pro Met Cys Thr His Tyr Thr Gln Met  
165 170 175

Val Trp Ala Thr Ser Asn Arg Ile Gly Cys Ala Ile His Ala Cys Gln  
180 185 190

Asn Met Asn Val Trp Gly Ser Val Trp Arg Arg Ala Val Tyr Leu Val  
195 200 205

Cys Asn Tyr Ala Pro Lys Gly Asn Trp Ile Gly Glu Ala Pro Tyr Lys  
210 215 220

Val Gly Val Pro Cys Ser Ser Cys Pro Pro Ser Tyr Gly Gly Ser Cys  
225 230 235 240

Thr Asp Asn Leu Cys Phe Pro Gly Val Thr Ser Asn Tyr Leu Tyr Trp  
245 250 255

Phe Lys

<210> 6  
<211> 258  
<212> PRT  
<213> human organism

<400> 6

Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu  
1 5 10 15

Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro  
20 25 30

Pro Thr Asn Asn Phe Thr Asp Ile Glu Ala Ala Leu Lys Ala Gln Leu  
35 40 45

Asp Ser Ala Asp Ile Pro Lys Ala Arg Arg Lys Arg Tyr Ile Ser Gln  
50 55 60

Asn Asp Met Ile Ala Ile Leu Asp Tyr His Asn Gln Val Arg Gly Lys  
65 70 75 80

Val Phe Pro Pro Ala Ala Asn Met Glu Tyr Met Val Trp Asp Glu Asn  
85 90 95

Leu Ala Lys Ser Ala Glu Ala Trp Ala Ala Thr Cys Ile Trp Asp His  
100 105 110

Gly Pro Ser Tyr Leu Leu Arg Phe Leu Gly Gln Asn Leu Ser Val Arg  
115 120 125

Thr Gly Arg Tyr Arg Ser Ile Leu Gln Leu Val Lys Pro Trp Tyr Asp  
130 135 140

Glu Val Lys Asp Tyr Ala Phe Pro Tyr Pro Gln Asp Cys Asn Pro Arg  
145 150 155 160

Cys Pro Met Arg Cys Phe Gly Pro Met Cys Thr His Tyr Thr Gln Met  
165 170 175

Val Trp Ala Thr Ser Asn Arg Ile Gly Cys Ala Ile His Thr Cys Gln  
180 185 190

Asn Met Asn Val Trp Gly Ser Val Trp Arg Arg Ala Val Tyr Leu Val  
195 200 205

Cys Asn Tyr Ala Pro Lys Gly Asn Trp Ile Gly Glu Ala Pro Tyr Lys  
210 215 220

Val Gly Val Pro Cys Ser Ser Cys Pro Pro Ser Tyr Gly Gly Ser Cys  
225 230 235 240

Thr Asp Asn Leu Cys Phe Pro Gly Val Thr Ser Asn Tyr Leu Tyr Trp  
245 250 255

Phe Lys

<210> 7  
<211> 2820  
<212> DNA  
<213> human organism

<400> 7  
ggcggttcg cgcccgaaag gctgagagct ggccgtgcgtc gtgcctgtg tgccagacgg 60  
cggagctccg cggccggacc ccgcggcccc gcttgctgc cgactggagt ttggggaaag 120  
aaactctcct gcgc(ccaaga agatttcttc ctccggaaag ggacagcgaa agatgagggt 180  
ggcaggaaga gaaggcgctt tctgtctgcc ggggtcgcaag cgccgagaggg cagtgcctatg 240  
ttcctctcca tccttagtggc gctgtgcctg tggctgcacc tggcgctggg cgtgcgcggc 300  
gcgcctgcg aggccgtgcg catccctatg tgccggcaca tgccctggaa catcacgcgg 360  
atgcccacc acctgtcacca cagcacgcag gagaacgcca tcctggccat cgagcagtac 420  
gaggagctgg tggacgtgaa ctgcagcgcc gtgctgcgtct tttttcttg tgccatgtac 480  
gcgc(ccattt gcaccctgga gttcctgcac gaccctatca agccgtgcaa gtcgggtgtc 540  
caacgcgcgc ggcacgactg cgagccctc atgaagatgt acaaccacag ctggcccgaa 600  
agcctggct ggcacgagct gcctgtctat gaccgtggcg tgtgcatttc gcctgaagcc 660  
atcgtcacgg acctcccgga ggatgttaag tggatagaca tcacaccaga catgtggta 720  
caggaaaggc ctcttgatgt tgactgtaaa cgcctaagcc ccgatcggtg caagtgtaaa 780  
aaggtaagc caactttggc aacgtatctc agcaaaaact acagctatgt tattcatgcc 840  
aaaataaaaag ctgtgcagag gagtggctgc aatgaggtca caacggtggt ggatgtaaaa 900  
gagatcttca agtcctcatc acccatccct cgaactcaag tcccgctcat tacaaattct 960  
tcttgccagt gtccacacat cctgccccat caagatgttc tcattatgtg ttacgagtgg 1020

cgttcaagga ttagttgaaa aatggagaga tcagcttagt 1080  
aaaagatcca tacagtggga agagaggctg caggaacagc ggagaacagt tcaggacaag 1140  
aagaaaacag ccgggcgcac cagtcgtagt aatccccca aaccaaaggg aaagccctcct 1200  
gctccaaac cagccagtcc caagaagaac attaaaacta ggagtgccca gaagagaaca 1260  
aacccgaaaa gagtgtgagc taactagttt ccaaagcgga gacttccgac ttcccttacag 1320  
gatgaggctg ggcattgcct gggacagcct atgttaaggcc atgtgcccct tgccctaaca 1380  
actcaactgca gtgcctttca tagacacatc ttgcagcatt tttcttaagg ctatgcctca 1440  
gttttctt gtaagccatc acaagccata gtggtagggtt tgcccttgg tacagaaggt 1500  
gagttaaagc tggtgaaaaa ggcttattgc attgcattca gagtaacctg tgtgcatact 1560  
ctagaagagt agggaaaata atgcattgtta caattcgacc taatatgtgc attgtaaaat 1620  
aaatgccata tttcaaaacaa aacacgtaat tttttacag tatgttttat tacctttga 1680  
tatctgttgt tgcaatgtta gtgatgttt aaaatgtgat gaaaatataa tgtttttaag 1740  
aaggaacagt agtggaatga atgttaaaag atctttatgt gtttatggtc tgcagaagga 1800  
ttttgtgat gaaagggat ttttgaaaaa attagagaag tagcatatgg aaaattataa 1860  
tgtgttttt taccaatgac ttcaatgttct gtttttagct agaaaacttaa aaacaaaaat 1920  
aataataaag aaaaataaaat aaaaaggaga ggcagacaat gtctggattc ctgttttttg 1980  
gttacctgat ttccatgatc atgatgcctc ttgtcaacac cctcttaagc agcaccagaa 2040  
acagtgagtt tgtctgtacc attaggagtt aggtactaat tagttggcta atgctcaagt 2100  
attttatacc cacaagagag gtatgtcaact catcttactt cccaggacat ccaccctgag 2160  
aataatttga caagctaaaa aatggccttc atgtgagtgc caaattttgt ttttcttcat 2220  
ttaaatattt tctttgccta aatacatgtg agaggagtt aatataaatg tacagagagg 2280  
aaagttgagt tccacctctg aatgagaat tacttgacag ttgggatact ttaatcagaa 2340  
aaaaagaact tatttgcagc attttatcaa caaatttcat aattgtggac aattggaggc 2400  
attttattta aaaaacaatt ttattggcct tttgctaaca cagtaagcat gtattttata 2460  
aggcattcaa taaatgcaca acgccccaaag gaaataaaat cctatctaatt cctactctcc 2520  
actacacaga ggtaatcaact attagtattt tggcatatta ttctccaggt gtttgcttat 2580  
gcacttataa aatgatttga acaaataaaa ctaggaacct gtatacatgt gtttcataac 2640  
ctgcctcctt tgcttggccc tttattgaga taagtttcc tgtcaagaaa gcagaaacca 2700

tctcatttctt aacagctgtg ttatattcca tagtatgcat tactcaacaa actgttgtgc 2760  
tattggatac ttaggtggtt tcttcactga caataactgaa taaacatctc accggaattc 2820

<210> 8  
<211> 346  
<212> PRT  
<213> human organism

<400> 8

Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp Leu His Leu Ala  
1 5 10 15

Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys  
20 25 30

Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His  
35 40 45

Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu  
50 55 60

Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met  
65 70 75 80

Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro  
85 90 95

Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met  
100 105 110

Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu  
115 120 125

Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr  
130 135 140

Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met  
145 150 155 160

Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp  
165 170 175

Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser

180	185	190
Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg		
195	200	205
Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe		
210	215	220
Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn		
225	230	240
Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile		
245	250	255
Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu		
260	265	270
Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu		
275	280	285
Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr		
290	295	300
Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro		
305	310	315
Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser		
325	330	335
Ala Gln Lys Arg Thr Asn Pro Lys Arg Val		
340	345	

<210> 9  
 <211> 381  
 <212> DNA  
 <213> human organism

<400> 9	60
gtccttcctc tccttagccta aggctgtcaa acagagcgcc actggggaggc tgaaaccttt	120
aggccgatgc ttgcttgcaa ggtcaggcaa gctggattct ggtccccacc tttgcagaga	180
gaacagcgat gttgtgcgcc catttctcaag atcaaggacc ggcccatctt actacctcca	240
agagtgttt tctctataat aagaaaacat ctactttgaa acatctactg ggcgagacca	

ggagtatgg ctcagcctgt aattctggaa tttcggagg ccgaggcagg aagattcctt 300  
gagcacagga gttccagacc agcctggca atgttagcaag acgctgtctc tatttataca 360  
ataaaaatttt tttaaaaaag g 381

<210> 10  
<211> 57  
<212> PRT  
<213> human organism

<400> 10

Met Leu Cys Ala His Phe Ser Asp Gln Gly Pro Ala His Leu Thr Thr  
1 5 10 15

Ser Lys Ser Ala Phe Leu Ser Asn Lys Lys Thr Ser Thr Leu Lys His  
20 25 30

Leu Leu Gly Glu Thr Arg Ser Asp Gly Ser Ala Cys Asn Ser Gly Ile  
35 40 45

Ser Gly Gly Arg Gly Arg Lys Ile Pro  
50 55

<210> 11  
<211> 1141  
<212> DNA  
<213> human organism

<400> 11  
tccttgggtt cgggtgaaag cgccctgggg ttcgtggcca tgatccccga gctgctggag 60  
aactgaaggc ggacagtctc ctgcgaaacc aggcaatggc ggagctggag tttgttcaga 120  
tcatcatcat cgtggtggtg atgatggtga tggtgtgggt gatcacgtgc ctgctgagcc 180  
actacaagct gtctgcacgg tccttcatca gccggcacag ccagggcg 240  
atgccctgtc ctcagaagga tgcctgtggc cctcggagag cacagtgtca ggcaacggaa 300  
tcccagagcc gcaggtctac gccccgcctc ggcccaccga ccgcctggcc gtgccgcct 360  
tcgcccagcg ggagcgcttc caccgcttcc agcccaccta tccgtacctg cagcacgaga 420  
tcgacctgccc acccaccatc tcgctgtcag acggggagga gcccccaccc taccaggccc 480  
cctgcaccct ccagcttcgg gaccccgagc agcagctgga actgaaccgg gagtcgggtc 540  
gcccacccccc aaacagaacc atcttcgaca gtgacctgat ggatagtgcc aggctggcg 600  
gcccctgccc ccccagcagt aactcgggca tcagcgccac gtgctacggc agcggcgggc 660

gcatggaggg	gccgcccggcc	acctacagcg	aggcatcg	ccactacccg	gggtcctcct	720
tccagcacca	gcagagcagt	ggccgcgcct	cttgctgga	ggggaccgg	ctccaccaca	780
cacacatcgc	gcccctagag	agcgcagcca	tctggagcaa	agagaaggat	aaacagaaaag	840
gacaccctct	ctagggtccc	caggggggccc	gggctggggc	tgcgttagtg	aaaaggcaga	900
acactccgcg	cttcttagaa	gaggagttag	aggaaggcgg	ggggcgcagc	aacgcacgt	960
gtggccctcc	cctcccacct	ccctgtgtat	aatatattac	atgtatgtc	tggtctgaat	1020
gcacaagcta	agagagctt	caaaaaaaaaa	aagaaaaaaag	aaaaaaaaaa	accacgtttc	1080
tttgtttagc	tgtgtcttga	aggcaaaaga	aaaaaaaaattt	ctacagtaaa	aaaaaaaaaa	1140
a						1141

<210> 12  
 <211> 252  
 <212> PRT  
 <213> human organism

<400> 12

Met	Ala	Glu	Leu	Glu	Phe	Val	Gln	Ile	Ile	Ile	Ile	Val	Val	Val	Met
1								5				10			15

Met	Val	Met	Val	Val	Val	Ile	Thr	Cys	Leu	Leu	Ser	His	Tyr	Lys	Leu
								20				25		30	

Ser	Ala	Arg	Ser	Phe	Ile	Ser	Arg	His	Ser	Gln	Gly	Arg	Arg	Arg	Glu
								35			40		45		

Asp	Ala	Leu	Ser	Ser	Glu	Gly	Cys	Leu	Trp	Pro	Ser	Glu	Ser	Thr	Val
								50			55		60		

Ser	Gly	Asn	Gly	Ile	Pro	Glu	Pro	Gln	Val	Tyr	Ala	Pro	Pro	Arg	Pro
								65			70		75	80	

Thr	Asp	Arg	Leu	Ala	Val	Pro	Pro	Phe	Ala	Gln	Arg	Glu	Arg	Phe	His
								85			90		95		

Arg	Phe	Gln	Pro	Thr	Tyr	Pro	Tyr	Leu	Gln	His	Glu	Ile	Asp	Leu	Pro
								100			105		110		

Pro	Thr	Ile	Ser	Leu	Ser	Asp	Gly	Glu	Glu	Pro	Pro	Pro	Tyr	Gln	Gly
								115			120		125		

Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn  
130 135 140

Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp  
145 150 155 160

Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro Ser Ser Asn  
165 170 175

Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg Met Glu Gly  
180 185 190

Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro Gly Ser Ser  
195 200 205

Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu Glu Gly Thr  
210 215 220

Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala Ala Ile Trp  
225 230 235 240

Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu  
245 250

<210> 13  
<211> 1807  
<212> DNA  
<213> human organism

gcacgaggga agagggtgat ccgaccgggg gaaggtcgct gggcagggcg agttgggaaa	60
gcggcagccc cccggcccccc cgcaaaaaat ttccttcatt tctccacgt cctatctgcc	120
tctcgcttggaa ggccaggcccg tgcatcg aagacaggag gaactggagc ctcattggcc	180
ggcccggggc gccggctcg ggctaaata ggagctccgg gctctggctg ggacccgacc	240
gctggccggcc gcgctcccg tcgttcgttcc gggtgtatggaa aaaccccgac ccggccggcg	300
ccctggggcaa ggccctctgc gcttccttcc tggccactct cggcgccggcc ggccagccctc	360
ttgggggaga gtccatctgt tccggccagag ccccgccaa atacagcatc accttcacgg	420
gcaagtggag ccagacggcc ttccccaaagc agtacccctt gttccggcccc cctgcgcagt	480
ggcttcgtt gctggggggcc gcgcatagct ccgactacag catgtggagg aagaaccagt	540

acgtcagtaa	cgggctgcgc	gactttgcgg	agcgccggcga	ggcctggcg	ctgatgaagg	600
agatcgaggc	ggcgaaaaag	gcgcgcaga	gcgtgcacgc	ggtgtttcg	gcgccccccg	660
tccccagcgg	caccggcag	acgtcggcgg	agctggaggt	gcagcgcagg	cactcgctgg	720
tctcgttgt	ggtgcgcata	gtgcccagcc	ccgactggtt	cgtgggcgtg	gacagcctgg	780
acctgtgcga	cggggaccgt	tggcgaaac	aggcggcgct	ggacctgtac	ccctacgacg	840
ccgggacgga	cagcggcttc	accttctcct	cccccaactt	cgccaccatc	ccgcaggaca	900
cggtgaccga	gataacgtcc	tcctctccca	gccacccggc	caactccttc	tactaccgc	960
ggctgaaggc	cctgcctccc	atgcggagg	tgacactgg	gcccgtgcga	cagagcccc	1020
gggccttcat	ccctcccgcc	ccagtcctgc	ccagcaggga	aatgagatt	gtagacagcg	1080
cctcagttcc	agaaaacgccc	ctggactgcg	aggctccct	gtggcgtcc	tggggactgt	1140
gcggaggcca	ctgtgggagg	ctcgggacca	agagcaggac	tcgctacgtc	cgggtccagc	1200
ccgccaacaa	cgggagcccc	tgcccccggc	tcgaagaaga	ggctgagtgc	gtccctgata	1260
actgcgtcta	agaccagagc	cccgccagccc	ctggggcccc	cggagccatg	gggtgtcg	1320
ggctcctgtg	caggctcatg	ctgcaggcgg	ccgaggcaca	gggggtttcg	cgctgctcct	1380
gaccgcggtg	aggccgcgcc	gaccatctct	gcactgaagg	gccctctgg	ggccggcagc	1440
ggcattggga	aacagcctcc	tcctttccca	accttgccttc	ttagggcc	ccgtgtcccg	1500
tctgctctca	gcctcctcct	cctgcaggat	aaagtcatcc	ccaaggctcc	agctactcta	1560
aattatggtc	tccttataag	ttattgctgc	tccaggagat	tgccttcat	cgtccagg	1620
cctggctccc	acgtgggtgc	agataacctca	gacctgggtgc	tctaggctgt	gctgagccca	1680
ctctcccgag	ggcgcatcca	agcgaaaaac	acttggaaag	tgaataaatg	gggcggtttc	1740
ggaagcgtca	gtgtttccat	gttatggatc	tctctgcgtt	tgaataaaaga	ctatctctgt	1800
					tgctcac	1807

<210> 14  
 <211> 331  
 <212> PRT  
 <213> human organism  
  
 <400> 14

Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys Ala  
 1 5 10 15

Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly Gly Glu  
20 25 30

Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile Thr Phe Thr  
35 40 45

Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg  
50 55 60

Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp  
65 70 75 80

Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp  
85 90 95

Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala  
100 105 110

Ala Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala  
115 120 125

Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg  
130 135 140

Arg His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp  
145 150 155 160

Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp  
165 170 175

Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp  
180 185 190

Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp  
195 200 205

Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser  
210 215 220

Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr  
225 230 235 240

Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro

245

250

255

Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro  
260 265 270

Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu  
275 280 285

Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr  
290 295 300

Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu  
305 310 315 320

Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val  
325 330

<210> 15  
<211> 786  
<212> DNA  
<213> human organism

<400> 15  
cgggcgaagc agcgccggca gcgagatgca gcaccgaggc ttccctcctcc tcaccctcct 60  
cgccctgctg ggcgtcacct ccgcggtcgc caaaaagaaa gataaggta agaaggcg 120  
ccccgggagc gagtgccgtg agtgggcctg ggggcctgc acccccagca gcaaggattg 180  
cggcgtgggt ttccgcgagg gcacctgcgg ggcccagacc cagcgcatcc ggtgcagggt 240  
gccctgcaac tggaaagaagg agtttggagc cgactgcaag tacaagtttgg 300  
tgcgtgtgat gggggcacag gcaccaaagt ccgccaaggc accctgaaga aggccgccta 360  
caatgctcaag tgccaggaga ccatccgcgt caccaagccc tgcaccccca agaccaaagc 420  
aaaggccaaa gccaagaaag ggaaggaaaa ggactagacg ccaagcctgg atgccaagga 480  
gccccctgggt tcacatgggg cctggccacg ccctccctct cccaggcccc agatgtgacc 540  
caccagtgcc ttctgtctgc tcgttagctt taatcaatca tgccctgcct tgtccctctc 600  
actccccagc cccaccccta agtgcggaaa gtggggaggg acaaggatt ctggaaagct 660  
tgagcctccc ccaaagcaat gtgagtccta gagcccgctt ttgttcttcc ccacaattcc 720  
attactaaga aacacatcaa ataaactgac ttttccccca caataaaagc tcttctttt 780  
taatat 786

<210> 16  
<211> 143  
<212> PRT  
<213> human organism

<400> 16

Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala  
1 5 10 15

Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly  
20 25 30

Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser  
35 40 45

Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln  
50 55 60

Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe  
65 70 75 80

Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly  
85 90 95

Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr  
100 105 110

Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro  
115 120 125

Lys Thr Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp  
130 135 140

<210> 17  
<211> 1617  
<212> DNA  
<213> human organism

<400> 17 atggtagaac tagtgatctc acccagcctc actgtaaaca gcgattgtct ggataaactg 60

aagtttaacc gtgctgacgc tgctgtgtgg actctgagtg acagacaagg catcaccaaa 120

tcggccccc tgagagtgtc ccagctttc tccagatctt gcccacgtgt cctccccgc 180

cagccttcca cagccatggc agcctacggc cagacgcagt acagtgcggg gatccagcag 240

gctacccct atacagctta cccaccccca gcacaaggcct atggaatccc ttcctacagc 300  
atcaagacag aagacagctt gaaccattcc cctggccaga gtggattcct cagctatggc 360  
tccagcttca gcaccctcacc cactggacag agccccataca cctaccagat gcacggcaca 420  
acagggttct atcaaggagg aaatggactg ggcaacgcag ccggtttcgg gagtgtgcac 480  
caggactatc cttcctaccc cggttcccc cagagccagt acccccaagta ttacggctca 540  
tcctacaacc ctccctacgt cccggccagc agcatctgcc cttcgccccct ctccacgtcc 600  
acctacgtcc tccaggaggc atctcacaac gtccccaaacc agagttccga gtcacttgct 660  
ggtaataca acacacacaa tggaccccttcc acaccagcga aagagggaga cacagacagg 720  
ccgcaccggg cctccgacgg gaagctccga ggccggtcta agaggagcag tgaccctgtcc 780  
ccggcagggg acaatgagat tgagcgtgt ttcgtgtggg acttggatga gacaataatt 840  
atttttcaact ccttactcac gggacattt gcatccagat acgggaagga caccacgacg 900  
tccgtgcgcac ttggccttat gatggaagag atgatcttca accttgcaga tacacatctg 960  
ttcttcaatg acctggagga ttgtgaccag atccacgttg atgacgtctc atcagatgac 1020  
aatggccaag atttaagcac atacaacttc tccgctgacg gcttccacag ttccggccca 1080  
ggagccaaacc tgtgcctggg ctctggcggt cacggcggcg tggactggat gaggaagctg 1140  
gccttccgct accggcgggt gaaggagatg tacaataacct acaagaacaa cgttggtggg 1200  
ttgataggca ctccccaaaag ggagacctgg ctacagctcc gagctgagct ggaagctctc 1260  
acagacctct ggctgaccca ctccctgaag gcaactaaacc tcatacaactc ccggcccaac 1320  
tgtgtcaatg tgctggtcac caccactcaa ctaattcctg ccctggccaa agtcctgcta 1380  
tatggcctgg ggtctgtgtt tcctatttag aacatctaca gtgcaaccaa gacagggaaag 1440  
gagagctgct tcgagaggat aatgcagaga ttccggcagaa aagctgtcta cgtgggtgatc 1500  
ggtgatggtg tggaagagga gcaaggagcg aaaaaggcaca acatgccttt ctggcggata 1560  
tcctqccacq caqacctggg ggcactgagg cacggccctgg aactggagta tttatag 1617

<210> 18  
<211> 538  
<212> PRT  
<213> human organism

<400> 18

Met Val Glu Leu Val Ile Ser Pro Ser Leu Thr Val Asn Ser Asp Cys  
1 5 10 15

Leu Asp Lys Leu Lys Phe Asn Arg Ala Asp Ala Ala Val Trp Thr Leu  
20 25 30

Ser Asp Arg Gln Gly Ile Thr Lys Ser Ala Pro Leu Arg Val Ser Gln  
35 40 45

Leu Phe Ser Arg Ser Cys Pro Arg Val Leu Pro Arg Gln Pro Ser Thr  
50 55 60

Ala Met Ala Ala Tyr Gly Gln Thr Gln Tyr Ser Ala Gly Ile Gln Gln  
65 70 75 80

Ala Thr Pro Tyr Thr Ala Tyr Pro Pro Pro Ala Gln Ala Tyr Gly Ile  
85 90 95

Pro Ser Tyr Ser Ile Lys Thr Glu Asp Ser Leu Asn His Ser Pro Gly  
100 105 110

Gln Ser Gly Phe Leu Ser Tyr Gly Ser Ser Phe Ser Thr Ser Pro Thr  
115 120 125

Gly Gln Ser Pro Tyr Thr Tyr Gln Met His Gly Thr Thr Gly Phe Tyr  
130 135 140

Gln Gly Gly Asn Gly Leu Gly Asn Ala Ala Gly Phe Gly Ser Val His  
145 150 155 160

Gln Asp Tyr Pro Ser Tyr Pro Gly Phe Pro Gln Ser Gln Tyr Pro Gln  
165 170 175

Tyr Tyr Gly Ser Ser Tyr Asn Pro Pro Tyr Val Pro Ala Ser Ser Ile  
180 185 190

Cys Pro Ser Pro Leu Ser Thr Ser Thr Tyr Val Leu Gln Glu Ala Ser  
195 200 205

His Asn Val Pro Asn Gln Ser Ser Glu Ser Leu Ala Gly Glu Tyr Asn  
210 215 220

Thr His Asn Gly Pro Ser Thr Pro Ala Lys Glu Gly Asp Thr Asp Arg  
225 230 235 240

Pro His Arg Ala Ser Asp Gly Lys Leu Arg Gly Arg Ser Lys Arg Ser  
245 250 255

Ser Asp Pro Ser Pro Ala Gly Asp Asn Glu Ile Glu Arg Val Phe Val  
260 265 270

Trp Asp Leu Asp Glu Thr Ile Ile Phe His Ser Leu Leu Thr Gly  
275 280 285

Thr Phe Ala Ser Arg Tyr Gly Lys Asp Thr Thr Thr Ser Val Arg Ile  
290 295 300

Gly Leu Met Met Glu Glu Met Ile Phe Asn Leu Ala Asp Thr His Leu  
305 310 315 320

Phe Phe Asn Asp Leu Glu Asp Cys Asp Gln Ile His Val Asp Asp Val  
325 330 335

Ser Ser Asp Asp Asn Gly Gln Asp Leu Ser Thr Tyr Asn Phe Ser Ala  
340 345 350

Asp Gly Phe His Ser Ser Ala Pro Gly Ala Asn Leu Cys Leu Gly Ser  
355 360 365

Gly Val His Gly Val Asp Trp Met Arg Lys Leu Ala Phe Arg Tyr  
370 375 380

Arg Arg Val Lys Glu Met Tyr Asn Thr Tyr Lys Asn Asn Val Gly Gly  
385 390 395 400

Leu Ile Gly Thr Pro Lys Arg Glu Thr Trp Leu Gln Leu Arg Ala Glu  
405 410 415

Leu Glu Ala Leu Thr Asp Leu Trp Leu Thr His Ser Leu Lys Ala Leu  
420 425 430

Asn Leu Ile Asn Ser Arg Pro Asn Cys Val Asn Val Leu Val Thr Thr  
435 440 445

Thr Gln Leu Ile Pro Ala Leu Ala Lys Val Leu Leu Tyr Gly Leu Gly  
450 455 460

Ser Val Phe Pro Ile Glu Asn Ile Tyr Ser Ala Thr Lys Thr Gly Lys  
465 470 475 480

Glu Ser Cys Phe Glu Arg Ile Met Gln Arg Phe Gly Arg Lys Ala Val  
485 490 495

Tyr Val Val Ile Gly Asp Gly Val Glu Glu Gln Gly Ala Lys Lys  
500 505 510

His Asn Met Pro Phe Trp Arg Ile Ser Cys His Ala Asp Leu Glu Ala  
515 520 525

Leu Arg His Ala Leu Glu Leu Glu Tyr Leu  
530 535

<210> 19  
<211> 2261  
<212> DNA  
<213> human organism

<400> 19  
ccgcggttcc ggctgctccg gcgaggcgac cttgggtcg gctgcggg cgaggtggc 60  
aggtaggtgg cggacggcc cgggttctcc ggcaagcgca ggcggcggag tcccccacgg 120  
ccccgaagc gcccccgca ccccccgcct ccagcggtga ggcgggggag tgaggagatg 180  
ccgaccaga gggacagcag caccatgtcc cacacggtcg caggcggcgg cagcgggac 240  
cattccacc agtccgggt gaaagcctac taccgcgggg atatcatgt aacacattt 300  
gaaccttcca tctccttga gggccttgc aatgaggttc gagacatgtg ttctttgac 360  
aacgaacagc tcttaccat gaaatggata gatgaggaag gagacccgtg tacagtatca 420  
tctcagttgg agttagaaga agcctttaga ctatgtgac taaacaagga ttctgaactc 480  
ttgattcatg tttcccttg tgtaccagaa cgtcctggga tgccttgtcc aggagaagat 540  
aaatccatct accgttagagg tgcacgcccgc tggagaaagc ttatgtgc caatggccac 600  
actttccaag ccaagcgaaa caacaggcgt gctcaatgtg ccatctgcac agaccgaaa 660  
tggggacttg gacgccaagg atataagtgc atcaactgca aactcttggt tcataagaag 720  
tgccataaac tcgtcacaat tgaatgtggg cggcattctt tgccacagga accagtgtatg 780  
cccatggatc agtcatccat gcattctgac catgcacaga cagtaattcc atataatcct 840  
tcaagtcatg agagtttggaa tcaagttggt gaagaaaaag aggcaatgaa caccaggaa 900  
agtggcaaag cttcatccag tctaggtctt caggatggatggatggc ggtaatagga 960

agaggaagtt atgccaaagt actgttggtt cgattaaaaa aaacagatcg tatTTATGCA	1020
atgaaaagttg tgaaaaaaga gcttgttaat gatgatgagg atattgattg ggtacagaca	1080
gagaagcatg tgTTTgagca ggcattcaat catcCTTCC ttgttggct gcattCTTGC	1140
tttcagacag aaagcagatt gttttgtt atagagatg taaatggagg agacctaATG	1200
tttcatatgc agcgacAAAG AAAACTTCCT gaagaACATG CCAGATTTC ctctgcAGAA	1260
atcAGTCTAG cattAAATTt TCTTCATGAG CGAGGGATAA TTtATAGAGA TTGAAACTG	1320
gacaATGTAT tactggactc tgaaggccac attAAACTCA CTGACTACGG CATGTGTAAG	1380
gaaggattac ggccaggaga tacaaccAGC acTTTCTGTG GTACTCCTAA TTACATTGCT	1440
cctgaaATTt taagaggaga agattatggT ttcAGTGTG ACTGGTGGC TCTTGGAGTG	1500
ctcatgtttg agatgatggc aggaaggTCT ccATTGATA TTGTTGGAG CTCCGATAAC	1560
cctgaccaga acacagagGA ttATCTCTC caAGTTATTt TGAAAACA ATTcGCATA	1620
ccacGTTCTC TGTCTGAAA AGCTGCAAGT GTTCTGAAGA GTTTCTTAA TAAGGACCT	1680
aAGGAACGAT TGGGTTGTCA TCCTCAAACA GGATTGCTG ATATTCAAGG ACACCGTTC	1740
ttCCGAAATG TTGATTGGGAT TATGATGGAG CAAAAACAGG TGGTACCTCC CTTAAACCA	1800
aatATTTCTG GGGAAATTGG TTTGGACAAC TTTGATTCTC AGTTTACTAA TGAACCTGTC	1860
cAGCTCACTC CAGATGACGA TGACATTGTG AGGAAGATTG ATCAGTCTGA ATTGAAAGGT	1920
TTTGAGTATA TCAATCCTCT TTTGATGTCT GCAGAAGAAAT GTGTCTGATC CTCATTTTC	1980
AACCATGTAT TCTACTCATG TTGCCATTa ATGCAATGGAT AAACATTGCTG CAAGCCTGGA	2040
TACAATTAAC CATTATAT TTGCCACCTA CAAAAAAACA CCCAATATCT TCTCTGTAG	2100
ACTATATGAA TCAATTATTA CATCTGTttT ACTATGAAAA AAAAATTAAT ACTACTAGCT	2160
TCCAGACAAAT CATGTCAAAA TTAGTTGAA CTGGTTTTC AGTTTTAAA AGGCCTACAG	2220
ATGAGTAATG AAGTTACCTT TTTGTttaa AAAAaaaaaaa G	2261

<210> 20  
 <211> 587  
 <212> PRT  
 <213> human organism  
  
 <400> 20

Met Ser His Thr Val Ala Gly Gly Ser Gly Asp His Ser His Gln  
 1 5 10 15

Val Arg Val Lys Ala Tyr Tyr Arg Gly Asp Ile Met Ile Thr His Phe  
20 25 30

Glu Pro Ser Ile Ser Phe Glu Gly Leu Cys Asn Glu Val Arg Asp Met  
35 40 45

Cys Ser Phe Asp Asn Glu Gln Leu Phe Thr Met Lys Trp Ile Asp Glu  
50 55 60

Glu Gly Asp Pro Cys Thr Val Ser Ser Gln Leu Glu Leu Glu Ala  
65 70 75 80

Phe Arg Leu Tyr Glu Leu Asn Lys Asp Ser Glu Leu Leu Ile His Val  
85 90 95

Phe Pro Cys Val Pro Glu Arg Pro Gly Met Pro Cys Pro Gly Glu Asp  
100 105 110

Lys Ser Ile Tyr Arg Arg Gly Ala Arg Arg Trp Arg Lys Leu Tyr Cys  
115 120 125

Ala Asn Gly His Thr Phe Gln Ala Lys Arg Phe Asn Arg Arg Ala His  
130 135 140

Cys Ala Ile Cys Thr Asp Arg Ile Trp Gly Leu Gly Arg Gln Gly Tyr  
145 150 155 160

Lys Cys Ile Asn Cys Lys Leu Leu Val His Lys Lys Cys His Lys Leu  
165 170 175

Val Thr Ile Glu Cys Gly Arg His Ser Leu Pro Gln Glu Pro Val Met  
180 185 190

Pro Met Asp Gln Ser Ser Met His Ser Asp His Ala Gln Thr Val Ile  
195 200 205

Pro Tyr Asn Pro Ser Ser His Glu Ser Leu Asp Gln Val Gly Glu Glu  
210 215 220

Lys Glu Ala Met Asn Thr Arg Glu Ser Gly Lys Ala Ser Ser Ser Leu  
225 230 235 240

Gly Leu Gln Asp Phe Asp Leu Leu Arg Val Ile Gly Arg Gly Ser Tyr

245	250	255
Ala Lys Val Leu Leu Val Arg Leu Lys Lys Thr Asp Arg Ile Tyr Ala		
260	265	270
Met Lys Val Val Lys Lys Glu Leu Val Asn Asp Asp Glu Asp Ile Asp		
275	280	285
Trp Val Gln Thr Glu Lys His Val Phe Glu Gln Ala Ser Asn His Pro		
290	295	300
Phe Leu Val Gly Leu His Ser Cys Phe Gln Thr Glu Ser Arg Leu Phe		
305	310	315
Phe Val Ile Glu Tyr Val Asn Gly Gly Asp Leu Met Phe His Met Gln		
325	330	335
Arg Gln Arg Lys Leu Pro Glu Glu His Ala Arg Phe Tyr Ser Ala Glu		
340	345	350
Ile Ser Leu Ala Leu Asn Tyr Leu His Glu Arg Gly Ile Ile Tyr Arg		
355	360	365
Asp Leu Lys Leu Asp Asn Val Leu Leu Asp Ser Glu Gly His Ile Lys		
370	375	380
Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly Leu Arg Pro Gly Asp Thr		
385	390	395
400		
Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Ile Leu		
405	410	415
Arg Gly Glu Asp Tyr Gly Phe Ser Val Asp Trp Trp Ala Leu Gly Val		
420	425	430
Leu Met Phe Glu Met Met Ala Gly Arg Ser Pro Phe Asp Ile Val Gly		
435	440	445
Ser Ser Asp Asn Pro Asp Gln Asn Thr Glu Asp Tyr Leu Phe Gln Val		
450	455	460
Ile Leu Glu Lys Gln Ile Arg Ile Pro Arg Ser Leu Ser Val Lys Ala		
465	470	475
480		

Ala Ser Val Leu Lys Ser Phe Leu Asn Lys Asp Pro Lys Glu Arg Leu  
485 490 495

Gly Cys His Pro Gln Thr Gly Phe Ala Asp Ile Gln Gly His Pro Phe  
500 505 510

Phe Arg Asn Val Asp Trp Asp Met Met Glu Gln Lys Gln Val Val Pro  
515 520 525

Pro Phe Lys Pro Asn Ile Ser Gly Glu Phe Gly Leu Asp Asn Phe Asp  
530 535 540

Ser Gln Phe Thr Asn Glu Pro Val Gln Leu Thr Pro Asp Asp Asp Asp  
545 550 555 560

Ile Val Arg Lys Ile Asp Gln Ser Glu Phe Glu Gly Phe Glu Tyr Ile  
565 570 575

Asn Pro Leu Leu Met Ser Ala Glu Glu Cys Val  
580 585

<210> 21

<211> 5011

<212> DNA

<213> human organism

<400> 21  
ccaggcggcg ttgcggcccc ggccccggct ccctgcgccc cccggccgc cgccggccgc 60  
gccggccgc cccggccag cgctagcgcc agcagccggg cccgatcacc cgccggccgg 120  
tgcccgccgc cccggccgc agcaaccggg cccgatcacc cgccggccgg tgcccgccgc 180  
ccggccgc accggcatgg cgctccgggg ctgtgcagc gccgatggct cccggccgc 240  
ctgggactgg aatgtcacgt ggaataccag caacccgac ttcaccaagt gttttcagaa 300  
cacggtcctc gtgtgggtgc ctgtttta cctctggcc tgttccct tctacttcct 360  
ctatcttcc cgacatgacc gaggctacat tcagatgaca cctctcaaca aaaccaaaaac 420  
tgccctggaa ttttgctgt ggatcgctcg ctggcagac ctcttctact ctttctggaa 480  
aagaagtcgg ggcattttcc tggcccccagt gtttctggtc agcccaactc tcttgggcat 540  
caccacgctg cttgctaccc tttaattca gctggagagg aggaagggag ttcagtcctc 600  
aggatcatg ctcactttct ggctggtagc cctagtgtgt gccctagcca tcctgagatc 660

caaaaattatg acagccttaa aagaggatgc ccaggtggac ctgtttcgta acatcaactt 720  
ctacgtctac tttccctct tactcattca gctcgcttg tcctgtttct cagatcgctc 780  
accctgttc tcggaaacca tccacgaccc taatccctgc ccagagtcca gcgcttcctt 840  
cctgtcgagg atcaccttct ggtggatcac agggttgatt gtccggggct accgccagcc 900  
cctggagggc agtgcacctct ggtccttaaa caaggaggac acgtcgaaac aagtcgtgcc 960  
tgtttggta aagaactgga agaaggaatg cgccaaagact aggaagcagc cggtgaaggt 1020  
tgtgtactcc tccaaggatc ctgcccagcc gaaagagagt tccaagggtgg atgcgaatga 1080  
ggaggtggag gctttgatcg tcaagtcggcc acagaaggag tggaacccct ctctgtttaa 1140  
ggtgttatac aagacctttg ggccctactt cctcatgagc ttcttcttca aggccatcca 1200  
cgacctgatg atgtttccg ggccgcagat cttaaagtttgc ctcataatgt tcgtgaatga 1260  
cacgaaggcc ccagactggc agggctactt ctacaccgtg ctgctgtttg tcactgcctg 1320  
cctgcagacc ctcgtgtgc accagtaattt ccacatctgc ttctgtcgtg gcatgaggat 1380  
caagaccgct gtcattgggg ctgtctatcg gaaggccctg gtgatcacca attcagccag 1440  
aaaatcctcc acggtcgggg agattgtcaa cctcatgtct gtggacgctc agaggtcat 1500  
ggacttggcc acgtacatta acatgatctg gtcagccccctt ctgcaagtca tccttgctct 1560  
ctacccctcg tggctgaatc tggcccttc cgtcctggct ggagtggcggt tgatggcct 1620  
catggtgcggc gtcaatgtcg tgatggcgat gaagaccaag acgtatcagg tggccacat 1680  
gaagagcaaa gacaatcgga tcaagctgat gaacgaaatt ctcaatggga tcaaagtgt 1740  
aaagctttat gcctgggagc tggcattcaa ggacaaggatg ctggccatca ggcaggagga 1800  
gctgaaggatg ctgaagaagt ctgcctaccc gtcagccgtg ggcacccatca cctgggtctg 1860  
cacgcctttt ctggtgccct tggtcacatt tgccgtctac gtgaccatttgc acgagaacaa 1920  
catcctggat gcccagacag cttcgtgtc tttggcccttgc ttcaacatcc tccggttcc 1980  
cctgaacatt ctccccatgg tcatcagcag catcgatcgagc gcgagtgtct ccctcaaacg 2040  
cctgaggatc tttctctccc atgaggagct ggaacctgac agcatcgagc gacggcctgt 2100  
caaagacggc gggggcacga acagcatcac cgtgaggaat gccacattca cctggccag 2160  
gagcgaccct cccacactga atggcatcac cttctccatc cccgaaggatg ctttgggtggc 2220  
cgtggtgggc caggtgggct gcgaaagtc gtcctgtc tcagccctct tggctgagat 2280  
ggacaaagtg gaggggcacg tggctatcaa gggctccgtg gcctatgtgc cacagcaggc 2340

ctggattcag aatgattctc tccgagaaaa catcctttt ggatgtcagc tggaggaacc 2400  
atattacagg tccgtgatac aggctgtgc cctcctccca gacctggaaa tcctgcccag 2460  
tggggatcg acagagattg gcgagaaggg cgtaacctg tctggggcc agaagcagcg 2520  
cgtgagcctg gcccggccg tgtactccaa cgctgacatt tacctttcg atgatcccct 2580  
ctcagcagtg gatccccatg tggaaaaaca catcttgaa aatgtgattg gccccaaagg 2640  
gatgctgaag aacaagacgc ggatcttgtt cacgcacagc atgagctact tgccgcaggt 2700  
ggacgtcatac atcgcatga gtggcggcaa gatctctgag atgggctcct accaggagct 2760  
gctggctcga gacggcgccct tcgctgagtt cctgcgtacc tatgccagca cagagcagga 2820  
gcaggatgca gaggagaacg gggtcacggg cgtcagcggt ccagggaaagg aagcaaagca 2880  
aatggagaat ggcatgctgg tgacggacag tgcagggaaag caactgcaga gacagctcag 2940  
cagctcctcc tcctatagtg gggacatcag caggcaccac aacagcacccg cagaactgca 3000  
gaaagctgag gccaaagaagg aggagacctg gaagctgatg gaggctgaca aggccgcagac 3060  
aggcaggc aagcttccg tgtactgggaa ctacatgaag gccatcgacat tcttcatttc 3120  
cttcctcagc atcttccttt tcatgtgtaa ccatgtgtcc gcgctggctt ccaactattg 3180  
gctcagcctc tggactgatg accccatcgt caacggact caggagcaca cgaaagtccg 3240  
gctgagcgcc tatggagccc tggcatttc acaagggatc gccgtgtttg gctactccat 3300  
ggccgtgtcc atcggggggta tcttggcttc ccgctgtctg cacgtggacc tgctgcacag 3360  
catcctgcgg tcacccatga gcttcttga gcgacccccc agtgggaacc tggtaaccg 3420  
cttctccaag gagctggaca cagtggactc catgatcccg gaggtcatca agatgttcat 3480  
gggctccctg ttcaacgtca ttggcgtctg catcgatccat ctgctggcca cgcccatcgc 3540  
cgccatcatc atcccgcccc ttggcctcat ctacttcttc gtccagaggt tctacgtggc 3600  
ttcctcccg cagctgaagc gcctcgagtc ggtcagccgc tccccggctt attccattt 3660  
caacgagacc ttgctggggg tcagcgatcat tcgagccttc gaggagcagg agcgcttcat 3720  
ccaccagagt gacctgaagg tggacgagaa ccagaaggcc tattacccca gcatcggttc 3780  
caacaggtgg ctggccgtgc ggctggagtg tgtggcaac tgcatcgatcc tggctgtgc 3840  
cctgtttgcg gtatctcca ggcacagccct cagtgcgtgc ttggggcc tctcagtgatc 3900  
ttactcattt caggtcacca cgtacttgaa ctggctggtt cggatgtcat ctgaaatgg 3960  
aaccaacatc gtggccgtgg agaggctcaa ggagtattca gagactgaga aggaggcgcc 4020  
ctggcaaatc caggagacag ctccgcccag cagctggccc caggtggccg gagtgaaatt 4080

ccggaactac	tgcctgcgct	accgagagga	cctggacttc	gttctcaggc	acatcaatgt	4140
cacgatcaat	gggggagaaaa	aggtcggcat	cgtggggcg	acgggagctg	ggaagtgc	4200
cctgaccctg	ggcttatttc	ggatcaacga	gtctgccgaa	ggagagatca	tcatcgatgg	4260
catcaacatc	gccaagatcg	gcctgcacga	cctccgcttc	aagatcacca	tcatccccca	4320
ggaccctgtt	ttgtttcgg	gttccctccg	aatgaacctg	gaccattca	gccagtactc	4380
ggatgaagaa	gtctggacgt	ccctggagct	ggcccacctg	aaggacttcg	tgtcagccct	4440
tcctgacaag	ctagaccatg	aatgtgcaga	aggcggggag	aacctcagtg	tcgggcagcg	4500
ccagcttgtg	tgcctagccc	ggccctgct	gaggaagacg	aagatccttg	tgttggatga	4560
ggccacggca	gccgtggacc	tggaaacgga	cgacctcatc	cagtccacca	tccggacaca	4620
gttcgaggac	tgcacccgtcc	tcaccatcgc	ccacccggctc	aacaccatca	tggactacac	4680
aagggtgatc	gtcttggaca	aaggagaaat	ccaggagtac	ggcgccccat	cggacccct	4740
gcagcagaga	ggtctttct	acagcatggc	caaagacgcc	ggcttggtgt	gagccccaga	4800
gctggcatat	ctggtcagaa	ctgcagggcc	tatatgccag	cgcccaggga	ggagtcagta	4860
ccctggtaa	accaaggctc	ccacactgaa	acaaaacat	aaaaacccaaa	cccagacaac	4920
caaaacatat	tcaaaggcgc	agccaccgccc	atccggtccc	ctgcctggaa	ctggctgtga	4980
agacccagga	gagacagaga	tgcgaaccac	c			5011

<210> 22  
 <211> 1531  
 <212> PRT  
 <213> human organism

<400> 22

Met	Ala	Leu	Arg	Gly	Phe	Cys	Ser	Ala	Asp	Gly	Ser	Asp	Pro	Leu	Trp
1								10						15	

Asp	Trp	Asn	Val	Thr	Trp	Asn	Thr	Ser	Asn	Pro	Asp	Phe	Thr	Lys	Cys
								25					30		

Phe	Gln	Asn	Thr	Val	Leu	Val	Trp	Val	Pro	Cys	Phe	Tyr	Leu	Trp	Ala
								40					45		

Cys	Phe	Pro	Phe	Tyr	Phe	Leu	Tyr	Leu	Ser	Arg	His	Asp	Arg	Gly	Tyr
								55				60			

Ile Gln Met Thr Pro Leu Asn Lys Thr Lys Thr Ala Leu Gly Phe Leu  
65 70 75 80

Leu Trp Ile Val Cys Trp Ala Asp Leu Phe Tyr Ser Phe Trp Glu Arg  
85 90 95

Ser Arg Gly Ile Phe Leu Ala Pro Val Phe Leu Val Ser Pro Thr Leu  
100 105 110

Leu Gly Ile Thr Thr Leu Leu Ala Thr Phe Leu Ile Gln Leu Glu Arg  
115 120 125

Arg Lys Gly Val Gln Ser Ser Gly Ile Met Leu Thr Phe Trp Leu Val  
130 135 140

Ala Leu Val Cys Ala Leu Ala Ile Leu Arg Ser Lys Ile Met Thr Ala  
145 150 155 160

Leu Lys Glu Asp Ala Gln Val Asp Leu Phe Arg Asp Ile Thr Phe Tyr  
165 170 175

Val Tyr Phe Ser Leu Leu Ile Gln Leu Val Leu Ser Cys Phe Ser  
180 185 190

Asp Arg Ser Pro Leu Phe Ser Glu Thr Ile His Asp Pro Asn Pro Cys  
195 200 205

Pro Glu Ser Ser Ala Ser Phe Leu Ser Arg Ile Thr Phe Trp Trp Ile  
210 215 220

Thr Gly Leu Ile Val Arg Gly Tyr Arg Gln Pro Leu Glu Gly Ser Asp  
225 230 235 240

Leu Trp Ser Leu Asn Lys Glu Asp Thr Ser Glu Gln Val Val Pro Val  
245 250 255

Leu Val Lys Asn Trp Lys Lys Glu Cys Ala Lys Thr Arg Lys Gln Pro  
260 265 270

Val Lys Val Val Tyr Ser Ser Lys Asp Pro Ala Gln Pro Lys Glu Ser  
275 280 285

Ser Lys Val Asp Ala Asn Glu Glu Val Glu Ala Leu Ile Val Lys Ser

290

295

300

Pro Gln Lys Glu Trp Asn Pro Ser Leu Phe Lys Val Leu Tyr Lys Thr  
305 310 315 320

Phe Gly Pro Tyr Phe Leu Met Ser Phe Phe Lys Ala Ile His Asp  
325 330 335

Leu Met Met Phe Ser Gly Pro Gln Ile Leu Lys Leu Leu Ile Lys Phe  
340 345 350

Val Asn Asp Thr Lys Ala Pro Asp Trp Gln Gly Tyr Phe Tyr Thr Val  
355 360 365

Leu Leu Phe Val Thr Ala Cys Leu Gln Thr Leu Val Leu His Gln Tyr  
370 375 380

Phe His Ile Cys Phe Val Ser Gly Met Arg Ile Lys Thr Ala Val Ile  
385 390 395 400

Gly Ala Val Tyr Arg Lys Ala Leu Val Ile Thr Asn Ser Ala Arg Lys  
405 410 415

Ser Ser Thr Val Gly Glu Ile Val Asn Leu Met Ser Val Asp Ala Gln  
420 425 430

Arg Phe Met Asp Leu Ala Thr Tyr Ile Asn Met Ile Trp Ser Ala Pro  
435 440 445

Leu Gln Val Ile Leu Ala Leu Tyr Leu Leu Trp Leu Asn Leu Gly Pro  
450 455 460

Ser Val Leu Ala Gly Val Ala Val Met Val Leu Met Val Pro Val Asn  
465 470 475 480

Ala Val Met Ala Met Lys Thr Lys Thr Tyr Gln Val Ala His Met Lys  
485 490 495

Ser Lys Asp Asn Arg Ile Lys Leu Met Asn Glu Ile Leu Asn Gly Ile  
500 505 510

Lys Val Leu Lys Leu Tyr Ala Trp Glu Leu Ala Phe Lys Asp Lys Val  
515 520 525

Leu Ala Ile Arg Gln Glu Glu Leu Lys Val Leu Lys Lys Ser Ala Tyr  
530 535 540

Leu Ser Ala Val Gly Thr Phe Thr Trp Val Cys Thr Pro Phe Leu Val  
545 550 555 560

Ala Leu Cys Thr Phe Ala Val Tyr Val Thr Ile Asp Glu Asn Asn Ile  
565 570 575

Leu Asp Ala Gln Thr Ala Phe Val Ser Leu Ala Leu Phe Asn Ile Leu  
580 585 590

Arg Phe Pro Leu Asn Ile Leu Pro Met Val Ile Ser Ser Ile Val Gln  
595 600 605

Ala Ser Val Ser Leu Lys Arg Leu Arg Ile Phe Leu Ser His Glu Glu  
610 615 620

Leu Glu Pro Asp Ser Ile Glu Arg Arg Pro Val Lys Asp Gly Gly Gly  
625 630 635 640

Thr Asn Ser Ile Thr Val Arg Asn Ala Thr Phe Thr Trp Ala Arg Ser  
645 650 655

Asp Pro Pro Thr Leu Asn Gly Ile Thr Phe Ser Ile Pro Glu Gly Ala  
660 665 670

Leu Val Ala Val Val Gly Gln Val Gly Cys Gly Lys Ser Ser Leu Leu  
675 680 685

Ser Ala Leu Leu Ala Glu Met Asp Lys Val Glu Gly His Val Ala Ile  
690 695 700

Lys Gly Ser Val Ala Tyr Val Pro Gln Gln Ala Trp Ile Gln Asn Asp  
705 710 715 720

Ser Leu Arg Glu Asn Ile Leu Phe Gly Cys Gln Leu Glu Glu Pro Tyr  
725 730 735

Tyr Arg Ser Val Ile Gln Ala Cys Ala Leu Leu Pro Asp Leu Glu Ile  
740 745 750

Leu Pro Ser Gly Asp Arg Thr Glu Ile Gly Glu Lys Gly Val Asn Leu  
755 760 765

Ser Gly Gly Gln Lys Gln Arg Val Ser Leu Ala Arg Ala Val Tyr Ser  
770 775 780

Asn Ala Asp Ile Tyr Leu Phe Asp Asp Pro Leu Ser Ala Val Asp Ala  
785 790 795 800

His Val Gly Lys His Ile Phe Glu Asn Val Ile Gly Pro Lys Gly Met  
805 810 815

Leu Lys Asn Lys Thr Arg Ile Leu Val Thr His Ser Met Ser Tyr Leu  
820 825 830

Pro Gln Val Asp Val Ile Ile Val Met Ser Gly Gly Lys Ile Ser Glu  
835 840 845

Met Gly Ser Tyr Gln Glu Leu Leu Ala Arg Asp Gly Ala Phe Ala Glu  
850 855 860

Phe Leu Arg Thr Tyr Ala Ser Thr Glu Gln Glu Gln Asp Ala Glu Glu  
865 870 875 880

Asn Gly Val Thr Gly Val Ser Gly Pro Gly Lys Glu Ala Lys Gln Met  
885 890 895

Glu Asn Gly Met Leu Val Thr Asp Ser Ala Gly Lys Gln Leu Gln Arg  
900 905 910

Gln Leu Ser Ser Ser Ser Tyr Ser Gly Asp Ile Ser Arg His His  
915 920 925

Asn Ser Thr Ala Glu Leu Gln Lys Ala Glu Ala Lys Lys Glu Glu Thr  
930 935 940

Trp Lys Leu Met Glu Ala Asp Lys Ala Gln Thr Gly Gln Val Lys Leu  
945 950 955 960

Ser Val Tyr Trp Asp Tyr Met Lys Ala Ile Gly Leu Phe Ile Ser Phe  
965 970 975

Leu Ser Ile Phe Leu Phe Met Cys Asn His Val Ser Ala Leu Ala Ser  
980 985 990

Asn Tyr Trp Leu Ser Leu Trp Thr Asp Asp Pro Ile Val Asn Gly Thr  
995 1000 1005

Gln Glu His Thr Lys Val Arg Leu Ser Val Tyr Gly Ala Leu Gly  
1010 1015 1020

Ile Ser Gln Gly Ile Ala Val Phe Gly Tyr Ser Met Ala Val Ser  
1025 1030 1035

Ile Gly Gly Ile Leu Ala Ser Arg Cys Leu His Val Asp Leu Leu  
1040 1045 1050

His Ser Ile Leu Arg Ser Pro Met Ser Phe Phe Glu Arg Thr Pro  
1055 1060 1065

Ser Gly Asn Leu Val Asn Arg Phe Ser Lys Glu Leu Asp Thr Val  
1070 1075 1080

Asp Ser Met Ile Pro Glu Val Ile Lys Met Phe Met Gly Ser Leu  
1085 1090 1095

Phe Asn Val Ile Gly Ala Cys Ile Val Ile Leu Leu Ala Thr Pro  
1100 1105 1110

Ile Ala Ala Ile Ile Ile Pro Pro Leu Gly Leu Ile Tyr Phe Phe  
1115 1120 1125

Val Gln Arg Phe Tyr Val Ala Ser Ser Arg Gln Leu Lys Arg Leu  
1130 1135 1140

Glu Ser Val Ser Arg Ser Pro Val Tyr Ser His Phe Asn Glu Thr  
1145 1150 1155

Leu Leu Gly Val Ser Val Ile Arg Ala Phe Glu Glu Gln Glu Arg  
1160 1165 1170

Phe Ile His Gln Ser Asp Leu Lys Val Asp Glu Asn Gln Lys Ala  
1175 1180 1185

Tyr Tyr Pro Ser Ile Val Ala Asn Arg Trp Leu Ala Val Arg Leu

1190

1195

1200

Glu Cys Val Gly Asn Cys Ile Val Leu Phe Ala Ala Leu Phe Ala  
1205 1210 1215

Val Ile Ser Arg His Ser Leu Ser Ala Gly Leu Val Gly Leu Ser  
1220 1225 1230

Val Ser Tyr Ser Leu Gln Val Thr Thr Tyr Leu Asn Trp Leu Val  
1235 1240 1245

Arg Met Ser Ser Glu Met Glu Thr Asn Ile Val Ala Val Glu Arg  
1250 1255 1260

Leu Lys Glu Tyr Ser Glu Thr Glu Lys Glu Ala Pro Trp Gln Ile  
1265 1270 1275

Gln Glu Thr Ala Pro Pro Ser Ser Trp Pro Gln Val Gly Arg Val  
1280 1285 1290

Glu Phe Arg Asn Tyr Cys Leu Arg Tyr Arg Glu Asp Leu Asp Phe  
1295 1300 1305

Val Leu Arg His Ile Asn Val Thr Ile Asn Gly Gly Glu Lys Val  
1310 1315 1320

Gly Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Thr Leu  
1325 1330 1335

Gly Leu Phe Arg Ile Asn Glu Ser Ala Glu Gly Glu Ile Ile Ile  
1340 1345 1350

Asp Gly Ile Asn Ile Ala Lys Ile Gly Leu His Asp Leu Arg Phe  
1355 1360 1365

Lys Ile Thr Ile Ile Pro Gln Asp Pro Val Leu Phe Ser Gly Ser  
1370 1375 1380

Leu Arg Met Asn Leu Asp Pro Phe Ser Gln Tyr Ser Asp Glu Glu  
1385 1390 1395

Val Trp Thr Ser Leu Glu Leu Ala His Leu Lys Asp Phe Val Ser  
1400 1405 1410

Ala Leu Pro Asp Lys Leu Asp His Glu Cys Ala Glu Gly Gly Glu  
1415 1420 1425

Asn Leu Ser Val Gly Gln Arg Gln Leu Val Cys Leu Ala Arg Ala  
1430 1435 1440

Leu Leu Arg Lys Thr Lys Ile Leu Val Leu Asp Glu Ala Thr Ala  
1445 1450 1455

Ala Val Asp Leu Glu Thr Asp Asp Leu Ile Gln Ser Thr Ile Arg  
1460 1465 1470

Thr Gln Phe Glu Asp Cys Thr Val Leu Thr Ile Ala His Arg Leu  
1475 1480 1485

Asn Thr Ile Met Asp Tyr Thr Arg Val Ile Val Leu Asp Lys Gly  
1490 1495 1500

Glu Ile Gln Glu Tyr Gly Ala Pro Ser Asp Leu Leu Gln Gln Arg  
1505 1510 1515

Gly Leu Phe Tyr Ser Met Ala Lys Asp Ala Gly Leu Val  
1520 1525 1530

<210> 23

<211> 1290

<212> DNA

<213> human organism

<400> 23

atggccggct ctggcgctg gaagcgctc aaatctatgc taaggaagga tcatgcggccg 60

ctgttttaa atgacaccag cgccttgac ttctcgatg aggccccggc cgaggggctt 120

tctcggttca acaaacttcg agttgtggtg gccgatgacg gttccgaagc cccggaaagg 180

cctgttaacg gggcgcaccc gaccctccag gccgacgatg attccttact ggaccaagac 240

ttacctttga ccaacagtca gctgagttt aaggtggact cctgtgacaa ctgcagcaaa 300

cagagagaga tactgaagca gagaaagggtg aaagccaggt tgaccattgc tgccgttctg 360

tacttgctt tcatgattgg agaacttgta ggtggataca ttgcaaatacg ccttagcaatc 420

atgacagatg cacttcatat gttaactgac ctaagcgcca tcatactcac cctgcttgct 480

ttgtggctat catcaaaaatc accaaccaaa agattcacct ttggatttca tcgcttagag 540

gttttgcag ctatgattag tggctgttg gtgtatatac ttatgggatt cctcttatat 600  
gaagctgtgc aaagaactat ccatatgaac tatgaaataa atggagatat aatgctcatc 660  
accgcagctg ttggagttgc agttaatgta ataatgggt ttctgttcaa ccagtctgg 720  
caccgtcact cccattccca ctccctgcct tcaaattccc ctaccagagg ttctgggtgt 780  
gaacgtaacc atgggcagga tagcctggca gtgagagctg catttgtaca tgctttggga 840  
gatttggtag agagtgttgg tgtgctaata gctgcataca tcatacgatt caagccagaa 900  
tacaagattt ctgatcccat ctgtacatac gtatttcatac tacttgtggc tttacaaca 960  
tttcgaatca tatgggatac agtagttata atactagaag gtgtgccaag ccatttgaat 1020  
gttagactata tcaaagaagc cttgatgaaa atagaagatg tatattcagt cgaagattta 1080  
aatatctggc ctctcacttc aggaaaatct actgccatag ttcacataca gctaattcct 1140  
ggaagttcat ctaaatggga ggaagtacag tccaaagcaa accattttatt attgaacaca 1200  
tttggcatgt atagatgtac tattcagctt cagagttaca ggcaagaagt ggacagaact 1260  
tgtgcaaatt gtcagagttc tagtccctga 1290

<210> 24

<211> 429

<212> PRT

<213> human organism

<400> 24

Met Ala Gly Ser Gly Ala Trp Lys Arg Leu Lys Ser Met Leu Arg Lys  
1 5 10 15

Asp Asp Ala Pro Leu Phe Leu Asn Asp Thr Ser Ala Phe Asp Phe Ser  
20 25 30

Asp Glu Ala Gly Asp Glu Gly Leu Ser Arg Phe Asn Lys Leu Arg Val  
35 40 45

Val Val Ala Asp Asp Gly Ser Glu Ala Pro Glu Arg Pro Val Asn Gly  
50 55 60

Ala His Pro Thr Leu Gln Ala Asp Asp Ser Leu Leu Asp Gln Asp  
65 70 75 80

Leu Pro Leu Thr Asn Ser Gln Leu Ser Leu Lys Val Asp Ser Cys Asp  
85 90 95

Asn Cys Ser Lys Gln Arg Glu Ile Leu Lys Gln Arg Lys Val Lys Ala  
100 105 110

Arg Leu Thr Ile Ala Ala Val Leu Tyr Leu Leu Phe Met Ile Gly Glu  
115 120 125

Leu Val Gly Gly Tyr Ile Ala Asn Ser Leu Ala Ile Met Thr Asp Ala  
130 135 140

Leu His Met Leu Thr Asp Leu Ser Ala Ile Ile Leu Thr Leu Leu Ala  
145 150 155 160

Leu Trp Leu Ser Ser Lys Ser Pro Thr Lys Arg Phe Thr Phe Gly Phe  
165 170 175

His Arg Leu Glu Val Leu Ser Ala Met Ile Ser Val Leu Leu Val Tyr  
180 185 190

Ile Leu Met Gly Phe Leu Leu Tyr Glu Ala Val Gln Arg Thr Ile His  
195 200 205

Met Asn Tyr Glu Ile Asn Gly Asp Ile Met Leu Ile Thr Ala Ala Val  
210 215 220

Gly Val Ala Val Asn Val Ile Met Gly Phe Leu Leu Asn Gln Ser Gly  
225 230 235 240

His Arg His Ser His Ser His Ser Leu Pro Ser Asn Ser Pro Thr Arg  
245 250 255

Gly Ser Gly Cys Glu Arg Asn His Gly Gln Asp Ser Leu Ala Val Arg  
260 265 270

Ala Ala Phe Val His Ala Leu Gly Asp Leu Val Gln Ser Val Gly Val  
275 280 285

Leu Ile Ala Ala Tyr Ile Ile Arg Phe Lys Pro Glu Tyr Lys Ile Ala  
290 295 300

Asp Pro Ile Cys Thr Tyr Val Phe Ser Leu Leu Val Ala Phe Thr Thr  
305 310 315 320

Phe Arg Ile Ile Trp Asp Thr Val Val Ile Ile Leu Glu Gly Val Pro  
325 330 335

Ser His Leu Asn Val Asp Tyr Ile Lys Glu Ala Leu Met Lys Ile Glu  
340 345 350

Asp Val Tyr Ser Val Glu Asp Leu Asn Ile Trp Ser Leu Thr Ser Gly  
355 360 365

Lys Ser Thr Ala Ile Val His Ile Gln Leu Ile Pro Gly Ser Ser Ser  
370 375 380

Lys Trp Glu Glu Val Gln Ser Lys Ala Asn His Leu Leu Leu Asn Thr  
385 390 395 400

Phe Gly Met Tyr Arg Cys Thr Ile Gln Leu Gln Ser Tyr Arg Gln Glu  
405 410 415

Val Asp Arg Thr Cys Ala Asn Cys Gln Ser Ser Ser Pro  
420 425

<210> 25

<211> 4526

<212> DNA

<213> human organism

<400> 25  
gccgagtcgg tggcggtcgc aggctggag ggagaagtgc tacgccttg cagggtggcg 60  
aagtggttcc aggctacccg gctagtctgg cacggccccg tcttctgcct cctccctccgt 120  
cgcgtggcgg cgggaactgt tgccgcgcg gcctcggaa cggcccaggt ccccgccccgc 180  
aggccccggg cagataacat agatcatcag tagaaaactt cttgaagttg ttcaagaaaa 240  
atttgaaaagt agcaaaatag aaaataaaga attaacagca gatacagagg acagcatgga 300  
agtgttgtct tagaaacag aacacagcag tgaaaaaaca gacaaaatcc gctcagatac 360  
aactgcagct gataatgtt tccggcttca atgtcttag agttggatc tctttgtca 420  
taatgtgcat ttttacatg ccaacagtaa actcttacc agaactgagt cctcagaaaat 480  
attttagtac attgcaacca ggtcttgaag aactgaatga ggctgttaga cctctgcagg 540  
actatggaat ttcagttgcc aaggtaatt gtgtcaaaga agaaatatca agatactgt 600  
gaaaagaaaa ggatttgatg aaagcatatt tattcaaggg caacatattg ctcagagaat 660

tccctactga caccttgttt gatgtaatg ccattgtcgc ccatgttctc tttgctctc 720  
tttttagtga agtcaaataat attaccaacc tggaagacct tcagaacata gaaaatgctc 780  
tgaaaggaaa agcaaataatt atattctcat atgtaagagc cattggaaata ccagagcaca 840  
gagcagtcat ggaagccggt tttgtgtatg ggactacata ccaatttgc ttaaccacag 900  
aaattgcct tttggaaagt attggctctg aggatgtgga atatgcacat ctctacttt 960  
ttcattgtaa actagtctg gacttgaccc agcaatgtag aagaacacta atggaacagc 1020  
cattgactac actgaacatt cacctgttta ttaagacaat gaaagcacct ctgttactg 1080  
aagttgctga agatcctcaa caagttcaa ctgtccatct ccaactggc ttaccactgg 1140  
tttttattgt tagccaacag gctacttatg aagctgatag aagaactgca gaatgggttg 1200  
cttggcgtct tctggaaaaa gcaggagttc tactcttgc aaggactct ttggaagtga 1260  
acattcctca agatgcta at gtggtcttca aaagagcaga agagggagtt ccagtggaaat 1320  
tttggtatt acatgatgtt gattaataa tatctcatgt ggaaaataat atgcacattg 1380  
agaaaataca agaagatgaa gacaatgaca tggaaggtcc agatataat gttcaggatg 1440  
atgaagtggc agaaactgtt ttcagagata ggaagagaaa attaccttg gaacttacag 1500  
tggaactaac agaagaaaca tttaatgcaa cagtgtatggc ttctgacagc atagtactct 1560  
tctatgctgg ttggcaagca gtatccatgg cattttgc atcctatatt gatgtggcag 1620  
ttaaactgaa aggcacatct actatgcttc ttactagaat aaactgtgca gattggctcg 1680  
atgtatgtac taagcaaaat gttactgaat ttcttatcat aaagatgtac aagaaaggcg 1740  
agaacccagt atcttatgct ggaatgttag gaaccaaaga tctcctaaaa tttatccagc 1800  
tcaacaggat ttcatatcca gtgaatataa catcgatcca agaagcagaa gaatattaa 1860  
gtgggaaatt atataaagac ctcatcttgc attctagtgt gtcagtattg ggactattta 1920  
gtccaaccat gaaaacagca aaagaagatt ttagtgaagc aggaaactac ctaaaaggat 1980  
atgttattcac tggaatttat tctgaagaag atgtttgc actgtcaacc aaatatgctg 2040  
caagtcttcc agccctgctg cttgccagac acacagaagg caaaatagag agcatcccac 2100  
tagctagcac acatgcacaa gacatagttc aaataataac agatgcacta ctggaaatgt 2160  
ttccggaaat cactgtggaa aatcttccca gttatttcag acttcagaaa ccattattga 2220  
ttttgttcag tgatggcact gtaaatcctc aatataaaaa agcaatattg acactggtaa 2280  
agcagaaaata cttggattca ttactccat gctggtaaa tctaaagaat actccagtg 2340  
ggagaggaat cttgcggca tattttgatc ctctgcctcc cttcctctt cttgtttgg 2400

tgaatctgca ttcaggtggc caagtatttgc catttccttc agaccaggct ataattgaag 2460  
aaaaccttgtt attgtggctg aagaaatttag aagcaggact agaaaatcat atcacaattt 2520  
tacctgctca agaatggaaa cctcctcttc cagcttatga ttttctaagt atgatagatg 2580  
ccgcaacatc tcaacgtggc actaggaaag ttcccaggat tatgaaagaa acagatgtgc 2640  
aggagaatga taaggaacaa catgaagata aatcgccagt cagaaaagaa ccgattgaaa 2700  
ctctgagaat aaagcattgg aatagaagta attgggtttaa agaagcagaa aaatcattta 2760  
gacgtgataa agagtttagga tgctcaaaag tgaactaatt ttataggcgt gtggttcca 2820  
aaattttttt ggcatgatag acttaattta ttcccttaaa gaataatatt aaatcatttc 2880  
aagtttgcag actagtgcua tccaaatagaa ttataatata agtcacatatt ttatattaa 2940  
attttctagt aactacatta aacaaagtaa aagttagcag ggcaaaataa ttttgatatt 3000  
acttttcacc cagtagtata cccaaaatag cgaaatata tag aatttattaa tgagatattt 3060  
tacatccctt tttgtaccaa gtcttctaaa tgcagtagat attttatact tactgcattt 3120  
cttacttccg agtagccata ttcaaggatgt tcattgccac atgtggcctg tgactactgt 3180  
atggacagt tcaagtacta aaaaaacta gcataattaa cttagttcta gccatgattt 3240  
ctatttggat taaaattaaa ctctaattcac agttaactcc acagtgcattt catgcagctg 3300  
acagttatat ttgttttatt ggagtcatga tattaaaatc agcgtttgtc aacctcaggg 3360  
gatatttagc aattgtcggg agacattttt gatgtcatga cttagggcagt tattgacattt 3420  
tagtgagtag aggccatgga tcctgctaaa taacctgcattt tggacagcgc cccacaacaa 3480  
agaattatcc tgccccaaat ggttagtcgtg ccaaggctga gtaaccttgtt gttaaaagta 3540  
acctgtggca gacttagttt ccagaatttc ctgggtctgc tcacgtatca tgtttggaaa 3600  
aattttggctt attaaagata tgtatttagat ggtcttattcc tgattattac ctggataacaa 3660  
cttgatcttt tctaattttt tcagaaatgt atgggataac cctagaagag gactcagaat 3720  
gatatttata tttaagtgaa gtcttaaaac ctcctttat ttctacaatgt tatatggcta 3780  
aatttcagat tgaacaggga ttccatcattc tgccatctcc tcattggaaag agaggctccc 3840  
tcattgtggaa cgtctctgaa atctaccctt gcaagttca gacaaatcag ttgtatctccc 3900  
tgagccacac ggcctcatcc tggatggag ggaaagatta gccaagatgtt taattttcat 3960  
tccaaatcac ttagctgtta gactgatctg tttgttagcag ttgtttgtctt cattttgtct 4020  
ctqtcattt tttgagacat ttgttgagaa tattctattt ggtgtctac tggattttc 4080

ttttaatat ctacttgata tcttgttctt taaattttct tcacatatgg tttgcctgat 4140  
acaactgatt ttataactg aaatttaagg aatctaacag ctaaaaactca gtaagtgcatt 4200  
mtatttcctt ataacataga cccgttgcta ctctcagcac cctctcctca atttttttc 4260  
ctgttagcatg tgatgcctga ttaaactcat tttcatttgc ttttatttct aatatggaa 4320  
caatgagagt gaactctaaa tataggttgt agtaataaaa catcatttgc ctaattatta 4380  
gaaaatgcta attaagtacc agcacataga aacatgaaat tgcttagtca ttgtacctt 4440  
gtcagcaatt ttgacagtca ttaatgtttg tcataattt aaataaaagtg tctgggttc 4500  
agaataacctt caaaaaaaaaaaaaa 4526

<210> 26  
<211> 807  
<212> PRT  
<213> human organism

<400> 26

Met Phe Ser Gly Phe Asn Val Phe Arg Val Gly Ile Ser Phe Val Ile  
1 5 10 15

Met Cys Ile Phe Tyr Met Pro Thr Val Asn Ser Leu Pro Glu Leu Ser  
20 25 30

Pro Gln Lys Tyr Phe Ser Thr Leu Gln Pro Gly Leu Glu Glu Leu Asn  
35 40 45

Glu Ala Val Arg Pro Leu Gln Asp Tyr Gly Ile Ser Val Ala Lys Val  
50 55 60

Asn Cys Val Lys Glu Glu Ile Ser Arg Tyr Cys Gly Lys Glu Lys Asp  
65 70 75 80

Leu Met Lys Ala Tyr Leu Phe Lys Gly Asn Ile Leu Leu Arg Glu Phe  
85 90 95

Pro Thr Asp Thr Leu Phe Asp Val Asn Ala Ile Val Ala His Val Leu  
100 105 110

Phe Ala Leu Leu Phe Ser Glu Val Lys Tyr Ile Thr Asn Leu Glu Asp  
115 120 125

Leu Gln Asn Ile Glu Asn Ala Leu Lys Gly Lys Ala Asn Ile Ile Phe

130                    135                    140  
Ser Tyr Val Arg Ala Ile Gly Ile Pro Glu His Arg Ala Val Met Glu  
145                    150                    155                    160  
  
Ala Gly Phe Val Tyr Gly Thr Thr Tyr Gln Phe Val Leu Thr Thr Glu  
165                    170                    175  
  
Ile Ala Leu Leu Glu Ser Ile Gly Ser Glu Asp Val Glu Tyr Ala His  
180                    185                    190  
  
Leu Tyr Phe Phe His Cys Lys Leu Val Leu Asp Leu Thr Gln Gln Cys  
195                    200                    205  
  
Arg Arg Thr Leu Met Glu Gln Pro Leu Thr Thr Leu Asn Ile His Leu  
210                    215                    220  
  
Phe Ile Lys Thr Met Lys Ala Pro Leu Leu Thr Glu Val Ala Glu Asp  
225                    230                    235                    240  
  
Pro Gln Gln Val Ser Thr Val His Leu Gln Leu Gly Leu Pro Leu Val  
245                    250                    255  
  
Phe Ile Val Ser Gln Gln Ala Thr Tyr Glu Ala Asp Arg Arg Thr Ala  
260                    265                    270  
  
Glu Trp Val Ala Trp Arg Leu Leu Gly Lys Ala Gly Val Leu Leu Leu  
275                    280                    285  
  
Leu Arg Asp Ser Leu Glu Val Asn Ile Pro Gln Asp Ala Asn Val Val  
290                    295                    300  
  
Phe Lys Arg Ala Glu Glu Gly Val Pro Val Glu Phe Leu Val Leu His  
305                    310                    315                    320  
  
Asp Val Asp Leu Ile Ile Ser His Val Glu Asn Asn Met His Ile Glu  
325                    330                    335  
  
Glu Ile Gln Glu Asp Glu Asp Asn Asp Met Glu Gly Pro Asp Ile Asp  
340                    345                    350  
  
Val Gln Asp Asp Glu Val Ala Glu Thr Val Phe Arg Asp Arg Lys Arg  
355                    360                    365

Lys Leu Pro Leu Glu Leu Thr Val Glu Leu Thr Glu Glu Thr Phe Asn  
370 375 380

Ala Thr Val Met Ala Ser Asp Ser Ile Val Leu Phe Tyr Ala Gly Trp  
385 390 395 400

Gln Ala Val Ser Met Ala Phe Leu Gln Ser Tyr Ile Asp Val Ala Val  
405 410 415

Lys Leu Lys Gly Thr Ser Thr Met Leu Leu Thr Arg Ile Asn Cys Ala  
420 425 430

Asp Trp Ser Asp Val Cys Thr Lys Gln Asn Val Thr Glu Phe Pro Ile  
435 440 445

Ile Lys Met Tyr Lys Lys Gly Glu Asn Pro Val Ser Tyr Ala Gly Met  
450 455 460

Leu Gly Thr Lys Asp Leu Leu Lys Phe Ile Gln Leu Asn Arg Ile Ser  
465 470 475 480

Tyr Pro Val Asn Ile Thr Ser Ile Gln Glu Ala Glu Glu Tyr Leu Ser  
485 490 495

Gly Glu Leu Tyr Lys Asp Leu Ile Leu Tyr Ser Ser Val Ser Val Leu  
500 505 510

Gly Leu Phe Ser Pro Thr Met Lys Thr Ala Lys Glu Asp Phe Ser Glu  
515 520 525

Ala Gly Asn Tyr Leu Lys Gly Tyr Val Ile Thr Gly Ile Tyr Ser Glu  
530 535 540

Glu Asp Val Leu Leu Ser Thr Lys Tyr Ala Ala Ser Leu Pro Ala  
545 550 555 560

Leu Leu Leu Ala Arg His Thr Glu Gly Lys Ile Glu Ser Ile Pro Leu  
565 570 575

Ala Ser Thr His Ala Gln Asp Ile Val Gln Ile Ile Thr Asp Ala Leu  
580 585 590

Leu Glu Met Phe Pro Glu Ile Thr Val Glu Asn Leu Pro Ser Tyr Phe  
595 600 605

Arg Leu Gln Lys Pro Leu Leu Ile Leu Phe Ser Asp Gly Thr Val Asn  
610 615 620

Pro Gln Tyr Lys Lys Ala Ile Leu Thr Leu Val Lys Gln Lys Tyr Leu  
625 630 635 640

Asp Ser Phe Thr Pro Cys Trp Leu Asn Leu Lys Asn Thr Pro Val Gly  
645 650 655

Arg Gly Ile Leu Arg Ala Tyr Phe Asp Pro Leu Pro Pro Leu Pro Leu  
660 665 670

Leu Val Leu Val Asn Leu His Ser Gly Gly Gln Val Phe Ala Phe Pro  
675 680 685

Ser Asp Gln Ala Ile Ile Glu Glu Asn Leu Val Leu Trp Leu Lys Lys  
690 695 700

Leu Glu Ala Gly Leu Glu Asn His Ile Thr Ile Leu Pro Ala Gln Glu  
705 710 715 720

Trp Lys Pro Pro Leu Pro Ala Tyr Asp Phe Leu Ser Met Ile Asp Ala  
725 730 735

Ala Thr Ser Gln Arg Gly Thr Arg Lys Val Pro Lys Cys Met Lys Glu  
740 745 750

Thr Asp Val Gln Glu Asn Asp Lys Glu Gln His Glu Asp Lys Ser Ala  
755 760 765

Val Arg Lys Glu Pro Ile Glu Thr Leu Arg Ile Lys His Trp Asn Arg  
770 775 780

Ser Asn Trp Phe Lys Glu Ala Glu Lys Ser Phe Arg Arg Asp Lys Glu  
785 790 795 800

Leu Gly Cys Ser Lys Val Asn  
805

<210> 27  
<211> 1195  
<212> DNA  
<213> human organism

<400> 27  
ccgagactca cggtaagct aaggcgaaga gtgggtggct gaagccatac tattttatag 60  
aattaatgga aagcagaaaa gacatcacaa accaagaaga actttggaaa atgaaggcta 120  
ggagaaattt agaagaagac gattattgc ataaggacac gggagagacc agcatgctaa 180  
aaagacctgt gctttgcat ttgcacccaaa cagcccatgc tgatgaattt gactgccctt 240  
cagaacttca gcacacacag gaactcttc cacagtggca cttgccaatt aaaatagctg 300  
ctattatagc atctctgact tttcttaca ctcttcttag ggaagtaatt caccctttag 360  
caactccccca tcaacaatat ttttataaaaa ttccaatcct ggtcatcaac aaagtcttgc 420  
caatggtttc catcaactctc ttggcattgg tttacctgcc aggtgtgata gcagcaattt 480  
tccaacttca taatggAACc aagtataaga agtttccaca ttgggtggat aagtggatgt 540  
taacaagaaaa gcagtttggg cttctcagtt tctttttgc tgtactgcat gcaatttata 600  
gtctgtctta cccaatgagg cgatcctaca gatacaagtt gctaaactgg gcataatcaac 660  
aggtccaaca aaataaaagaa gatgcctgga ttgagcatga tgtttggaga atggagattt 720  
atgtgtctct gggatttgtg ggattggcaa tactggctct gttggctgtg acatctattc 780  
catctgttag tgactcttg acatggagag aatttcacta tattcagagc aagctaggaa 840  
ttgtttccct tctactgggc acaatacacg cattgatttt tgccctggaaat aagtggatag 900  
atataaaaca atttgtatgg tatacacaccc caacttttat gatagctgtt ttccttccaa 960  
ttgttgtcct gatatttaaa agcatactat tcctgccatg cttgaggaag aagatactga 1020  
agatttagaca tgggtggaa gacgtcacca aaattaacaa aactgagata tgttcccagt 1080  
tgtagaatta ctgtttcacac acattttgt tcaatattga tatattttat caccaacatt 1140  
tcaaqttqt atttgttaat aaaatgatta ttcaaggaaa aaaaaaaaaaaa aaaaaa 1195

<210>	28
<211>	339
<212>	PRT
<213>	human organism

<400> 28

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met  
1 5 10 15

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr  
20 25 30

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln  
35 40 45

Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr  
50 55 60

Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile  
65 70 75 80

Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His  
85 90 95

Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu  
100 105 110

Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu  
115 120 125

Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly  
130 135 140

Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr  
145 150 155 160

Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala  
165 170 175

Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu  
180 185 190

Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp  
195 200 205

Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile  
210 215 220

Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser  
225 230 235 240

Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys  
245 250 255

Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe  
260 265 270

Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro  
275 280 285

Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe  
290 295 300

Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile  
305 310 315 320

Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys  
325 330 335

Ser Gln Leu

<210> 29  
<211> 2541  
<212> DNA  
<213> human organism

<400> 29  
atgagttcct gcaacttcac acatgccacc tttgtgctta ttggtatccc aggatttagag 60  
aaagccatt tctgggttgg cttccccctc ctttccatgt atgttagtggc aatgtttgga 120  
aactgcatcg tggtcttcat cgtaaggacg gaacgcagcc tgcacgctcc gatgtacctc 180  
tttctctgca tgcttgagc cattgacctg gccttatcca catccaccat gcctaagatc 240  
cttgccctt tctgggttga ttcccagagat attagcttg aggcctgtct tacccagatg 300  
ttctttattc atgcctctc agccattgaa tccaccatcc tgctggccat ggcctttgac 360  
cgttatgtgg ccatctgcca cccactgcgc catgctgcag tgctcaacaa tacagtaaca 420  
gcccagattt gcatcggtgc tgggtccgc ggatccctct ttttttccc actgcctctg 480  
ctgatcaagc ggctggcctt ctgccactcc aatgtcctct cgcactccta ttgtgtccac 540  
caggatgtaa tgaagttggc ctatgcagac actttgccca atgtggtata tggtcttact 600  
gccattctgc tggtcatggg cgtggacgta atgttcatct ctttgtccctt ttttctgata 660  
atacgaacgg ttctgcaact gccttccaag tcagagcggg ccaaggcctt tggaacctgt 720

gtgtcacaca ttggtgtggt actcgcccttc tatgtgccac ttattggcct ctcagtgta 780  
caccgcttg gaaacagcct tcatacccatt gtgcgtgttgc tcatgggtga catctacactg 840  
ctgctgcctc ctgtcatcaa tcccatcatc tatggtgcca aaaccaaaca gatcagaaca 900  
cggtgctgg ctatgttcaa gatcagctgt gacaaggact tgcaggctgt gggaggcaag 960  
tgacccttaa cactacactt ctccttatct ttattggctt gataaacata attatttcta 1020  
acactagctt atttccagtt gcccataagc acatcagtac ttttctctgg ctggaaatagt 1080  
aaactaaagt atggtacatc tacctaaagg actattatgt ggaataatac atactaatga 1140  
agtattacat gattaaaga ctacaataaa accaaacatg ctataacat taagaaaaac 1200  
aataaagata catgattgaa accaagttga aaaatagcat atgccttggg ggaaatgtgc 1260  
tcaaattact aatgatttag tgggtccct actttctctc tctttttct ttctttttt 1320  
tttattatgg ttagctgtca catacaactt ttttttttt tgagatgggg tctcgctctg 1380  
tcaccaggct ggagtgcagt ggcgcgatct cggctcaactg caacctccac atcccatgtt 1440  
gaagtaattc ttctgcctca gcctcccgag tagctggac tagaggaacg tgccaccatg 1500  
actggctaattttctgttatttttagtaga gacagagttt caccatgttgc cccaggatgg 1560  
tctcgatctc ctgacccctgt gatccaccccg cctcagcctc ccaaagtgtt gggattacag 1620  
gtgtgaacca ctgtgcccgg cctgtgtaca actttttaaa taggaaatat gatacgctcg 1680  
catgggtggtgc tgcacctata gcctccactg cctggaaagc tgaggtggga gaatcgcttg 1740  
agtccaggag tttgaggtta cagtgtatcca cgatcgtaacc actacactcc agcctggca 1800  
acagagcaag accctgtctc aaagcataaa atgaaataac atatcaaatg aaacagggaa 1860  
aatgaagctg acaatttatg gaagccaggg cttgtcacag tctctactgt tattatgcat 1920  
tacctggaa tttatataag cccttaataa tartgccaat gaacatctca tgtgtgctca 1980  
caatgttctg gcactattat aagtgttca caggtttat gtgttcttcg taactttatg 2040  
gagtaggtac catttgttgc tctttattat aagtgagaga aatgaagttt atattatcaa 2100  
ggggactaaa gtcacacggc ttgtggcac tggccaaaga tttaaaatta aatttgtatgg 2160  
ttgaatacag ttacttaatg accatgttattt attgcttcct gtgtacatc tgccatttat 2220  
ttcctcagct gtacaaatcc tctgtttct ctctgttaca cactaacatc aatggctttg 2280  
tacttgtat gagagataac cttggccctag ttgtggcaaa cacatgcaga ataatcctgt 2340  
tttacagctg ccttcgtga tcttattgtc tgctttttc cagattcagg gagaatgttgc 2400

ttgtctat tt gtc tttaca ttc cttgat catgtttca tttttaatg tgctctgtac 2460  
ctgtcaaaaa ttttgaatgt acaccacatg ctattgtctg aacttgagta taagataaaa 2520  
taaaatttta ttttaaattt t 2541

<210> 30  
<211> 320  
<212> PRT  
<213> human organism

<400> 30

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile  
1 5 10 15

Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser  
20 25 30

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val  
35 40 45

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
50 55 60

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile  
65 70 75 80

Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys  
85 90 95

Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr  
100 105 110

Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro  
115 120 125

Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly  
130 135 140

Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu  
145 150 155 160

Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser  
165 170 175

Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu  
180 185 190

Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val  
195 200 205

Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val  
210 215 220

Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys  
225 230 235 240

Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly  
245 250 255

Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg  
260 265 270

Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro  
275 280 285

Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala  
290 295 300

Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys  
305 310 315 320

<210> 31  
<211> 1020  
<212> DNA  
<213> human organism

<400> 31	
atgaactggg agctgctgct gtggctgctg gtgctgtgcg cgctgctcct gctcttggtg	60
cagctgctgc gtttcctgag ggctgacggc gacctgacgc tactatgggc cgagtggcag	120
ggacgacgccc cagaatggga gctgactgat atgggttgtt gggtgactgg agcctcgagt	180
ggaaattggtg aggagctggc ttaccagttt tctaaactag gagtttctct tgtgctgtca	240
gccagaagag tgcatacgact ggaaagggtg aaaagaagat gccttagagaa tggcaattta	300
aaagaaaaag atataacttgt tttgccccctt gacctgaccc acactggttc ccatgaagcg	360
gctacccaaag ctgttctcca ggagtttgtt agaatcgaca ttctggtcaa caatggtgaa	420

atgtcccagc	480
gttctctgtg	
catggatacc	
agcttggatg	
tctacagaaa	
gctaatacgag	
cttaactact	540
tagggacggt	
gtccttgaca	
aatgtgttc	
tgcctcacat	
gatcgagagg	
aagcaaggaa	600
agattgttac	
tgtgaatagc	
atcctggta	
tcatatctgt	
acctcttcc	
attggatact	660
gtgctagcaa	
gcatgctctc	
cggggttttt	
ttaatggcct	
tcgaacagaa	
cttgcacat	720
acccaggtat	
aatagttct	
aacattgcc	
caggacctgt	
gcaatcaa	
attgtggaga	780
attcccttagc	
tggagaagtc	
acaaagacta	
taggcaataa	
tggagaccag	
tcccacaaga	840
tgacaaccag	
tcgttgtgtg	
cggctgatgt	
taatcagcat	
ggccaatgtat	
ttgaaagaag	900
tttggatctc	
agaacaacct	
ttcttggtag	
taacatattt	
gtggcaatac	
atgccaacct	960
gggcctggtg	
gataaccaac	
aagatgggaa	
agaaaaggat	
tgagaacttt	
aagagtggtg	1020
tggatgcaga	
ctcttcttat	
tttaaaatct	
ttaagacaaa	
acatgactga	

<210> 32  
 <211> 339  
 <212> PRT  
 <213> human organism

<400> 32

Met			
Asn			
Trp			
Glu			
Leu			
Leu			
Leu			
Trp			
Leu			
Leu			
Val			
Cys			
Ala			
Leu			
Leu			
1	5	10	15

Leu		
Leu		
Leu		
Val		
Gln		
Leu		
Leu		
Arg		
Phe		
Leu		
Arg		
Ala		
Asp		
Gly		
Asp		
Leu		
20	25	30

Thr		
Leu		
Leu		
Trp		
Ala		
Glu		
Trp		
Gln		
Gly		
Arg		
Arg		
Pro		
Glu		
Trp		
Glu		
Leu		
35	40	45

Thr		
Asp		
Met		
Val		
Val		
Trp		
Val		
Thr		
Gly		
Ala		
Ser		
Ser		
Gly		
Ile		
Gly		
Glu		
50	55	60

Glu			
Leu			
Ala			
Tyr			
Gln			
Leu			
Ser			
Lys			
Leu			
Gly			
Val			
Ser			
Leu			
Val			
Leu			
Ser			
65	70	75	80

Ala	
Arg	
Arg	
Val	
His	
Glu	
Leu	
Glu	
Arg	
Val	
Lys	
95	

Asn		
Gly		
Asn		
Leu		
Lys		
Glu		
Lys		
Asp		
Ile		
Leu		
Val		
Leu		
Pro		
Leu		
Asp		
Leu		
100	105	110

Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu

115

120

125

Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly Met Ser Gln Arg  
130 135 140

Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg Lys Leu Ile Glu  
145 150 155 160

Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His  
165 170 175

Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu  
180 185 190

Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His  
195 200 205

Ala Leu Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr  
210 215 220

Pro Gly Ile Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn  
225 230 235 240

Ile Val Glu Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn  
245 250 255

Asn Gly Asp Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu  
260 265 270

Met Leu Ile Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu  
275 280 285

Gln Pro Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp  
290 295 300

Ala Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe  
305 310 315 320

Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys Thr  
325 330 335

Lys His Asp

<210> 33  
 <211> 1186  
 <212> DNA  
 <213> human organism

<400> 33

aggaaatctgc	gctcgggttc	cgcagatgca	gagggtttaggg	tggctgcggg	actggaaagtc	60
atcgggcaga	ggtctcacag	cagccaaagga	acctggggcc	cgtccctccc	ccctccaggc	120
catgaggatt	ctgcagttaa	tcctgcttgc	tctggcaaca	gggctttag	ggggagagac	180
caggatcatc	aaggggttcg	agtgcagacc	tcactcccag	ccctggcagg	cagccctgtt	240
cgagaagacg	cggctactct	gtggggcgac	gctcatcgcc	cccagatggc	tcctgacagc	300
agcccactgc	ctcaagcccc	gctacatagt	tcacctgggg	cagcacaacc	tccagaagga	360
ggagggctgt	gagcagaccc	ggacagccac	tgagtccctc	ccccaccccg	gcttcaacaa	420
cagcctcccc	aacaaagacc	accgcaatga	catcatgctg	gtgaagatgg	catcgccagt	480
ctccatcacc	tgggctgtgc	gaccctcac	cctctcctca	cgtgtgtca	ctgctggcac	540
cagctgcctc	atttccggct	ggggcagcac	gtccagcccc	cagttacgccc	tgcctcacac	600
cttgcgtgc	gccaacatca	ccatcattga	gcaccagaag	tgtgagaacg	cctacccgg	660
caacatcaca	gacaccatgg	tgtgtgccag	cgtgcaggaa	gggggcaagg	actcctgcca	720
gggtgactcc	ggggccctc	tggtctgtaa	ccagtctctt	caaggcatta	tctcctgggg	780
ccaggatccg	tgtgcgtca	cccgaaagcc	tggtgtctac	acgaaaagtct	gcaaataatgt	840
ggactggatc	caggagacga	tgaagaacaa	ttagactgga	cccacccacc	acagcccatc	900
accctccatt	tccacttggt	gtttggttcc	tgttcaactct	gttaataaga	aaccctaagc	960
caagaccctc	tacgaacatt	cttggccct	cctggactac	aggagatgct	gtcacttaat	1020
aatcaacctg	gggttcgaaa	tcagtgagac	ctggattcaa	attctgcctt	gaaatattgt	1080
gactctggga	atgacaacac	ctggtttgtt	ctctgttcta	tccccagccc	caaagacagc	1140
tcctggccat	atatcaaggt	ttcaataaaat	atttgctaaa	tgagtg		1186

<210> 34  
 <211> 250  
 <212> PRT  
 <213> human organism

<400> 34

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val

1                   5                   10                   15  
Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser  
20   25                                     30  
  
Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly  
35   40                                     45  
  
Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu  
50   55                                     60  
  
Lys Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu  
65   70                                     80  
  
Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro  
85   90                                     95  
  
Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met  
100   105                                     110  
  
Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro  
115   120                                     125  
  
Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile  
130   135                                     140  
  
Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr  
145   150                                     160  
  
Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn  
165   170                                     175  
  
Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln  
180   185                                     190  
  
Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val  
195   200                                     205  
  
Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys  
210   215                                     220  
  
Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val  
225   230                                     240



Asp Trp Ile Gln Glu Thr Met Lys Asn Asn  
245 250

<210> 35  
<211> 1233  
<212> DNA  
<213> human organism

<400> 35  
ctaaagctct cttgctgcct agcctcctgc cggcctcatc ttcgcccagc caaccccgcc 60  
tggagcccta tggccaactg cgagttcagc ccgggtgtccg gggacaaaacc ctgctgccgg 120  
ctctcttagga gagcccaact ctgtcttggc gtcagtatcc tggcctgtat cctcgtcgtg 180  
gtgctcgccgg tggtcgtccc gaggtggcgc cagacgtgga gcgggtccggg caccaccaag 240  
cgctttcccg agaccgtcct ggcgcgatgc gtcaagtaca ctgaaattca tcctgagatg 300  
agacatgttag actgccaaag tgtatggat gcttcaagg gtgcatttat ttcaaaacat 360  
ccttgcaaca ttactgaaga agactatcag ccactaatga agttggaaac tcagaccgta 420  
ccttgcaaca agattcttct ttggagcaga ataaaagatc tggcccatca gttcacacag 480  
gtccagcggg acatgttcac cctggaggac acgctgctag gctacccctgc tcatgacctc 540  
acatggtgtg gtgaattcaa cacttccaaa ataaaactatc aatcttgcgg agactggaga 600  
aaggactgca gcaacaaccc tgtttcagta ttctggaaaa cggtttcccg caggtttgc 660  
gaagctgcct gtgatgtggt ccatgtgatg ctcaatggat cccgcagtaa aatcttgac 720  
aaaaacagca cttttggag tgtggaaagtc cataatttgc aaccagagaa ggttcagaca 780  
ctagaggcct gggtgataca tggtggaaaga gaagattcca gagactttag ccaggatccc 840  
accataaaag agctggaaatc gattataagc aaaaggaata ttcaattttc ctgcaagaat 900  
atctacagac ctgacaagtt tcttcagtgt gtgaaaaatc ctgaggattc atcttgcaca 960  
tctgagatct gagccagtcg ctgtgggtgt tttagctcct tgactccttg tggtttatgt 1020  
catcatacat gactcagcat acctgctggc gcagagctga agatttggc gggcctcca 1080  
caataaggcgtc aatgccagag acggaagcct tttccccaa agtctaaaa taacttat 1140  
catcagcata cctttattgt gatctatcaa tagtcaagaa aaattattgt ataagattag 1200  
aatgaaaatt gtatgttaag ttacttcctt tag 1233

<210> 36  
<211> 300

<212> PRT

<213> human organism

<400> 36

Met Ala Asn Cys Glu Phe Ser Pro Val Ser Gly Asp Lys Pro Cys Cys  
1 5 10 15

Arg Leu Ser Arg Arg Ala Gln Leu Cys Leu Gly Val Ser Ile Leu Val  
20 25 30

Leu Ile Leu Val Val Val Leu Ala Val Val Val Pro Arg Trp Arg Gln  
35 40 45

Thr Trp Ser Gly Pro Gly Thr Thr Lys Arg Phe Pro Glu Thr Val Leu  
50 55 60

Ala Arg Cys Val Lys Tyr Thr Glu Ile His Pro Glu Met Arg His Val  
65 70 75 80

Asp Cys Gln Ser Val Trp Asp Ala Phe Lys Gly Ala Phe Ile Ser Lys  
85 90 95

His Pro Cys Asn Ile Thr Glu Glu Asp Tyr Gln Pro Leu Met Lys Leu  
100 105 110

Gly Thr Gln Thr Val Pro Cys Asn Lys Ile Leu Leu Trp Ser Arg Ile  
115 120 125

Lys Asp Leu Ala His Gln Phe Thr Gln Val Gln Arg Asp Met Phe Thr  
130 135 140

Leu Glu Asp Thr Leu Leu Gly Tyr Leu Ala Asp Asp Leu Thr Trp Cys  
145 150 155 160

Gly Glu Phe Asn Thr Ser Lys Ile Asn Tyr Gln Ser Cys Pro Asp Trp  
165 170 175

Arg Lys Asp Cys Ser Asn Asn Pro Val Ser Val Phe Trp Lys Thr Val  
180 185 190

Ser Arg Arg Phe Ala Glu Ala Ala Cys Asp Val Val His Val Met Leu  
195 200 205

Asn Gly Ser Arg Ser Lys Ile Phe Asp Lys Asn Ser Thr Phe Gly Ser  
210 215 220

Val Glu Val His Asn Leu Gln Pro Glu Lys Val Gln Thr Leu Glu Ala  
225 230 235 240

Trp Val Ile His Gly Gly Arg Glu Asp Ser Arg Asp Leu Cys Gln Asp  
245 250 255

Pro Thr Ile Lys Glu Leu Glu Ser Ile Ile Ser Lys Arg Asn Ile Gln  
260 265 270

Phe Ser Cys Lys Asn Ile Tyr Arg Pro Asp Lys Phe Leu Gln Cys Val  
275 280 285

Lys Asn Pro Glu Asp Ser Ser Cys Thr Ser Glu Ile  
290 295 300

<210> 37

<211> 3315

<212> DNA

<213> human organism

<400> 37  
atgcctttc gggcagccag gtcagcatg aggaacagaa ggaatgacac tctggacagc 60  
accggaccc tgtactccag cgcgtctcg agcacagact tgtcttacag tgaaagcgac 120  
tttgtaatt ttattcaagc aaatttaag aaacgagaat gtgtcttctt taccaaagat 180  
tccaaggcca cggagaatgt gtgcaagtgt ggctatgcc agagccagca catggaaggc 240  
accagatca accaaagtga gaaatggaac tacaagaaac acaccaagga attcctacc 300  
gacgccttg gggatattca gttgagaca ctgggagaaga aagggaaagta tatacgtctg 360  
tcctgcgaca cggacgcgga aatccttac gagctgctga cccagcactg gcacctgaaa 420  
acacccaacc tggtcatttc tgtgaccggg ggcgccaaga acttcgcctt gaagccgcgc 480  
atgcgcaaga tcattcagccg gctcatctac atcgcgact ccaaagggtgc ttggattctc 540  
acgggaggca cccattatgg cctgatgaag tacatcgaaa aggtggtag agataaacacc 600  
atcagcagga gttcagagga gaatattgtg gccattggca tagcagctt gggcatggtc 660  
tccaaccggg acaccctcat caggaattgc gatgctgagg gctatcccc agcccactac 720  
cttatggatg acttcacaag agatccactg tatatcctgg acaacaacca cacacatttgc 780  
ctgctcgtgg acaatggctg tcatggacat cccactgtcg aagcaaagct ccggaatcag 840

ctagagaagt atatctctga gcgcactatt caagattcca actatggtgg caagatcccc 900  
attgtgtgtt ttgcccagg aggtggaaaa gagacttga aagccatcaa tacctccatc 960  
aaaaataaaa ttccttgtt ggtggggaa ggctcgcc agatcgctga tgtgatcgct 1020  
agcctggtgg aggtggagga tgccctgaca tcttctgccc tcaaggagaa gctggtgcbc 1080  
ttttacccc gcacgggtgtc ccggctgcct gaggaggaga ctgagagttg gatcaaatgg 1140  
ctcaaagaaa ttctcgaatg ttctcaccta ttaacagtta ttaaaaatgga agaagctggg 1200  
gatgaaattg tgagcaatgc catctcctac gctctataca aagccttcag caccagttag 1260  
caagacaagg ataactggaa tggcagctg aagcttctgc tggagtggaa ccagctggac 1320  
ttagccaatg atgagattt caccaatgac cgccgatggg agtctgctga cttcaagaa 1380  
gtcatgttta cggctctcat aaaggacaga cccaagttt tccgcctt tctggagaat 1440  
ggcttgaacc tacggaagtt tctcacccat gatgtcctca ctgaactctt ctccaaccac 1500  
ttcagcacgc ttgtgtaccg gaatctgcag atcgccaaga attcctataa tgatgccctc 1560  
ctcacgttg tctggaaact ggttgcgaac ttccgaagag gcttccggaa ggaagacaga 1620  
aatggccggg acgagatgga catagaactc cacgacgtgt ctccattac tcggcacccc 1680  
ctgcaagctc tcttcatctg gccattttt cagaataaga aggaactctc caaagtcatt 1740  
tggagcaga ccaggggctg cactctggca gccctggag ccagcaagct tctgaagact 1800  
ctggccaaag tgaagaacga catcaatgct gctggggagt ccgaggagct ggctaattgag 1860  
tacgagaccc gggctgttga gctgttcaact gagtgttaca gcagcgatga agacttggca 1920  
gaacagctgc tggcttattc ctgtgaagct tgggtggaa gcaactgtct ggagctggcg 1980  
gtggaggcca cagaccagca tttcatcgcc cagcctgggg tccagaattt tcttcctaag 2040  
caatggtatg gagagatttcc cgagacacc aagaactgga agattatccct gtgtctgtt 2100  
attataccct tggtggctg tggcttgtt tcatttagga agaaacctgt cgacaagcac 2160  
aagaagctgc ttggacta tggcgttcc ttcacccccc cttcggtt cttctctgg 2220  
aatgtggct tctacatcgc cttccctctg ctgtttgcct acgtgctgct catggatttcc 2280  
cattcggtgc cacacccccc cgagctggtc ctgtactcgc tggctttgtt cttctctgt 2340  
gatgaagtga gacagtggta cgtaaatggg gtgaattatt ttactgaccc gtggaaatgt 2400  
atggacacgc tggggctttt ttacttcata gcaggaattt tatttcggct ccactttct 2460  
aataaaagct ctttgttattc tggacgagtc atttctgtc tggactacat tatttcact 2520

ctaagattga tccacat	ttt tactgt	aaaggc gacccaa	gat tataatgctg	2580		
cagaggatgc tgatcgatgt	gttcttc	ctgttcc	tgtcggtgtg gatgg	2640		
tttggcgtgg ccaggcaagg	gatccttagg	cagaatgagc	agcgctggag gtggat	2700		
cgttcggtca tctacgagcc	ctacctggcc	atgttcggcc	agggtcccag tgacgtggat	2760		
ggtaccacgt atgactttgc	ccactgcacc	ttca	ctgggaa atgagtccaa gccactgtgt	2820		
gtggagctgg atgagcacaa	cctgccccgg	ttccccgagt	ggatcaccat cccctgg	2880		
tgcata	taca	tggtcaacc	tgctggcgc catgttggc	2940		
tacacggtgg gcaccgtcca	ggagaacaat	gaccagg	tctggtcca gaggtacttc	3000		
ctgg	tcagg	actgcag ccgcctcaat	atccc	ttccatcg	cttcgcttac	3060
ttctacatgg tggtaagaa	gtgttcaag	tgttgctgca	aggagaaaaa catggagtct	3120		
tctgtctgct	gtttcaaaaa	tgaagacaat	gagactctgg catggaggg tgtcatgaag	3180		
gaaaactacc ttgtcaagat	caacacaaaa	gccaacgaca	cctcagagga aatgaggcat	3240		
cgatttagac aactggatac	aaagcttaat	gatctcaagg	gtcttctgaa agagattgct	3300		
aataaaatca aatga				3315		

<210> 38  
 <211> 1104  
 <212> PRT  
 <213> human organism

<400> 38

Met	Ser	Phe	Arg	Ala	Ala	Arg	Leu	Ser	Met	Arg	Asn	Arg	Arg	Asn	Asp
1								10							15

Thr	Leu	Asp	Ser	Thr	Arg	Thr	Leu	Tyr	Ser	Ser	Ala	Ser	Arg	Ser	Thr
															20
															25
															30

Asp	Leu	Ser	Tyr	Ser	Glu	Ser	Asp	Leu	Val	Asn	Phe	Ile	Gln	Ala	Asn
															35
															40
															45

Phe	Lys	Lys	Arg	Glu	Cys	Val	Phe	Phe	Thr	Lys	Asp	Ser	Lys	Ala	Thr
															50
															55
															60

Glu	Asn	Val	Cys	Lys	Cys	Gly	Tyr	Ala	Gln	Ser	Gln	His	Met	Glu	Gly
															65
															70
															75
															80

Thr Gln Ile Asn Gln Ser Glu Lys Trp Asn Tyr Lys Lys His Thr Lys

85

90

95

Glu Phe Pro Thr Asp Ala Phe Gly Asp Ile Gln Phe Glu Thr Leu Gly  
100 105 110

Lys Lys Gly Lys Tyr Ile Arg Leu Ser Cys Asp Thr Asp Ala Glu Ile  
115 120 125

Leu Tyr Glu Leu Leu Thr Gln His Trp His Leu Lys Thr Pro Asn Leu  
130 135 140

Val Ile Ser Val Thr Gly Gly Ala Lys Asn Phe Ala Leu Lys Pro Arg  
145 150 155 160

Met Arg Lys Ile Phe Ser Arg Leu Ile Tyr Ile Ala Gln Ser Lys Gly  
165 170 175

Ala Trp Ile Leu Thr Gly Gly Thr His Tyr Gly Leu Met Lys Tyr Ile  
180 185 190

Gly Glu Val Val Arg Asp Asn Thr Ile Ser Arg Ser Ser Glu Glu Asn  
195 200 205

Ile Val Ala Ile Gly Ile Ala Ala Trp Gly Met Val Ser Asn Arg Asp  
210 215 220

Thr Leu Ile Arg Asn Cys Asp Ala Glu Gly Tyr Phe Leu Ala Gln Tyr  
225 230 235 240

Leu Met Asp Asp Phe Thr Arg Asp Pro Leu Tyr Ile Leu Asp Asn Asn  
245 250 255

His Thr His Leu Leu Leu Val Asp Asn Gly Cys His Gly His Pro Thr  
260 265 270

Val Glu Ala Lys Leu Arg Asn Gln Leu Glu Lys Tyr Ile Ser Glu Arg  
275 280 285

Thr Ile Gln Asp Ser Asn Tyr Gly Gly Lys Ile Pro Ile Val Cys Phe  
290 295 300

Ala Gln Gly Gly Lys Glu Thr Leu Lys Ala Ile Asn Thr Ser Ile  
305 310 315 320

Lys Asn Lys Ile Pro Cys Val Val Val Glu Gly Ser Gly Gln Ile Ala  
325 330 335

Asp Val Ile Ala Ser Leu Val Glu Val Glu Asp Ala Leu Thr Ser Ser  
340 345 350

Ala Val Lys Glu Lys Leu Val Arg Phe Leu Pro Arg Thr Val Ser Arg  
355 360 365

Leu Pro Glu Glu Glu Thr Glu Ser Trp Ile Lys Trp Leu Lys Glu Ile  
370 375 380

Leu Glu Cys Ser His Leu Leu Thr Val Ile Lys Met Glu Glu Ala Gly  
385 390 395 400

Asp Glu Ile Val Ser Asn Ala Ile Ser Tyr Ala Leu Tyr Lys Ala Phe  
405 410 415

Ser Thr Ser Glu Gln Asp Lys Asp Asn Trp Asn Gly Gln Leu Lys Leu  
420 425 430

Leu Leu Glu Trp Asn Gln Leu Asp Leu Ala Asn Asp Glu Ile Phe Thr  
435 440 445

Asn Asp Arg Arg Trp Glu Ser Ala Asp Leu Gln Glu Val Met Phe Thr  
450 455 460

Ala Leu Ile Lys Asp Arg Pro Lys Phe Val Arg Leu Phe Leu Glu Asn  
465 470 475 480

Gly Leu Asn Leu Arg Lys Phe Leu Thr His Asp Val Leu Thr Glu Leu  
485 490 495

Phe Ser Asn His Phe Ser Thr Leu Val Tyr Arg Asn Leu Gln Ile Ala  
500 505 510

Lys Asn Ser Tyr Asn Asp Ala Leu Leu Thr Phe Val Trp Lys Leu Val  
515 520 525

Ala Asn Phe Arg Arg Gly Phe Arg Lys Glu Asp Arg Asn Gly Arg Asp  
530 535 540

Glu Met Asp Ile Glu Leu His Asp Val Ser Pro Ile Thr Arg His Pro  
545 550 555 560

Leu Gln Ala Leu Phe Ile Trp Ala Ile Leu Gln Asn Lys Lys Glu Leu  
565 570 575

Ser Lys Val Ile Trp Glu Gln Thr Arg Gly Cys Thr Leu Ala Ala Leu  
580 585 590

Gly Ala Ser Lys Leu Leu Lys Thr Leu Ala Lys Val Lys Asn Asp Ile  
595 600 605

Asn Ala Ala Gly Glu Ser Glu Glu Leu Ala Asn Glu Tyr Glu Thr Arg  
610 615 620

Ala Val Glu Leu Phe Thr Glu Cys Tyr Ser Ser Asp Glu Asp Leu Ala  
625 630 635 640

Glu Gln Leu Leu Val Tyr Ser Cys Glu Ala Trp Gly Gly Ser Asn Cys  
645 650 655

Leu Glu Leu Ala Val Glu Ala Thr Asp Gln His Phe Ile Ala Gln Pro  
660 665 670

Gly Val Gln Asn Phe Leu Ser Lys Gln Trp Tyr Gly Glu Ile Ser Arg  
675 680 685

Asp Thr Lys Asn Trp Lys Ile Ile Leu Cys Leu Phe Ile Ile Pro Leu  
690 695 700

Val Gly Cys Gly Phe Val Ser Phe Arg Lys Lys Pro Val Asp Lys His  
705 710 715 720

Lys Lys Leu Leu Trp Tyr Tyr Val Ala Phe Phe Thr Ser Pro Phe Val  
725 730 735

Val Phe Ser Trp Asn Val Val Phe Tyr Ile Ala Phe Leu Leu Phe  
740 745 750

Ala Tyr Val Leu Leu Met Asp Phe His Ser Val Pro His Pro Pro Glu  
755 760 765

Leu Val Leu Tyr Ser Leu Val Phe Val Leu Phe Cys Asp Glu Val Arg  
770 775 780

Gln Trp Tyr Val Asn Gly Val Asn Tyr Phe Thr Asp Leu Trp Asn Val  
785 790 795 800

Met Asp Thr Leu Gly Leu Phe Tyr Phe Ile Ala Gly Ile Val Phe Arg  
805 810 815

Leu His Ser Ser Asn Lys Ser Ser Leu Tyr Ser Gly Arg Val Ile Phe  
820 825 830

Cys Leu Asp Tyr Ile Ile Phe Thr Leu Arg Leu Ile His Ile Phe Thr  
835 840 845

Val Ser Arg Asn Leu Gly Pro Lys Ile Ile Met Leu Gln Arg Met Leu  
850 855 860

Ile Asp Val Phe Phe Leu Phe Leu Phe Ala Val Trp Met Val Ala  
865 870 875 880

Phe Gly Val Ala Arg Gln Gly Ile Leu Arg Gln Asn Glu Gln Arg Trp  
885 890 895

Arg Trp Ile Phe Arg Ser Val Ile Tyr Glu Pro Tyr Leu Ala Met Phe  
900 905 910

Gly Gln Val Pro Ser Asp Val Asp Gly Thr Thr Tyr Asp Phe Ala His  
915 920 925

Cys Thr Phe Thr Gly Asn Glu Ser Lys Pro Leu Cys Val Glu Leu Asp  
930 935 940

Glu His Asn Leu Pro Arg Phe Pro Glu Trp Ile Thr Ile Pro Leu Val  
945 950 955 960

Cys Ile Tyr Met Leu Ser Thr Asn Ile Leu Leu Val Asn Leu Leu Val  
965 970 975

Ala Met Phe Gly Tyr Thr Val Gly Thr Val Gln Glu Asn Asn Asp Gln  
980 985 990

Val Trp Lys Phe Gln Arg Tyr Phe Leu Val Gln Glu Tyr Cys Ser Arg

995	1000	1005
Leu Asn Ile Pro Phe Pro Phe Ile Val Phe Ala Tyr Phe Tyr Met		
1010	1015	1020
Val Val Lys Lys Cys Phe Lys Cys Cys Cys Lys Glu Lys Asn Met		
1025	1030	1035
Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp Asn Glu Thr Leu		
1040	1045	1050
Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val Lys Ile Asn		
1055	1060	1065
Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg Phe Arg		
1070	1075	1080
Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys Glu		
1085	1090	1095
Ile Ala Asn Lys Ile Lys		
1100		
<210> 39		
<211> 558		
<212> DNA		
<213> human organism		
<400> 39		
atgcctcgcc tggctttgtt ccacctgcta gaattctgtt tactactgaa ccaattttcc		60
agagcagtcg cggccaaatg gaaggacgat gttattaaat tatgcggccg cgaatttagtt		120
cgcgcgcaga ttgccatgg cggcatgagc acctggagca aaaggtctct gagccaggaa		180
gatgctcctc agacacctag accagtggca gaaattgtac catccttcat caacaaagat		240
acagaaaacta taattatcat gttggaaattc attgctaatt tgccaccgga gctgaaggca		300
gcccttatctg agaggcaacc atcattacca gagctacagc agtatgtacc tgcattaaag		360
gattccaatc ttagcttga agaatttaag aaacttattc gcaataggca aagtgaagcc		420
gcagacagca atccttcaga attaaaatac ttaggcttgg atactcattc tcaaaaaaaag		480
agacgaccct acgtggcaact gtttgagaaa tggcttaaa ttgggttgtac caaaaggct		540
cttgctaaat attgctga		558

<210> 40  
<211> 185  
<212> PRT  
<213> human organism

<400> 40

Met Pro Arg Leu Phe Leu Phe His Leu Leu Glu Phe Cys Leu Leu Leu  
1 5 10 15

Asn Gln Phe Ser Arg Ala Val Ala Ala Lys Trp Lys Asp Asp Val Ile  
20 25 30

Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly  
35 40 45

Met Ser Thr Trp Ser Lys Arg Ser Leu Ser Gln Glu Asp Ala Pro Gln  
50 55 60

Thr Pro Arg Pro Val Ala Glu Ile Val Pro Ser Phe Ile Asn Lys Asp  
65 70 75 80

Thr Glu Thr Ile Ile Ile Met Leu Glu Phe Ile Ala Asn Leu Pro Pro  
85 90 95

Glu Leu Lys Ala Ala Leu Ser Glu Arg Gln Pro Ser Leu Pro Glu Leu  
100 105 110

Gln Gln Tyr Val Pro Ala Leu Lys Asp Ser Asn Leu Ser Phe Glu Glu  
115 120 125

Phe Lys Lys Leu Ile Arg Asn Arg Gln Ser Glu Ala Ala Asp Ser Asn  
130 135 140

Pro Ser Glu Leu Lys Tyr Leu Gly Leu Asp Thr His Ser Gln Lys Lys  
145 150 155 160

Arg Arg Pro Tyr Val Ala Leu Phe Glu Lys Cys Cys Leu Ile Gly Cys  
165 170 175

Thr Lys Arg Ser Leu Ala Lys Tyr Cys  
180 185

<210> 41

<211> 3978  
 <212> DNA  
 <213> human organism

<400> 41						
atgctgcccg	tgtaccagga	ggtgaagccc	aacccgctgc	aggacgcgaa	cctctgctca	60
cgctgttct	tctggtggtct	caatcccttg	tttaaaattt	gccataaaacg	gagatttagag	120
gaagatgata	tgtattcagt	gctgccagaa	gaccgctcac	agcaccttgg	agaggagttg	180
caagggttct	gggataaaaga	agtttaaga	gctgagaatg	acgcacagaa	gccttctta	240
acaagagcaa	tcataaaagt	ttactggaaa	tcttatttt	tttggaaat	tttacgtta	300
attgaggaaa	gtgccaaagt	aatccagccc	atattttgg	aaaaaattat	taattatttt	360
gaaaattatg	atcccatgga	ttctgtggct	ttgaacacag	cgtacgccta	tgccacggtg	420
ctgactttt	gcacgctcat	tttggctata	ctgcatca	tatattttta	tcacgtttag	480
tgtgctggga	tgaggttacg	agtagccatg	tgccatata	tttatcgaa	ggcacttcgt	540
cttagtaaca	tggccatggg	gaagacaacc	acaggccaga	tagtcaatct	gctgtccaaat	600
gatgtgaaca	agtttgcata	ggtgacagt	ttcttacact	tcctgtggc	aggaccactg	660
cagggcgtcg	cagtgactgc	cctactctgg	atggagatag	gaatatcg	ccttgcgtgg	720
atggcagttc	taatcattct	cctgccc	caaagctgtt	ttggaaagt	gttctcatca	780
ctgaggagta	aaactgcaac	ttcacggat	gccaggatca	ggaccatgaa	tgaagttata	840
actggtataa	ggataataaa	aatgtacg	cccc	tggaaaagt	catttcaaa	900
aatttgagaa	agaaggagat	ttccaagatt	ctgagaagtt	cctgcctcag	ggggatgaat	960
ttggcttcgt	tttcagtg	aagcaaaatc	atcg	tggttt	tgaccttcac	1020
ctcctcggca	gtgtgatcac	agccagccgc	gtgtcg	cgtgacgct	gtatgggct	1080
gtgcggctga	cggtaacc	cttcttcccc	tca	gaccattt	agagggtgtc	1140
gtcagcatcc	gaagaatcca	gac	ttttt	ctacttgat	agatatcaca	1200
cagctgccgt	cagatggtaa	aaagatgg	tg	catgtgcagg	atttactgc	1260
aaggcatcag	agacccaaac	tctacaaggc	ctt	c	tgtcagacc	1320
ttagctgtgg	tcggccccgt	gggagcaggg	aagt	catcac	tgttaagtgc	1380
gaattggccc	caagtacgg	gctggtcagc	gtgc	atggaa	tgtgtctcag	1440
cagccctggg	tgttctcggg	aactctgagg	agtaatattt	tatttggaa	gaaatacgaa	1500
aaggaacgat	atgaaaaagt	cataaaggct	tgtgctctga	aaaaggattt	acagctgtt	1560

gaggatggtg atctgactgt gataggagat cggggAACCA cgctgagtgg agggcagaaa 1620  
gcacggtaa accttgcAAG agcagtgtat caagatgctg acatctatct cctggacgat 1680  
cctctcagtG cagtagatgc ggaagttAGC agacacttgt tcgaactgtg tatttgcAA 1740  
atttgcATG agaagatcac aattttAGTg actcatcAGt tgcaGtACt caaAGtgcA 1800  
agtcaGATTc tgatattgaa agatggtaaA atggtgCAGA aggggacttA cactgagtTC 1860  
ctaaaatctG gtatagattt tggctccCTt ttaaAGAAGG ataAtgagGA aagtGAacAA 1920  
cctccAGTTc caggaACTCC cacACTAAGG aatcgtaCt tctcAGAGtC ttcggTTGG 1980  
tctcaacaat cttctAGACC ctccTTgAAA gatggtgctc tggagAGCCA agatacAGAG 2040  
aatgtcccAG ttacactATC agaggagaAC cgTTCTgAAG gaaaAGTTGG ttttcaggCC 2100  
tataAGAAatt acttcAGAGC tggtgctcAc tggattgtct tcatttCCTt tatttcCCTA 2160  
aacactgcAG ctcAGGTTGC ctatgtGCTt caagattggT ggCTTTcATA ctgggcaaAC 2220  
aaACAAAGTA tgctAAatgt cactgtAAat ggaggAGGAA atgtAAccGA gaAGctAGAT 2280  
cttaactggT acttagGAat ttattcAGGT ttaactgtAG ctaccGTTCT ttttggcATA 2340  
gcaAGatCTC tattggTatt ctacgtcCtt gttaactCtt cacAAacttt gcacaACAAA 2400  
atgtttgAGT caattctgAA agctccggTA ttattcttG atagAAatCC aatAGGAAGA 2460  
attttaaATC gtttctccAA agacattggA cacttggATG atttgctGCC gctgacgttt 2520  
ttagatttCA tccAGACATT gctacaAGtG gttggTgtgg tctctgtggc tgtggccgtG 2580  
attcCTTggA tcgcaataCC ctTggTTccc ctTggAAatCA ttttcatttt tcttcggcGA 2640  
tatTTTTggA aaACgtcaAG agatgtGAAG cgcctggAAt ctacaactCG gagtccAGtG 2700  
ttttcccact tgcataCTTC tctccAGggg ctctggacCA tccgggcATA caaAGcAGAA 2760  
gagaggTgtC aggaactgtt tgatgcACAC caggatttAC attcAGAGGC ttggTTCTG 2820  
ttttgacAA cgtcccgtG gttcgccgtC cgtctggatG ccatctgtGC catgtttgtC 2880  
atcatcgTT ccttgggtC cctgattctG gcaAAactC tggatGCCgg gcaggTTggT 2940  
ttggcactgt cctatGCCt cAcgtcAtG gggatTTtC agtggTgtGT tcgacaAAAGt 3000  
gctgaAGttG agaAtAtgtA gatctcAGtA gaaAGggTCA ttgaAtAcAC agacCttgAA 3060  
aaAGAAGCAC ctTggGAATA tcAgAAACgC ccAccAccAG cctggccccA tgaAGggAGt 3120  
ataAtcttG acaAtgtgAA ctTcatgtAC agtccAGgtG ggCCTCTggT actgaAGcat 3180  
ctgacAGCAC tcattaAATC acaAGAAAAG gttggcATTG tggGAAGAAC cggAGctggA 3240  
aaaAGttccc tcAtctcAGC ctttttAGA ttgtcAGAAc ccGAAGgtAA aatttggatt 3300

gataagatct tgacaactga aattggactt cacgattaa ggaagaaaat gtcaatcata	3360
cctcaggaac ctgtttgtt cactggaaca atgaggaaaa acctggatcc cttaatgag	3420
cacacggatg aggaactgtg gaatgcctta caagaggtac aacttaaaga aaccattgaa	3480
gatttcctg gtaaaatgga tactgaatta gcagaatcag gatccaattt tagtggta	3540
caaagacaac tggtgtgcct tgccaggca attctcagga aaaatcagat attgattatt	3600
gatgaagcga cggcaaatgt ggatccaaga actgatgagt taataaaaaaaaatccgg	3660
gagaaatttg cccactgcac cgtgctaacc attgcacaca gattgaacac cattattgac	3720
agcgacaaga taatggttt agattcagga agactgaaag aatatgatga gccgtatgtt	3780
ttgctgcaaa ataaagagag cctatttac aagatggtgc aacaactggg caaggcagaa	3840
gccgctgccc tcactgaaac agcaaaacag gtataactca aaagaaaatttacccatatt	3900
ggtcacactg accacatggt tacaaacact tccaatggac agccctcgac cttaactatt	3960
ttcgagacag cactgtga	3978

<210> 42

<211> 1325

<212> PRT

<213> human organism

<400> 42

Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala			
1	5	10	15

Asn Leu Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys			
20	25	30	

Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu			
35	40	45	

Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp			
50	55	60	

Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu			
65	70	75	80

Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly			
85	90	95	

Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe  
100 105 110

Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser  
115 120 125

Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys  
130 135 140

Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln  
145 150 155 160

Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg  
165 170 175

Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Gly  
180 185 190

Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val  
195 200 205

Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala  
210 215 220

Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly  
225 230 235 240

Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys  
245 250 255

Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg  
260 265 270

Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met  
275 280 285

Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys  
290 295 300

Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn  
305 310 315 320

Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe

325

330

335

Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe  
340 345 350

Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe  
355 360 365

Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg  
370 375 380

Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg  
385 390 395 400

Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr  
405 410 415

Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser  
420 425 430

Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly  
435 440 445

Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro  
450 455 460

Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln  
465 470 475 480

Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly  
485 490 495

Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala  
500 505 510

Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile  
515 520 525

Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn  
530 535 540

Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp  
545 550 555 560

Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu  
565 570 575

Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His  
580 585 590

Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp  
595 600 605

Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly  
610 615 620

Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln  
625 630 635 640

Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu  
645 650 655

Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly  
660 665 670

Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu  
675 680 685

Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr  
690 695 700

Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu  
705 710 715 720

Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser  
725 730 735

Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly  
740 745 750

Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr  
755 760 765

Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu  
770 775 780

Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys  
785 790 795 800

Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn  
805 810 815

Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu  
820 825 830

Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu  
835 840 845

Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile  
850 855 860

Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg  
865 870 875 880

Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr  
885 890 895

Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser Leu Gln Gly Leu Trp  
900 905 910

Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys Gln Glu Leu Phe Asp  
915 920 925

Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr  
930 935 940

Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val  
945 950 955 960

Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala  
965 970 975

Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met  
980 985 990

Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile  
995 1000 1005

Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu Glu Lys Glu Ala  
1010 1015 1020

Pro Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp Pro His Glu  
1025 1030 1035

Gly Val Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser Pro Gly  
1040 1045 1050

Gly Pro Leu Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln  
1055 1060 1065

Glu Lys Val Gly Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser  
1070 1075 1080

Leu Ile Ser Ala Leu Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile  
1085 1090 1095

Trp Ile Asp Lys Ile Leu Thr Thr Glu Ile Gly Leu His Asp Leu  
1100 1105 1110

Arg Lys Lys Met Ser Ile Ile Pro Gln Glu Pro Val Leu Phe Thr  
1115 1120 1125

Gly Thr Met Arg Lys Asn Leu Asp Pro Phe Asn Glu His Thr Asp  
1130 1135 1140

Glu Glu Leu Trp Asn Ala Leu Gln Glu Val Gln Leu Lys Glu Thr  
1145 1150 1155

Ile Glu Asp Leu Pro Gly Lys Met Asp Thr Glu Leu Ala Glu Ser  
1160 1165 1170

Gly Ser Asn Phe Ser Val Gly Gln Arg Gln Leu Val Cys Leu Ala  
1175 1180 1185

Arg Ala Ile Leu Arg Lys Asn Gln Ile Leu Ile Ile Asp Glu Ala  
1190 1195 1200

Thr Ala Asn Val Asp Pro Arg Thr Asp Glu Leu Ile Gln Lys Lys  
1205 1210 1215

Ile Arg Glu Lys Phe Ala His Cys Thr Val Leu Thr Ile Ala His

1220	1225	1230
Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys Ile Met Val Leu Asp		
1235	1240	1245
Ser Gly Arg Leu Lys Glu Tyr Asp Glu Pro Tyr Val Leu Leu Gln		
1250	1255	1260
Asn Lys Glu Ser Leu Phe Tyr Lys Met Val Gln Gln Leu Gly Lys		
1265	1270	1275
Ala Glu Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Val Tyr Phe		
1280	1285	1290
Lys Arg Asn Tyr Pro His Ile Gly His Thr Asp His Met Val Thr		
1295	1300	1305
Asn Thr Ser Asn Gly Gln Pro Ser Thr Leu Thr Ile Phe Glu Thr		
1310	1315	1320
Ala Leu		
1325		
<210> 43		
<211> 1140		
<212> DNA		
<213> human organism		
<400> 43		
atggggaaag tgtcctgctg tggcatgaaa taaatgaaac agaaaatgat ggcaagactg		60
ctaagaacat ctttgcttt gcttttcctt ggcctcttg gggtgctggg ggcagcaaca		120
atttcatgca gaaatgaaga agggaaagct gtggactggt ttactttta taagttacct		180
aaaagacaaa acaaggaaag tggagagact gggtagagt acctgtacct agactctaca		240
actagaagct ggaggaagag tgagcaacta atgaatgaca ccaagagtgt tttggaaagg		300
acattacaac agctatatga agcatatgcc tctaagagta acaacacagc ctatctaata		360
tacaatgatg gagtcctaa acctgtgaat tacatgaa agtatggaca caccaaaggt		420
ttactgctgt ggaacagagt tcaagggttc tggctgattc attccatccc tcagttcct		480
ccaattccgg aagaaggcta tgattatcca cccacaggga gacgaaatgg acaaagtggc		540
atctgcataa ctttcaagta caaccagtat gaggcaatag attctcagct cttggctgc		600

aaccccaacg tctatacgccatccca gccacccccc accaggagct cattcacatg 660  
ccccagctgt gcaccagggc cagtcatca gagattcctg gcaggctcct caccacactt 720  
cagtcggccc agggacaaaa attcctccat ttgc当地 780  
atctttgcag cctggatggc tcaacggctg aagacacact tgttaacaga aacctggcag 840  
cgaaaaagac aagagcttcc ttcaaactgc tcccttcctt accatgtcta caatataaaa 900  
gcaattaaat tatcacgaca ctcttatttc agttcttatac aagatcacgc caagtggtgt 960  
atttcccaaa agggcaccaa aaatcgctgg acatgtattg gagacctaaa tcggagtcca 1020  
caccaagcct tcagaagtgg aggattcatt tgtacccaga attggcaaatttaccaagca 1080  
tttcaaaqqat tagtattata ctatgaaagc tgtaagtaaa cttggtgaaa ggacacaggt 1140

<210> 44  
<211> 357  
<212> PRT  
<213> human organism

<400> 44

Met Met Ala Arg Leu Leu Arg Thr Ser Phe Ala Leu Leu Phe Leu Gly  
1 5 10 15

Leu Phe Gly Val Leu Gly Ala Ala Thr Ile Ser Cys Arg Asn Glu Glu  
20 25 30

Gly Lys Ala Val Asp Trp Phe Thr Phe Tyr Lys Leu Pro Lys Arg Gln  
35 40 45

Thr Thr Arg Ser Trp Arg Lys Ser Glu Gln Leu Met Asn Asp Thr Lys  
65 70 75 80

Ser Val Leu Gly Arg Thr Leu Gln Gln Leu Tyr Glu Ala Tyr Ala Ser  
85 90 95

Lys Ser Asn Asn Thr Ala Tyr Leu Ile Tyr Asn Asp Gly Val Pro Lys  
           100             105             110

Pro Val Asn Tyr Ser Arg Lys Tyr Gly His Thr Lys Gly Leu Leu Leu  
115 120 125

Trp Asn Arg Val Gln Gly Phe Trp Leu Ile His Ser Ile Pro Gln Phe  
130 135 140

Pro Pro Ile Pro Glu Glu Gly Tyr Asp Tyr Pro Pro Thr Gly Arg Arg  
145 150 155 160

Asn Gly Gln Ser Gly Ile Cys Ile Thr Phe Lys Tyr Asn Gln Tyr Glu  
165 170 175

Ala Ile Asp Ser Gln Leu Leu Val Cys Asn Pro Asn Val Tyr Ser Cys  
180 185 190

Ser Ile Pro Ala Thr Phe His Gln Glu Leu Ile His Met Pro Gln Leu  
195 200 205

Cys Thr Arg Ala Ser Ser Glu Ile Pro Gly Arg Leu Leu Thr Thr  
210 215 220

Leu Gln Ser Ala Gln Gly Gln Lys Phe Leu His Phe Ala Lys Ser Asp  
225 230 235 240

Ser Phe Leu Asp Asp Ile Phe Ala Ala Trp Met Ala Gln Arg Leu Lys  
245 250 255

Thr His Leu Leu Thr Glu Thr Trp Gln Arg Lys Arg Gln Glu Leu Pro  
260 265 270

Ser Asn Cys Ser Leu Pro Tyr His Val Tyr Asn Ile Lys Ala Ile Lys  
275 280 285

Leu Ser Arg His Ser Tyr Phe Ser Ser Tyr Gln Asp His Ala Lys Trp  
290 295 300

Cys Ile Ser Gln Lys Gly Thr Lys Asn Arg Trp Thr Cys Ile Gly Asp  
305 310 315 320

Leu Asn Arg Ser Pro His Gln Ala Phe Arg Ser Gly Gly Phe Ile Cys  
325 330 335

Thr Gln Asn Trp Gln Ile Tyr Gln Ala Phe Gln Gly Leu Val Leu Tyr  
340 345 350

Tyr Glu Ser Cys Lys

355

<210> 45  
<211> 2243  
<212> DNA  
<213> human organism

<400> 45  
cggtgcctg gggtaata tccctacga atttaaccaa gcggacttta atgccactgt 60  
gcagttcatc caaaaccact tggatgacat ggatgtcaaa aagggtgtct cctggaccac  
catccgctac atgataggag agattcaata tggaggcaga gtcactgacg actatgataa 120  
gagattgtt aacacattt ctaaggttt gttcagtgaa aatatgtttt gaccagattt  
cagttttac caaggataca atattccaaa atgcagcaca gtggataact atcttcagta 180  
tatccagagt ttgcctgcct atgacagccc tgagggttt gggctgcacc ccaatgctga 240  
catcacctac cagagcaagc tggccaagga cgtgctggac accatcctag gcatccaacc  
caaggacacc tctggtggag gggatgagac ccgggaggcg gtggggccc ggctggctga 300  
tgatatgctg gagaagctgc ccccagacta tgtccccctt gaagtaaaag agaggctgca 360  
gaagatgggg ccattccagc ctatgaacat tttcctcagg caggaaatag acagaatgca 420  
aagggtactc agccttgtcc gcagcacccct cactgagctg aaacttgcta ttgatggcac  
catcatcatg agcgaaaatc tgcaagatgc attggattgc atgtttgcattt ctagaatccc 480  
tgcttggtgg aaaaaagctt cttgggttt tagtacactg ggtttctggg ttactgaact  
tatagaaaga aacagccagt ttacctcggt ggtttcaat ggccgaccc actgctttt 540  
gatgacgggt ttttttaacc cccaggatt ttaactgca atgcgacagg aaataactcg 600  
ggccaacaaa ggctgggctc tggacaatat ggtgcttgc aatgaagtca ccaaatggat  
gaaggacgac atttctaccc ctccccacaga ggggtctat gtctatggct tataatcttga 660  
aggtgctggc tgggacaaga ggaacatgaa actcattgaa tcaaagccaa aagtgtcttt  
tgagttgatg cctgtcataa ggatttatgc agaaaacaat actttacgag atcctcggtt 720  
ttactcctgt cccatctata agaagccagt tcgaacggac ttgaactaca ttgccgctgt  
ggatctcagg acagccaga cccctgaaca ctgggtgctc cgtggggttt cccttctgtg 780  
tgatgtcaag taacatgtgg ggagtgtccc cacccaatgc tttggaaaat gcaagatcta 840  
aattattgtt acctttatctt ctgtatgact gctggacagt gtatgttagg tcgtttatgc  
aattaatgag ctgcataatgtt tttccccact ccttaattgg atgcttatat tttacttgg 900  
1020  
1080  
1140  
1200  
1260  
1320  
1380  
1440

tcatcattag tgaccaatgt ctgagttgt tgaaaatgtt atttagtgat ataaaagtaa 1500  
atttacagca tcctaatgaa gtgtggccct caaatccaca gtagtatatt ttcttcttac 1560  
ttcgctccga agactgactg tgattataac agcaaataa tttgcattgtg gacaaagatt 1620  
agatggcaag atagaaaaat aagaacagat gtgatagcaa gaattatagt tggcttggaa 1680  
aaatgtgatg atcaggagaa aaaataaaaa aagggttagaa atattagacg gtgcgttaggg 1740  
actttctatg gacttttatt aattaggaaa cattatcaaa ggaacttttc acgtatTTT 1800  
ctttaaattc tggttagatg ttattaataa ttcttcatct aacctactga ctagaaaata 1860  
tagtcagtac taaatttagaa ttgtggTTTA taaaacttttgg gttagctctg gatctgtata 1920  
actgcatttt ttggataaaa cagttttgg taggtggata ccgggagaca agtgtgggtc 1980  
cctctcactg ggcttcattc tgtggaccag gatcatttt tcattgtcat gatcatgaga 2040  
gttaggactg agtggctcct gtgactcccc caatcttgc tgatactgtt ttcttgtgag 2100  
ttctttcttt tggtgtggat tagtatatca gttgatttgt gtgaattgtg gtgaaacaat 2160  
catttcattt tgaaaagcaa gtaatgaaaa tgcaggcatc ataggaattt ataaaatgtt 2220  
tttactaaaa aaaaaaaaaaaa aaa 2243

<210> 46  
<211> 394  
<212> PRT  
<213> human organism

<400> 46

Met Asp Val Lys Lys Gly Val Ser Trp Thr Thr Ile Arg Tyr Met Ile  
1 5 10 15

Gly Glu Ile Gln Tyr Gly Gly Arg Val Thr Asp Asp Tyr Asp Lys Arg  
20 25 30

Pro Asp Phe Ser Phe Tyr Gln Gly Tyr Asn Ile Pro Lys Cys Ser Thr  
           50                 55                         60

Val Asp Asn Tyr Leu Gln Tyr Ile Gln Ser Leu Pro Ala Tyr Asp Ser  
65 70 75 80

Pro Glu Val Phe Gly Leu His Pro Asn Ala Asp Ile Thr Tyr Gln Ser  
85 90 95

Lys Leu Ala Lys Asp Val Leu Asp Thr Ile Leu Gly Ile Gln Pro Lys  
100 105 110

Asp Thr Ser Gly Gly Asp Glu Thr Arg Glu Ala Val Val Ala Arg  
115 120 125

Leu Ala Asp Asp Met Leu Glu Lys Leu Pro Pro Asp Tyr Val Pro Phe  
130 135 140

Glu Val Lys Glu Arg Leu Gln Lys Met Gly Pro Phe Gln Pro Met Asn  
145 150 155 160

Ile Phe Leu Arg Gln Glu Ile Asp Arg Met Gln Arg Val Leu Ser Leu  
165 170 175

Val Arg Ser Thr Leu Thr Glu Leu Lys Leu Ala Ile Asp Gly Thr Ile  
180 185 190

Ile Met Ser Glu Asn Leu Gln Asp Ala Leu Asp Cys Met Phe Asp Ala  
195 200 205

Arg Ile Pro Ala Trp Trp Lys Lys Ala Ser Trp Val Phe Ser Thr Leu  
210 215 220

Gly Phe Trp Phe Thr Glu Leu Ile Glu Arg Asn Ser Gln Phe Thr Ser  
225 230 235 240

Trp Val Phe Asn Gly Arg Pro His Cys Phe Trp Met Thr Gly Phe Phe  
245 250 255

Asn Pro Gln Gly Phe Leu Thr Ala Met Arg Gln Glu Ile Thr Arg Ala  
260 265 270

Asn Lys Gly Trp Ala Leu Asp Asn Met Val Leu Cys Asn Glu Val Thr  
275 280 285

Lys Trp Met Lys Asp Asp Ile Ser Thr Pro Pro Thr Glu Gly Val Tyr  
290 295 300

Val Tyr Gly Leu Tyr Leu Glu Gly Ala Gly Trp Asp Lys Arg Asn Met

305                    310                    315                    320

Lys Leu Ile Glu Ser Lys Pro Lys Val Leu Phe Glu Leu Met Pro Val  
                   325                   330                   335

Ile Arg Ile Tyr Ala Glu Asn Asn Thr Leu Arg Asp Pro Arg Phe Tyr  
 340 345 350

Ser Cys Pro Ile Tyr Lys Lys Pro Val Arg Thr Asp Leu Asn Tyr Ile  
           355               360               365

Ala Ala Val Asp Leu Arg Thr Ala Gln Thr Pro Glu His Trp Val Leu  
370 375 380

Arg Gly Val Ala Leu Leu Cys Asp Val Lys  
385 390

<210> 47  
<211> 6041  
<212> DNA  
<213> human organism

<400> 47  
ggagcagcct acaacttcac aaccagaaaac cactaccctt caggggttgc tttcagataa 60  
agatgacatg ggaaggagaa atgctggcat agatttcgga tccagaaaaag catcagcagc  
acagcccata cctgaaaaca tggacaattc catggttagt gatccacaac cataccatga 120  
agatcagct tctggagctg agaagacaga agccagagct tctctcac tgatggtgg 180  
aagctttct acaacccaag aggaggccat tctctcagta gcagcagagg ctcaggtgtt 240  
tatgaatcct tctcatatcc agttagaaga tcaagaagct ttcagcttg atttacaaaa 300  
ggcccaatcc aaaatggagt cagcccagga tgttcaaact atctgcaaag aaaagccttc 360  
tggaaatgtt caccagacct ttacagcaag tgaaaaatgggtt atgacaagta ctacagccaa 420  
aggagatgtt tatgccaaga ctctgcctcc cagaagcctt tttcagtcctt caaggaagcc 480  
tgatgctgaa gaagtctcctt cagattcaga gaatattcctt gaggaggggg atggttctga 540  
agaactggct catggtcact cttcccagtc cttggggaaag tttgaagatg aacaagaagt 600  
cttctcagaa tcaaaaaagt ttgtttaggaa cttgagcagc tctgaggagg agctggacct 660  
cagatgcctc tcccaggctt tagaggagcc tgaagatgca gaagtcttca cagaatcaag 720  
catgttatgtt gaaaagtaca acacttctga tgattgcagc agctcagagg aagacctgcc 780  
840

tctcagacac cctgctcagg ccttgggaaa gccccaaaaac caacaagaag ttcctctgc 900  
ttcaaataat actcctgaag agcagaatga ttttatgcag cagctgcctt ccagatgcc 960  
ttctcagccc attatgaatc ctactgttca gcaacaagtc cccaccagtt cagtggcac 1020  
ttctataaaa cagagcgatt ccgtggagcc aatccctcca agacaccctt tccagccatg 1080  
ggtaaccct aaagtggagc aagaagttc ctcatctcca aagagcatgg ctgttgaaga 1140  
gagcatttct atgaagcctc tgccctctaa acttcttgc cagcccttga tgaatcctaa 1200  
agttcaacaa aacatgttct caggttcaga ggacattgct gttgagagag tcatttctgt 1260  
ggagccacta ctccccagat atttcctca gtccttgaca gatcctcaaa tccggcaaat 1320  
ctcagaaagc acagctgttgc aggaaggcac ttatgtggaa ccgctgcctc ccagatgcct 1380  
ttcccgccc tcggagaggc ctaagttcct ggactcaatg agtacttctg cagaatggag 1440  
cagtcctgtg gcaccaacac ctccaaata cactccccg ccatgggtga cccctaaatt 1500  
tgaggaactg tatcaactct ctgcacatcc agaaagcact actgttgaag aggacattc 1560  
taaggagcag ctgcttccca gacatcttc ccagttgact gtgggaaata aagtccagca 1620  
actgtcctca aatttcgagc gggctgctat tgagggcagac atttctggga gtccattgcc 1680  
tccccaatat gctaccagt tcttaaagag gtctaaagtt cagggaaatga cctcacgact 1740  
agagaaaatg gctgttgaag gcacttctaa caaatcaccg attcccgagc gtccgacc 1800  
gtcattcgtg aaatttatgg cacagcaaat ctttcagag agctctgctc ttaagagggg 1860  
cagtgtatgtg gcacccctgc ctcccaatct tccttccaaa tctttatcaa agcctgaagt 1920  
caagcaccaa gtttctcag attcagggag tgctaattcct aagggaggca tttctcaaa 1980  
gatgctacct atgaagcacc cttaacagtc ctggggagg cctgaagacc cacagaaagt 2040  
tttctcttat tcagagagag ctccctggaa gtgcagcagt tttaaagagc agctgtctcc 2100  
caggcagctt tcccaggcct tgagggaaacc tgagtatgag caaaaagttt cccctgtttc 2160  
tgccagttct cctaaagagt ggaggaattc taaaaagcag ctgcctccca aacattctc 2220  
ccaaggcctca gataggctca aattccagcc acagatgtca tcaaaggccc cagtaatgt 2280  
acctgttaaag cagagcagcg gtgagaagca cctgccttca agtagtcctt tccagcaaca 2340  
ggttcattca agttctgtga atgctgctgc taggcgatct gttttgaga gcaattctga 2400  
caattggttc ctaggaagag atgaagctt tgcaatcaaa accaagaaat tcagccaagg 2460  
ttccaaaaac cccataaaaga gcattccagc ccctgctacc aaacctggga agttcaccat 2520  
tgctcctgtc aggcaaacat ccacttctgg gggcatttac tctaagaaag aagatcttga 2580

gagtggtgat ggtaataata accagcatgc aaaccttatcc aatcaggatg atgttggaaa 2640  
gcttttgga gttcgactga aaagagcccc tccctcgag aagtataaga gtgagaaaca 2700  
agataacttc acccagcttgc ttcaagtgc ctcggccca atttcattcct ctgttaggcag 2760  
gggacataaa atcagaagca cttcccaggg gtcctggat gctgcaggga acctcaccaa 2820  
aatatcttac gttgcagata agcaacagag caggccaaa tctgaaagca tggccaagaa 2880  
gcaacctgct tgcaagaccc cagggaaagcc tgctggtcaa cagtcagatt atgctgtctc 2940  
agagccggtt tggataacta tggcaaagca gaagcagaag agtttcaagg cccacatttc 3000  
tgtgaaagag ctgaaaacta agagcaatgc tggagccat gctgagacta aggaggctaa 3060  
atatgagggg gctggctctg caaatgaaaaa ccaacctaataa aagatgttca cttccagtgt 3120  
ccataaacag gagaagacag cacagatgaa gccacctaag cctacaaaat cagttggatt 3180  
tgaagctcag aagataactgc aagttcctgc catggaaaaa gaaaccaaacc gatcttcaac 3240  
tctcccagcc aagttccaga acccagttga gccaatttagg cctgtctgg tctcactggc 3300  
caggaagaaa gccaaagcat ggagccacat ggcagaaatc acgcaataaa gagctttgt 3360  
gtggagcatc agcatttatt ttattnattt tttttttttt tttttttttt gagacagagt 3420  
ctcgctctgt tacccagatt ggagtgcagt ggcgcgatct ccgctcactg caagctccgc 3480  
ctcccggtt cacgccactc tccgcctca gtctccgac tagctggac tacaggcgcc 3540  
cgccatcactg cccggctaat ttgtttcg tatttttagt agagacgggg tttcaccatg 3600  
ttggccagga tggcttgat ctccgtacct cgtatccgc ccgcctcagc ctcccaaag 3660  
ctgggattac aggcgtgagc caccgcgccc ggcacgat cagcgtttta aatgataatt 3720  
gctaatacgat gtattaattc tatgttagtga tcttttact gtgaccactt gtattaagca 3780  
aaataagtat taagcaaaact aagaatttat taagcaaaat aagaatttat taagcaaaat 3840  
agccttagaa atgcaaaatta aaacataatt atttgaatga aataaatgcc atgaatgctt 3900  
aaccttccac gtagtcactg ccagcacccca gaaacccagc atttcctcta taaaaactat 3960  
cgaaaacatt tgcactgctg taaaattgca aaatcttaa cttggacaa tgtgcttttag 4020  
aagggagaaa gcaaaaacat ttgtttggag caactagaaa attgtcattt ccctcaacca 4080  
aataaaagtaa ttctaatgga aacattcaga tgatttgacc taaagattgg cctttaggtt 4140  
ttatgagcct agatagatgc cgcaattttt tgggttgtgc tctaagctt gcaagggatc 4200  
ctaaaagagg cggtggaagt gaaaattctg ggtctccaag aaaatttctg cacagccagt 4260

tctccaatca gccttatcacc cttgaaaca tcttccctgt gtccctgggg gcccctgatg 4320  
ctttctcctt gggtgatagt aacatgcaga gcacttacac aaagctccct ctttggacat 4380  
accccacgtc gacctgtcac aggctggct gtagcgagca cttccctatg acgcagaatg 4440  
cttcttggga attatcttac tcctctggag gtttagtcca tcaatgtttt gtttcttgc 4500  
ccaatactac tgtgaccctc tctgatcgca cagaaatcac tgcctatcac atatatcctg 4560  
ttaaggactg aagaccctat tgaaattaga gttctacaga tgccaaaagc tgtactttcc 4620  
atcaggcaga tggcaagctt actgccttga tgcacatctg gagccactgg agctccttcc 4680  
tctctggttc cagcattaag gtggagaact ccatgttagct tcttgcctt tcccctcagc 4740  
tgtctttgct tcacaagggtt ttagcccaa gcaagagtgc aatcccaaag ccacagagaa 4800  
atgaactttc cgctacctgg aagcttaag tgagtaaatac agctttccc ctctcattcc 4860  
tagaggcaca cacctcaaaa gttacttaggc tggagagacc ctaccttcca gtgaccact 4920  
catcccccaag ccacggagaa gagggaagac caaaaaggga gagtgagaaa gaggatgaga 4980  
gggatggtca gctgtgaggg gagggggcaa gtggcccagc aaatgttgc gctcccttc 5040  
ccatcttgc acacggtctt ttcttttgc agcacagcct ccattaataa ctctcggct 5100  
gaggatgaag atgttaggcac cttaaaaaa agagccagtt ccttaattgg ctggctttct 5160  
gagatgcaga ccaccctaga atctcatcta ggttcaactag aagttagtta aatcttcctt 5220  
tctctgtctt tctcttcatt ccatccccca aacccaccaa acactaaggg agagctccct 5280  
ttggatgtct gggcagtaaa cctagctcat tttcttagga gacccagaag tgacttctga 5340  
gtagttatca ctgtgtctgc ctctgttaca ctgtgtctgct ttgcttaaac agaaatgcag 5400  
gcctggacat ctgactgtgc cttaatattc tgagtgggt gctggcccat gaaaaaaaaat 5460  
ccagagaggt agtgagggtc cagagctaaa cacttggtgc tgggtttgt tgatgttgt 5520  
ataatgtgac acagtacaat tacatgctaa atttgcatt ttctctatata aacatctatt 5580  
tttcctgata ctgtgcctt gccatttga taatgttatt ttgattgagt gaattttatt 5640  
tcctttgtat tcccatagtg aacaatataa taaggtagat gccctttatc tggtaactcc 5700  
tggttagatta gctgttacac ctcccttccc tttttacag tgaacctgta ttcatgttatt 5760  
gtcactctga gaactctcca ataacaattt ctttccaca gttaacaaca cagctgttac 5820  
acctcccttc ctttttca cagtgaacct gtattcagct attctcactc tgagaactct 5880  
ccaataacaa tttctttcc acagttaca acaaagttct gttttaaat gaagagatta 5940  
agttctttt aaatgcctaa aggcatattc tgacaacttt tctacttctt taacttttt 6000

gatttaagat atatgcaaag caaataaaatt caataaaagcc t

6041

<210> 48  
<211> 1115  
<212> PRT  
<213> human organism

<400> 48

Glu Gln Pro Thr Thr Ser Gln Pro Glu Thr Thr Thr Pro Gln Gly Leu  
1 5 10 15

Leu Ser Asp Lys Asp Asp Met Gly Arg Arg Asn Ala Gly Ile Asp Phe  
20 25 30

Gly Ser Arg Lys Ala Ser Ala Ala Gln Pro Ile Pro Glu Asn Met Asp  
35 40 45

Asn Ser Met Val Ser Asp Pro Gln Pro Tyr His Glu Asp Ala Ala Ser  
50 55 60

Gly Ala Glu Lys Thr Glu Ala Arg Ala Ser Leu Ser Leu Met Val Glu  
65 70 75 80

Ser Leu Ser Thr Thr Gln Glu Glu Ala Ile Leu Ser Val Ala Ala Glu  
85 90 95

Ala Gln Val Phe Met Asn Pro Ser His Ile Gln Leu Glu Asp Gln Glu  
100 105 110

Ala Phe Ser Phe Asp Leu Gln Lys Ala Gln Ser Lys Met Glu Ser Ala  
115 120 125

Gln Asp Val Gln Thr Ile Cys Lys Glu Lys Pro Ser Gly Asn Val His  
130 135 140

Gln Thr Phe Thr Ala Ser Val Leu Gly Met Thr Ser Thr Thr Ala Lys  
145 150 155 160

Gly Asp Val Tyr Ala Lys Thr Leu Pro Pro Arg Ser Leu Phe Gln Ser  
165 170 175

Ser Arg Lys Pro Asp Ala Glu Glu Val Ser Ser Asp Ser Glu Asn Ile  
180 185 190

Pro Glu Glu Gly Asp Gly Ser Glu Glu Leu Ala His His Ser Ser  
195 200 205

Gln Ser Leu Gly Lys Phe Glu Asp Glu Gln Glu Val Phe Ser Glu Ser  
210 215 220

Lys Ser Phe Val Glu Asp Leu Ser Ser Ser Glu Glu Glu Leu Asp Leu  
225 230 235 240

Arg Cys Leu Ser Gln Ala Leu Glu Glu Pro Glu Asp Ala Glu Val Phe  
245 250 255

Thr Glu Ser Ser Ser Tyr Val Glu Lys Tyr Asn Thr Ser Asp Asp Cys  
260 265 270

Ser Ser Ser Glu Glu Asp Leu Pro Leu Arg His Pro Ala Gln Ala Leu  
275 280 285

Gly Lys Pro Lys Asn Gln Gln Glu Val Ser Ser Ala Ser Asn Asn Thr  
290 295 300

Pro Glu Glu Gln Asn Asp Phe Met Gln Gln Leu Pro Ser Arg Cys Pro  
305 310 315 320

Ser Gln Pro Ile Met Asn Pro Thr Val Gln Gln Val Pro Thr Ser  
325 330 335

Ser Val Gly Thr Ser Ile Lys Gln Ser Asp Ser Val Glu Pro Ile Pro  
340 345 350

Pro Arg His Pro Phe Gln Pro Trp Val Asn Pro Lys Val Glu Gln Glu  
355 360 365

Val Ser Ser Ser Pro Lys Ser Met Ala Val Glu Glu Ser Ile Ser Met  
370 375 380

Lys Pro Leu Pro Pro Lys Leu Leu Cys Gln Pro Leu Met Asn Pro Lys  
385 390 395 400

Val Gln Gln Asn Met Phe Ser Gly Ser Glu Asp Ile Ala Val Glu Arg  
405 410 415

Val Ile Ser Val Glu Pro Leu Leu Pro Arg Tyr Ser Pro Gln Ser Leu  
420 425 430

Thr Asp Pro Gln Ile Arg Gln Ile Ser Glu Ser Thr Ala Val Glu Glu  
435 440 445

Gly Thr Tyr Val Glu Pro Leu Pro Pro Arg Cys Leu Ser Gln Pro Ser  
450 455 460

Glu Arg Pro Lys Phe Leu Asp Ser Met Ser Thr Ser Ala Glu Trp Ser  
465 470 475 480

Ser Pro Val Ala Pro Thr Pro Ser Lys Tyr Thr Ser Pro Pro Trp Val  
485 490 495

Thr Pro Lys Phe Glu Glu Leu Tyr Gln Leu Ser Ala His Pro Glu Ser  
500 505 510

Thr Thr Val Glu Glu Asp Ile Ser Lys Glu Gln Leu Pro Arg His  
515 520 525

Leu Ser Gln Leu Thr Val Gly Asn Lys Val Gln Gln Leu Ser Ser Asn  
530 535 540

Phe Glu Arg Ala Ala Ile Glu Ala Asp Ile Ser Gly Ser Pro Leu Pro  
545 550 555 560

Pro Gln Tyr Ala Thr Gln Phe Leu Lys Arg Ser Lys Val Gln Glu Met  
565 570 575

Thr Ser Arg Leu Glu Lys Met Ala Val Glu Gly Thr Ser Asn Lys Ser  
580 585 590

Pro Ile Pro Arg Arg Pro Thr Gln Ser Phe Val Lys Phe Met Ala Gln  
595 600 605

Gln Ile Phe Ser Glu Ser Ser Ala Leu Lys Arg Gly Ser Asp Val Ala  
610 615 620

Pro Leu Pro Pro Asn Leu Pro Ser Lys Ser Leu Ser Lys Pro Glu Val  
625 630 635 640

Lys His Gln Val Phe Ser Asp Ser Gly Ser Ala Asn Pro Lys Gly Gly  
645 650 655

Ile Ser Ser Lys Met Leu Pro Met Lys His Pro Leu Gln Ser Leu Gly  
660 665 670

Arg Pro Glu Asp Pro Gln Lys Val Phe Ser Tyr Ser Glu Arg Ala Pro  
675 680 685

Gly Lys Cys Ser Ser Phe Lys Glu Gln Leu Ser Pro Arg Gln Leu Ser  
690 695 700

Gln Ala Leu Arg Lys Pro Glu Tyr Glu Gln Lys Val Ser Pro Val Ser  
705 710 715 720

Ala Ser Ser Pro Lys Glu Trp Arg Asn Ser Lys Lys Gln Leu Pro Pro  
725 730 735

Lys His Ser Ser Gln Ala Ser Asp Arg Ser Lys Phe Gln Pro Gln Met  
740 745 750

Ser Ser Lys Gly Pro Val Asn Val Pro Val Lys Gln Ser Ser Gly Glu  
755 760 765

Lys His Leu Pro Ser Ser Pro Phe Gln Gln Gln Val His Ser Ser  
770 775 780

Ser Val Asn Ala Ala Ala Arg Arg Ser Val Phe Glu Ser Asn Ser Asp  
785 790 795 800

Asn Trp Phe Leu Gly Arg Asp Glu Ala Phe Ala Ile Lys Thr Lys Lys  
805 810 815

Phe Ser Gln Gly Ser Lys Asn Pro Ile Lys Ser Ile Pro Ala Pro Ala  
820 825 830

Thr Lys Pro Gly Lys Phe Thr Ile Ala Pro Val Arg Gln Thr Ser Thr  
835 840 845

Ser Gly Gly Ile Tyr Ser Lys Lys Glu Asp Leu Glu Ser Gly Asp Gly  
850 855 860

Asn Asn Asn Gln His Ala Asn Leu Ser Asn Gln Asp Asp Val Glu Lys

865	870	875	880
Leu Phe Gly Val Arg Leu Lys Arg Ala Pro Pro Ser Gln Lys Tyr Lys			
	885	890	895
Ser Glu Lys Gln Asp Asn Phe Thr Gln Leu Ala Ser Val Pro Ser Gly			
	900	905	910
Pro Ile Ser Ser Ser Val Gly Arg Gly His Lys Ile Arg Ser Thr Ser			
	915	920	925
Gln Gly Leu Leu Asp Ala Ala Gly Asn Leu Thr Lys Ile Ser Tyr Val			
	930	935	940
Ala Asp Lys Gln Gln Ser Arg Pro Lys Ser Glu Ser Met Ala Lys Lys			
	945	950	955
960			
Gln Pro Ala Cys Lys Thr Pro Gly Lys Pro Ala Gly Gln Gln Ser Asp			
	965	970	975
Tyr Ala Val Ser Glu Pro Val Trp Ile Thr Met Ala Lys Gln Lys Gln			
	980	985	990
Lys Ser Phe Lys Ala His Ile Ser Val Lys Glu Leu Lys Thr Lys Se			
	995	1000	1005
Lys			
Asn Ala Gly Ala Asp Ala Glu Thr Lys Glu Pro Lys Tyr Glu Gly			
	1010	1015	1020
Ala Gly Ser Ala Asn Glu Asn Gln Pro Lys Lys Met Phe Thr Ser			
	1025	1030	1035
Ser Val His Lys Gln Glu Lys Thr Ala Gln Met Lys Pro Pro Lys			
	1040	1045	1050
Pro Thr Lys Ser Val Gly Phe Glu Ala Gln Lys Ile Leu Gln Val			
	1055	1060	1065
Pro Ala Met Glu Lys Glu Thr Lys Arg Ser Ser Thr Leu Pro Ala			
	1070	1075	1080
Lys Phe Gln Asn Pro Val Glu Pro Ile Glu Pro Val Trp Phe Ser			
	1085	1090	1095

Leu Ala Arg Lys Lys Ala Lys Ala Trp Ser His Met Ala Glu Ile  
1100 1105 1110

Thr Gln  
1115

<210> 49  
<211> 5976  
<212> DNA  
<213> human organism

<400> 49  
gcttccttt ctaaagtaga agaggatgat tatccctctg aagaactact agaggatgaa 60  
aacgctataa atgcaaaaacg gtctaaagaa aaaaaccctg ggaatcaggg caggcagtt 120  
gatgttaatc tgcaagtccc tgacagagca gttttaggga ccattcatcc agatccagaa 180  
attgaagaaa gcaagcaaga aactagtatg attttggata gtaaaaaaac aagtgagact 240  
gctgccaaag gggtcaacac aggaggcagg gaaccaaata caatggtgaa aaaagaacgc 300  
cctctggcag ataagaaaac acagagacca tttgaacgaa gtgacttttc tgacagcata 360  
aaaattcaga ctccagaatt aggtgaagtg tttcagaata aagattctga ttatctgaag 420  
aacgacaacc ctgaggaaca tctgaagacc tcagggcttg caggggagcc tgagggagaa 480  
ctctcaaaag aggaccatgg gaacacagag aagtacatgg gcacagaaag ccaggggtct 540  
gctgctgcag aacctgaaga tgactcggttc cactggactc cacatacaag tgtagagcca 600  
ggccatagtg acaagaggaa ggacttactt atcataagca gcttctttaa agaacaacag 660  
tctttgcagc ggttccagaa gtacttaat gtccatgagc tggaaagcctt gctacaagaa 720  
atgtcatcaa aactgaagtc agcgcagcag gagagcctgc cctataatat ggaaaaagtc 780  
ctagataagg tcttccgtgc ttctgagtca caaattctga gcatagcaga aaaaatgctt 840  
gatactcgtg tggctgaaaa tagagatctg ggaatgaacg aaaataacat atttgaagag 900  
gctgcagtgc ttgatgacat tcaagacctc atctatgg tcaggtacaa gcactccaca 960  
gcagaggaga cagccacact ggtgatggca ccaccccttag aggaaggctt gggggagca 1020  
atggaagaga tgcaaccact gcatgaagat aatttctcac gagagaagac agcagaactt 1080  
aatgtgcagg ttccctgaaga acccaccac ttggaccaac gtgtgattgg ggacactcat 1140  
gcctcagaag tgtcacagaa gccaaatact gagaaagacc tggacccagg gccagttaca 1200  
acagaagaca ctcctatgga tgctattgat gcaaacaagc aaccagagac agccgcccga 1260

gagccggcaa gtgtcacacc tttggaaaac gcaatccttc taatatattc attcatgttt 1320  
tattaacta agtcgctagt tgctacattg cctgatgatg ttcaagcctgg gcctgatttt 1380  
tatggactgc catggaaacc tgtatattatc actgccttct tgggaattgc ttcgttgcc 1440  
attttcttat ggagaactgt ccttggatgt aaggatagag tataatcaagt cacggaacag 1500  
caaatttctg agaagttgaa gactatcatg aaagaaaata cagaacttgt aaaaaattg 1560  
tcaaattatg aacagaagat caaggaatca aagaaacatg ttcaggaaac cagggaaacaa 1620  
aatatgattc tctctgatga agcaattaaa tataaggata aaatcaagac acttgaaaaaa 1680  
aatcaggaaa ttctggatga cacagctaaa aatcttcgtg ttatgctaga atctgagaga 1740  
gaacagaatg tcaagaatca ggacttgata tcagaaaaca agaaatctat agagaagtta 1800  
aaggatgtta tttcaatgaa tgccctagaa ttttcagagg ttcagattgc acttaatgaa 1860  
gctaagctta gtgaagagaa ggtgaagtct gaatgccatc gggttcaaga agaaaatgct 1920  
aggcttaaga agaaaaaaga gcagttgcag cagggaaatcg aagactggag taaattacat 1980  
gctgagctca gtgagcaaat caaatcattt gagaagtctc agaaagattt ggaagtagct 2040  
cttactcaca aggatgataa tattaatgct ttgactaact gcattacaca gttgaatctg 2100  
ttagagtgtg aatctgaatc tgagggtcaa aataaagggtg gaaatgattc agatgaatta 2160  
gcaaatggag aagtggggagg tgaccggaat gagaagatga aaaatcaaataa taagcagatg 2220  
atggatgtct ctggacaca gactgcaata tcggtagttg aagaggatct aaagctttta 2280  
cagcttaagc taagagcctc cgtgtccact aaatgttaacc tggaaagacca ggtaaaagaaaa 2340  
ttggaagatg accgcaactc actacaagct gccaaagctg gactggaaaga tgaatgcaaa 2400  
accttgaggc agaaaagtggaa gattctgaat gagctctatc agcagaagga gatggctttg 2460  
caaaaagaaa tgagtcaaga agagtatgaa cggcaagaaa gagagcacag gctgtcagct 2520  
gcagatgaaa aggcaagtttc ggctgcagag gaagtaaaaaa cttacaagcg gagaattgaa 2580  
gaaatggagg atgaattaca gaagacagag cggtcattta aaaaccagat cgctacccat 2640  
gagaagaaaatg ctcataaaaa ctggctcaaa gctcgtgctg cagaaagagc tataatgaa 2700  
gagaaaagg aagctgccaat tttgagacac aaattatttag aattaacaca aaagatggca 2760  
atgctgcaag aagaacctgt gattgtaaaa ccaatgccag gaaaacccaaa tacacaaaac 2820  
cctccacgga gaggtccctct gagccagaat ggcttttg gcccattcccc tgtgagtgg 2880  
ggagaatgct cccctccatt gacagtggag ccacccgtga gacctctctc tgctactctc 2940

aatcgaagag atatgcctag aagtgaattt ggatcagtgg acggggcctct acctcatcct 3000  
cgatggtcag ctgaggcatac tggaaaccc tctccttctg atccaggatc tggtagact 3060  
accatgatga acagcagctc aagaggctct tcccctacca ggtactcga tgaaggcaag 3120  
gttaatatgg ctccaaaagg gccccctcct ttcccaggag tccctctcat gagcaccccc 3180  
atggaggcc ctgtaccacc acccattcga tatggaccac cacctcagct ctgcggac 3240  
tttggcctc ggccacttcc tccacccttt ggccctggta tgcgtccacc actaggctt 3300  
agagaatttg caccaggcgt tccaccagga agacgggacc tgccctcca ccctcgggga 3360  
ttttacctg gacacgcacc atttagacct ttaggtcac ttggcccaag agagtactt 3420  
attcctggta cccgattacc acccccaacc catggcccc agaataaccc accaccac 3480  
gctgtaagag acttactgcc gtcaggctct agagatgagc ctccacctgc ctctcagagc 3540  
actagccagg actgttcaca ggcttaaaa cagagccat aaaactatga cctctgaggt 3600  
ttcattggaa agaaagtgtt ctgtgcatta tccattacag taaaggattt cattggctc 3660  
aaaaatccaaa agtttatttt aaaaggtttt ttgttagaac taagctgcct tggcagtgtg 3720  
cattttgag ccaaacaatt caaaaatgtc atttcttccc taaataaaaaa tcaccttta 3780  
agctagagcg tccttacaac ttgaaatgt gcaataaaga atacctgtgt ttagcta 3840  
gtagcatatg taattgcaaa atgattttaga atgtcatgaa aaatatgaac atttcctgtg 3900  
gaaatgctt aagaacatgt atttccatta tcctatttt agtgtacacc agctgaatac 3960  
ggagcaatgg tgtttataag cgtttttta aactatctgg tcacaaagac tggtacgcta 4020  
aaaatgttta ctaaaagatc actaaactat ctccctctt gctgaagttc ttgttagtaa 4080  
tagctcataa aaatttgtt attaatattt cccaaatgtc tggtgactca ttggactgtt 4140  
atgaggctt tgccatttgg ggaacatgtt aactcaggct cccagaactg aagatggtgg 4200  
ctgggtgcac acttccggct gtcctccgt cacatgtgaa ctctacaagt gatgttttt 4260  
tatttcaaag aagtttattt cccacttgc tagcattcac atgcttctt tacgatcctc 4320  
attgtctatt tgagaatggt ttctgagag tgagttaca ttagtagcaa gagttgtttg 4380  
acctgatgtt ccattgtttt taccattcct gtagaaaaag ggtgcacaac agaaaaatga 4440  
aaatgatgtg tcatggccat aaaagtatag aaatctttaa aaattttaaa atgtacagtc 4500  
ccttatctat cttccatt cttgccact gatTTTgag gaatataataaaaagattgg 4560  
aagagtataa tgccatgaga aagaatgatt taggactgtg agggttataa catgccctag 4620  
gtcagcaacc aagggttgaa atcagttctg ttttaggggg aaatgggggg ggcgacagat 4680

attattccaa aattaatatt aattaatatt taaacgttgg tgttttatt taaaaatcg	4740
taactaacca tctggaattt caccatactt aaagtcttat ccattactac actgtctta	4800
aaacaatgtt tctttaataa ctctacaacg tttctaagaa cgaacttcag acattttaat	4860
tacagtaata atagcactcc ttttaaggag tttcagatcc acactaaaac taaaatcata	4920
aaaggctgat acttttgtt gctgcttaggc tatattcttc cattcttga agtcctatga	4980
tgtaatattt ttgaaaccta gtgtatgtct tgcactgtt gtgatattta atcgattaag	5040
aataccttgt aaaaaggagc aaaagcttca atgtgaaaca attttctctc tttatactaa	5100
acaactgaag atagatagtt tagaaagata aggaccttg aaagaagaca actctgtcaa	5160
agttcataag gaatataaaa attctcagg aaaagagaat tcaatctata tgtcctcccg	5220
tttaatatca agaatagaag aaattaagag gaaaactcca cagaagagca taggccactt	5280
ttagccatgt aaaaataaga ttaagtcaca aatacaactt ttgaatttac ctgtcaatat	5340
ctcttagga cacaaaacaa tgctgaagtt aatataattt ctaattttaa atgtcattta	5400
agttagatt atgccatcta ggaaggtaag taggaaaggt aaattaaatc tattttaaa	5460
attcaaaata ttagagtatt ttccccctct aaagcctttt ttgggtgatta ttctgtatct	5520
gacataattt agaaactggt aagctgtaaa gattccagtg tagttctct gagaagttgt	5580
gagccagtcataactgctt cctcacatcc atctgattgc accattctg cagcaaaccc	5640
caaagcaggg tgccaatatg cagatggcat agggagtatc atccctcagc caaatcactt	5700
ttccatctct aaagtttcat ctattttggaa agtcatctcc aactaattgt gtctggattt	5760
agttgctaaa attgtcttat ttatattatga agcagcaata ttcagcctga aagcatttct	5820
gccatagttg ttgttagttat atcgccaatg gctgattttt ttcattggaa agtaaattta	5880
agtaattcgt gggatgtggt atattctgtg tcaacttcaa gataatcact catttctcg	5940
ttatattcag gtctgaatta aagttaagtt aatcac	5976

<210> 50  
 <211> 1193  
 <212> PRT  
 <213> human organism  
  
 <400> 50

Ala Phe Leu Ser Lys Val Glu Glu Asp Asp Tyr Pro Ser Glu Glu Leu  
 1 5 10 15

Leu Glu Asp Glu Asn Ala Ile Asn Ala Lys Arg Ser Lys Glu Lys Asn  
20 25 30

Pro Gly Asn Gln Gly Arg Gln Phe Asp Val Asn Leu Gln Val Pro Asp  
35 40 45

Arg Ala Val Leu Gly Thr Ile His Pro Asp Pro Glu Ile Glu Glu Ser  
50 55 60

Lys Gln Glu Thr Ser Met Ile Leu Asp Ser Glu Lys Thr Ser Glu Thr  
65 70 75 80

Ala Ala Lys Gly Val Asn Thr Gly Gly Arg Glu Pro Asn Thr Met Val  
85 90 95

Glu Lys Glu Arg Pro Leu Ala Asp Lys Lys Ala Gln Arg Pro Phe Glu  
100 105 110

Arg Ser Asp Phe Ser Asp Ser Ile Lys Ile Gln Thr Pro Glu Leu Gly  
115 120 125

Glu Val Phe Gln Asn Lys Asp Ser Asp Tyr Leu Lys Asn Asp Asn Pro  
130 135 140

Glu Glu His Leu Lys Thr Ser Gly Leu Ala Gly Glu Pro Glu Gly Glu  
145 150 155 160

Leu Ser Lys Glu Asp His Gly Asn Thr Glu Lys Tyr Met Gly Thr Glu  
165 170 175

Ser Gln Gly Ser Ala Ala Ala Glu Pro Glu Asp Asp Ser Phe His Trp  
180 185 190

Thr Pro His Thr Ser Val Glu Pro Gly His Ser Asp Lys Arg Glu Asp  
195 200 205

Leu Leu Ile Ile Ser Ser Phe Phe Lys Glu Gln Gln Ser Leu Gln Arg  
210 215 220

Phe Gln Lys Tyr Phe Asn Val His Glu Leu Glu Ala Leu Leu Gln Glu  
225 230 235 240

Met Ser Ser Lys Leu Lys Ser Ala Gln Gln Glu Ser Leu Pro Tyr Asn

245

250

255

Met Glu Lys Val Leu Asp Lys Val Phe Arg Ala Ser Glu Ser Gln Ile  
260 265 270

Leu Ser Ile Ala Glu Lys Met Leu Asp Thr Arg Val Ala Glu Asn Arg  
275 280 285

Asp Leu Gly Met Asn Glu Asn Asn Ile Phe Glu Glu Ala Ala Val Leu  
290 295 300

Asp Asp Ile Gln Asp Leu Ile Tyr Phe Val Arg Tyr Lys His Ser 'Thr  
305 310 315 320

Ala Glu Glu Thr Ala Thr Leu Val Met Ala Pro Pro Leu Glu Glu Gly  
325 330 335

Leu Gly Gly Ala Met Glu Glu Met Gln Pro Leu His Glu Asp Asn Phe  
340 345 350

Ser Arg Glu Lys Thr Ala Glu Leu Asn Val Gln Val Pro Glu Glu Pro  
355 360 365

Thr His Leu Asp Gln Arg Val Ile Gly Asp Thr His Ala Ser Glu Val  
370 375 380

Ser Gln Lys Pro Asn Thr Glu Lys Asp Leu Asp Pro Gly Pro Val Thr  
385 390 395 400

Thr Glu Asp Thr Pro Met Asp Ala Ile Asp Ala Asn Lys Gln Pro Glu  
405 410 415

Thr Ala Ala Glu Glu Pro Ala Ser Val Thr Pro Leu Glu Asn Ala Ile  
420 425 430

Leu Leu Ile Tyr Ser Phe Met Phe Tyr Leu Thr Lys Ser Leu Val Ala  
435 440 445

Thr Leu Pro Asp Asp Val Gln Pro Gly Pro Asp Phe Tyr Gly Leu Pro  
450 455 460

Trp Lys Pro Val Phe Ile Thr Ala Phe Leu Gly Ile Ala Ser Phe Ala  
465 470 475 480

Ile Phe Leu Trp Arg Thr Val Leu Val Val Lys Asp Arg Val Tyr Gln  
485 490 495

Val Thr Glu Gln Gln Ile Ser Glu Lys Leu Lys Thr Ile Met Lys Glu  
500 505 510

Asn Thr Glu Leu Val Gln Lys Leu Ser Asn Tyr Glu Gln Lys Ile Lys  
515 520 525

Glu Ser Lys Lys His Val Gln Glu Thr Arg Lys Gln Asn Met Ile Leu  
530 535 540

Ser Asp Glu Ala Ile Lys Tyr Lys Asp Lys Ile Lys Thr Leu Glu Lys  
545 550 555 560

Asn Gln Glu Ile Leu Asp Asp Thr Ala Lys Asn Leu Arg Val Met Leu  
565 570 575

Glu Ser Glu Arg Glu Gln Asn Val Lys Asn Gln Asp Leu Ile Ser Glu  
580 585 590

Asn Lys Lys Ser Ile Glu Lys Leu Lys Asp Val Ile Ser Met Asn Ala  
595 600 605

Ser Glu Phe Ser Glu Val Gln Ile Ala Leu Asn Glu Ala Lys Leu Ser  
610 615 620

Glu Glu Lys Val Lys Ser Glu Cys His Arg Val Gln Glu Glu Asn Ala  
625 630 635 640

Arg Leu Lys Lys Lys Glu Gln Leu Gln Gln Glu Ile Glu Asp Trp  
645 650 655

Ser Lys Leu His Ala Glu Leu Ser Glu Gln Ile Lys Ser Phe Glu Lys  
660 665 670

Ser Gln Lys Asp Leu Glu Val Ala Leu Thr His Lys Asp Asp Asn Ile  
675 680 685

Asn Ala Leu Thr Asn Cys Ile Thr Gln Leu Asn Leu Glu Cys Glu  
690 695 700

Ser Glu Ser Glu Gly Gln Asn Lys Gly Gly Asn Asp Ser Asp Glu Leu  
705 710 715 720

Ala Asn Gly Glu Val Gly Gly Asp Arg Asn Glu Lys Met Lys Asn Gln  
725 730 735

Ile Lys Gln Met Met Asp Val Ser Arg Thr Gln Thr Ala Ile Ser Val  
740 745 750

Val Glu Glu Asp Leu Lys Leu Leu Gln Leu Lys Leu Arg Ala Ser Val  
755 760 765

Ser Thr Lys Cys Asn Leu Glu Asp Gln Val Lys Lys Leu Glu Asp Asp  
770 775 780

Arg Asn Ser Leu Gln Ala Ala Lys Ala Gly Leu Glu Asp Glu Cys Lys  
785 790 800

Thr Leu Arg Gln Lys Val Glu Ile Leu Asn Glu Leu Tyr Gln Gln Lys  
805 810 815

Glu Met Ala Leu Gln Lys Lys Leu Ser Gln Glu Glu Tyr Glu Arg Gln  
820 825 830

Glu Arg Glu His Arg Leu Ser Ala Ala Asp Glu Lys Ala Val Ser Ala  
835 840 845

Ala Glu Glu Val Lys Thr Tyr Lys Arg Arg Ile Glu Glu Met Glu Asp  
850 855 860

Glu Leu Gln Lys Thr Glu Arg Ser Phe Lys Asn Gln Ile Ala Thr His  
865 870 875 880

Glu Lys Lys Ala His Glu Asn Trp Leu Lys Ala Arg Ala Ala Glu Arg  
885 890 895

Ala Ile Ala Glu Glu Lys Arg Glu Ala Ala Asn Leu Arg His Lys Leu  
900 905 910

Leu Glu Leu Thr Gln Lys Met Ala Met Leu Gln Glu Glu Pro Val Ile  
915 920 925

Val Lys Pro Met Pro Gly Lys Pro Asn Thr Gln Asn Pro Pro Arg Arg  
930 935 940

Gly Pro Leu Ser Gln Asn Gly Ser Phe Gly Pro Ser Pro Val Ser Gly  
945 950 955 960

Gly Glu Cys Ser Pro Pro Leu Thr Val Glu Pro Pro Val Arg Pro Leu  
965 970 975

Ser Ala Thr Leu Asn Arg Arg Asp Met Pro Arg Ser Glu Phe Gly Ser  
980 985 990

Val Asp Gly Pro Leu Pro His Pro Arg Trp Ser Ala Glu Ala Ser Gly  
995 1000 1005

Lys Pro Ser Pro Ser Asp Pro Gly Ser Gly Thr Ala Thr Met Met  
1010 1015 1020

Asn Ser Ser Ser Arg Gly Ser Ser Pro Thr Arg Val Leu Asp Glu  
1025 1030 1035

Gly Lys Val Asn Met Ala Pro Lys Gly Pro Pro Pro Phe Pro Gly  
1040 1045 1050

Val Pro Leu Met Ser Thr Pro Met Gly Gly Pro Val Pro Pro Pro  
1055 1060 1065

Ile Arg Tyr Gly Pro Pro Pro Gln Leu Cys Gly Pro Phe Gly Pro  
1070 1075 1080

Arg Pro Leu Pro Pro Pro Phe Gly Pro Gly Met Arg Pro Pro Leu  
1085 1090 1095

Gly Leu Arg Glu Phe Ala Pro Gly Val Pro Pro Gly Arg Arg Asp  
1100 1105 1110

Leu Pro Leu His Pro Arg Gly Phe Leu Pro Gly His Ala Pro Phe  
1115 1120 1125

Arg Pro Leu Gly Ser Leu Gly Pro Arg Glu Tyr Phe Ile Pro Gly  
1130 1135 1140

Thr Arg Leu Pro Pro Pro Thr His Gly Pro Gln Glu Tyr Pro Pro

1145	1150	1155
Pro Pro Ala Val Arg Asp Leu	Leu Pro Ser Gly Ser	Arg Asp Glu
1160	1165	1170
Pro Pro Pro Ala Ser Gln Ser	Thr Ser Gln Asp Cys	Ser Gln Ala
1175	1180	1185
Leu Lys Gln Ser Pro		
1190		
<210> 51		
<211> 3287		
<212> DNA		
<213> human organism		
<400> 51		
agactgaggc ggaggcagcc ccgcgcgcg ccggaccga gcatattca ttttctgtca		60
ttggactttg agccattaga accatgagca actacagtgt gtcactgggtt ggcccagctc		120
cttggggttt ccggctgcag ggcggtaagg atttcaacat gcctctgaca atctctagtc		180
taaaagatgg cggcaaggca gcccaggca atgtaagaat aggcatgtg gttctcagca		240
ttgatggaat aaatgcacaa ggaatgactc atcttgaagc ccagaataag attaagggtt		300
gtacaggctc tttgaatatg actctgcaaa gagcatctgc tgcacccaag cctgagccgg		360
ttcctgttca aaagggagaa cctaaagaag tagttaaacc tgtgccatt acatctcctg		420
ctgtgtccaa agtcacttcc acaaacaaca tggcctacaa taaggcacca cggccttttgc		480
gttctgtgtc ttcacccaaa gtcacatcca tcccatcacc atcgtctgcc ttcacccccag		540
cccatgcgac cacctcatca catgcttccc cttcacccgt ggctgccgtc actcctcccc		600
tgttcgtgtc atctggactg catgctaattt ccaatcttag tgctgaccag tctccatctg		660
cactgagcgc tggtaaaact gcagttaatg tcccacggca gcccacagtc accagcgtgt		720
gttccgagac ttctcaggag cttagcagagg gacagagaag aggatcccag ggtgacagta		780
aacagcaaaa tggccacca agaaaacaca ttgtggagcg ctatacagag ttttatcatg		840
tacccactca cagtgtatgcc agcaagaaga gactgattga ggatactgaa gactggcg		900
caagaactgg aacaactcag tctcgcttt tccgaatcct tgcccgatc actggactg		960
aacatttgaa agaatctgaa gccgataata caaagaaggc aaataactct caggagc		1020
ctccgcagtt ggcttcctt gtagcttcca cacggagcat gcccgagagc ctggacagcc		1080

caacacctgg cagaccaggg gttaccagcc tcacaactgc agtcgccttc aaggcctgttag 1140  
gatccactgg cgtcatcaag tcaccaagct ggcaacggcc aaacccaagga gtaccttcca 1200  
ctggaaagaat ctcaaacagc gctacttact caggatcagt ggccaccagcc aactcagctt 1260  
tgggacaaac ccagccaaatg gaccaggaca ctttagtgca aagagctgag cacattccag 1320  
caggaaacg aactccgatg tgcccccatt gtaaccaggt catcagagga ccattcttag 1380  
tggcactggg gaaatcttgg cacccagaag aattcaactg cgctcactgc aaaaatacaa 1440  
tggcctacat tggatttgta gaggagaaag gagccctgta ttgtgagctg tgctatgaga 1500  
aattcttgc ccctgaatgt ggtcgatgcc aaaggaagat ccttggagaa gtcatcaatg 1560  
cggtgaaaca aacttggcat gttccctgtt ttgtgtgtgt agcctgtgga aagcccattc 1620  
ggaacaatgt ttttcaacttg gaggatggtg aaccctactg tgagactgat tattatgcc 1680  
tctttggcac tatatccat ggtgtgaat ttcccataga agctggtgac atgttccctgg 1740  
aagctctggg ctacacctgg catgacactt gctttgtatg ctcagtgtgt tgtgaaagtt 1800  
tggaaaggta gaccttttc tccaagaagg acaagccccgt gtgtaagaaa catgctcatt 1860  
ctgtgaattt ttgaaagtca acagttcagg agaagagaag gaatttgaag agaaaaagga 1920  
aaattaaaaat tactaattaa ttttagatt caatatttat atggagttt gaaaaataat 1980  
agtggccctg aaggaataaa ttccagctt aaaaaccaag tctgagggaaa tatttggctt 2040  
cataaagtaa agagacggtt tggcatttat tattacttt tcctgtattt tatgcccata 2100  
aaataagctt tataaaaaacc aatttcctga tggacttatta aattcatctt agaataaatt 2160  
agtgaagaat ttaatttttag aataaataat ccaatctgaa ataattatac cttcttcct 2220  
tgttaggtatg ttatgagtaa atctgaaaaa ggcaatgaaa atgccttaaa ttttatcaat 2280  
aacagaattt ttgtatttaa aaaaaaacta atacttatct ttaaaatagt aaataggatt 2340  
ttaaacagag aattttatca gtaataggtg tcagtttta aaaaattgct tgtaggctga 2400  
gcgcgggtggc tcacgcctgt aatcccagca ctttgggagg ccaaggtggg tggaccacat 2460  
gaggtcagga gtttgagatc agcctggcca acatggtaa accccatctc tactaaaaat 2520  
acaaaaaatta gccggacgca gtggcacgca cctgtaatcc cagctactca agaggctgag 2580  
gcacgagaat cacttgaacc cggggagggag aggttgcagt gagccaagat cgtaccactg 2640  
cactccagcc tgggtgacag agttagactc cgtctccaaa aaaaaacttt gcttgtatat 2700  
tattttgcc ttacagtggta tcattcttagt aggaaaggac aataagattt tttatcaaaa 2760  
tgtgtcatgc cagtaagaga tggttatattc ttttcttatt tcttccccac ccaaaaataaa 2820

gctaccatat agcttataag tctcaaattt ttgccttta ctaaaatgtg attgtttctg	2880
ttcattgtgt atgcttcatc acctatatta ggcaaattcc attttttccc ttgcgctaag	2940
gtaaagattt aattaaataa ttttggcctc tcatagtttt ctctctctt aaagagaata	3000
aatagagggc caggtgtggc ggctcacgac tgtgatccc gcactttggg aggccaagac	3060
ggcgatca tgaggtcaag agatcaagat catcctggcc aacatggta aaccctgtct	3120
ctactaaaaa tacaaaaatg agctggcat ggtgggcgt gcctgtagtc ccatgtactt	3180
gggaggctga ggcaggaaaa ttcttgaacc caggagacgg aagttgcagt gagctgagat	3240
cacaccactg cactccagcc tggtgacaga gcaagactcc ggctctt	3287

<210> 52  
<211> 596  
<212> PRT  
<213> human organism

<400> 52

Met Ser Asn Tyr Ser Val Ser Leu Val Gly Pro Ala Pro Trp Gly Phe	
1	5
	10
	15

Arg Leu Gln Gly Gly Lys Asp Phe Asn Met Pro Leu Thr Ile Ser Ser	
20	25
	30

Leu Lys Asp Gly Gly Lys Ala Ala Gln Ala Asn Val Arg Ile Gly Asp	
35	40
	45

Val Val Leu Ser Ile Asp Gly Ile Asn Ala Gln Gly Met Thr His Leu	
50	55
	60

Glu Ala Gln Asn Lys Ile Lys Gly Cys Thr Gly Ser Leu Asn Met Thr	
65	70
	75
	80

Leu Gln Arg Ala Ser Ala Ala Pro Lys Pro Glu Pro Val Pro Val Gln	
85	90
	95

Lys Gly Glu Pro Lys Glu Val Val Lys Pro Val Pro Ile Thr Ser Pro	
100	105
	110

Ala Val Ser Lys Val Thr Ser Thr Asn Asn Met Ala Tyr Asn Lys Ala	
115	120
	125

Pro Arg Pro Phe Gly Ser Val Ser Ser Pro Lys Val Thr Ser Ile Pro  
130 135 140

Ser Pro Ser Ser Ala Phe Thr Pro Ala His Ala Thr Thr Ser Ser His  
145 150 155 160

Ala Ser Pro Ser Pro Val Ala Ala Val Thr Pro Pro Leu Phe Ala Ala  
165 170 175

Ser Gly Leu His Ala Asn Ala Asn Leu Ser Ala Asp Gln Ser Pro Ser  
180 185 190

Ala Leu Ser Ala Gly Lys Thr Ala Val Asn Val Pro Arg Gln Pro Thr  
195 200 205

Val Thr Ser Val Cys Ser Glu Thr Ser Gln Glu Leu Ala Glu Gly Gln  
210 215 220

Arg Arg Gly Ser Gln Gly Asp Ser Lys Gln Gln Asn Gly Pro Pro Arg  
225 230 235 240

Lys His Ile Val Glu Arg Tyr Thr Glu Phe Tyr His Val Pro Thr His  
245 250 255

Ser Asp Ala Ser Lys Lys Arg Leu Ile Glu Asp Thr Glu Asp Trp Arg  
260 265 270

Pro Arg Thr Gly Thr Thr Gln Ser Arg Ser Phe Arg Ile Leu Ala Gln  
275 280 285

Ile Thr Gly Thr Glu His Leu Lys Glu Ser Glu Ala Asp Asn Thr Lys  
290 295 300

Lys Ala Asn Asn Ser Gln Glu Pro Ser Pro Gln Leu Ala Ser Leu Val  
305 310 315 320

Ala Ser Thr Arg Ser Met Pro Glu Ser Leu Asp Ser Pro Thr Ser Gly  
325 330 335

Arg Pro Gly Val Thr Ser Leu Thr Ala Ala Ala Phe Lys Pro Val  
340 345 350

Gly Ser Thr Gly Val Ile Lys Ser Pro Ser Trp Gln Arg Pro Asn Gln

355

360

365

Gly Val Pro Ser Thr Gly Arg Ile Ser Asn Ser Ala Thr Tyr Ser Gly  
370 375 380

Ser Val Ala Pro Ala Asn Ser Ala Leu Gly Gln Thr Gln Pro Ser Asp  
385 390 395 400

Gln Asp Thr Leu Val Gln Arg Ala Glu His Ile Pro Ala Gly Lys Arg  
405 410 415

Thr Pro Met Cys Ala His Cys Asn Gln Val Ile Arg Gly Pro Phe Leu  
420 425 430

Val Ala Leu Gly Lys Ser Trp His Pro Glu Glu Phe Asn Cys Ala His  
435 440 445

Cys Lys Asn Thr Met Ala Tyr Ile Gly Phe Val Glu Glu Lys Gly Ala  
450 455 460

Leu Tyr Cys Glu Leu Cys Tyr Glu Lys Phe Phe Ala Pro Glu Cys Gly  
465 470 475 480

Arg Cys Gln Arg Lys Ile Leu Gly Glu Val Ile Asn Ala Leu Lys Gln  
485 490 495

Thr Trp His Val Ser Cys Phe Val Cys Val Ala Cys Gly Lys Pro Ile  
500 505 510

Arg Asn Asn Val Phe His Leu Glu Asp Gly Glu Pro Tyr Cys Glu Thr  
515 520 525

Asp Tyr Tyr Ala Leu Phe Gly Thr Ile Cys His Gly Cys Glu Phe Pro  
530 535 540

Ile Glu Ala Gly Asp Met Phe Leu Glu Ala Leu Gly Tyr Thr Trp His  
545 550 555 560

Asp Thr Cys Phe Val Cys Ser Val Cys Cys Glu Ser Leu Glu Gly Gln  
565 570 575

Thr Phe Phe Ser Lys Lys Asp Lys Pro Leu Cys Lys Lys His Ala His  
580 585 590

Ser Val Asn Phe  
595

<210> 53  
<211> 1115  
<212> DNA  
<213> human organism

<400> 53  
atggccaaact gtaaaatgac caaaaagcatc aggttccctg ccctggagca ctgctatact 60  
ggcgaaaaagg tcgtgttgcc caaggatcatc gaggagtggaa aaagacggac gggcattctg 120  
ctctacgaga actatggca gtcggaaacg ggactaattt gtgccaccta ctggggaaatg 180  
aagatcaagc cgggtttcat gggaaaggcc actccaccct atgacgtcca gtttcatatg 240  
gaggcctcag ttgaaaactg cattattgtg agcatgaaca ccgcgtgaccc tggcagccag 300  
ggcatcacac acagcctctt gctacaggc attgatgaca agggcagcat cctgccacct 360  
aacacagaag gaaacattgg catcagaatc aaacctgtca ggcctgtgag cctcttcattg 420  
tgctatgagg gtgaccaga gaagacagct aaagtggaaat gtggggactt ctacaacact 480  
ggggacagag gaaagatgga tgaagagggc tacatttgg tccctgggag gagtgatgac 540  
atcattaatg cctctggta tcgcattcggg cctgcagagg ttgaaagcgc tttggggag 600  
cacccagcgg tggcgagtc agccgtggtg ggcagccag acccgattcg aggggaggtg 660  
gtgaaggcct ttattgtcct gacccccacag ttcctgtccc atgacaaggaa tcagctgacc 720  
aaggaactgc agcagcatgt caagtcagtg acagccccat acaagtaccc aaggaagggtg 780  
gagtttgtct cagagctgcc aaaaaccatc actggcaaga ttgaacggaa ggaacttcgg 840  
aaaaaggaga ctggtcagat gtaatcggca gtgaactcag aacgcactgc acacctgagg 900  
caaattccctg gccactttag tctcccaact atggtgagga cgagggtggg gcattgagag 960  
tggatggatggatggatggatggatggatggatggatggatggatggatggatggatggatgg 1020  
aattcagttg ctctgcttcc tccaaatgtcc ctgtatctt agaatttccc aggtgagcac 1080  
tcataacgca agtaataaaa tactgatatc aacaa 1115

<210> 54  
<211> 287  
<212> PRT  
<213> human organism

<400> 54

Met Ala Asn Cys Lys Met Thr Lys Ser Ile Arg Phe Pro Ala Leu Glu  
1 5 10 15

His Cys Tyr Thr Gly Gly Glu Val Val Leu Pro Lys Asp Gln Glu Glu  
20 25 30

Trp Lys Arg Arg Thr Gly Leu Leu Tyr Glu Asn Tyr Gly Gln Ser  
35 40 45

Glu Thr Gly Leu Ile Cys Ala Thr Tyr Trp Gly Met Lys Ile Lys Pro  
50 55 60

Gly Phe Met Gly Lys Ala Thr Pro Pro Tyr Asp Val Gln Phe His Met  
65 70 75 80

Glu Ala Ser Val Glu Asn Cys Ile Ile Val Ser Met Asn Thr Ala Asp  
85 90 95

Pro Gly Ser Gln Gly Ile Thr His Ser Leu Leu Leu Gln Val Ile Asp  
100 105 110

Asp Lys Gly Ser Ile Leu Pro Pro Asn Thr Glu Gly Asn Ile Gly Ile  
115 120 125

Arg Ile Lys Pro Val Arg Pro Val Ser Leu Phe Met Cys Tyr Glu Gly  
130 135 140

Asp Pro Glu Lys Thr Ala Lys Val Glu Cys Gly Asp Phe Tyr Asn Thr  
145 150 155 160

Gly Asp Arg Gly Lys Met Asp Glu Glu Gly Tyr Ile Cys Phe Leu Gly  
165 170 175

Arg Ser Asp Asp Ile Ile Asn Ala Ser Gly Tyr Arg Ile Gly Pro Ala  
180 185 190

Glu Val Glu Ser Ala Leu Val Glu His Pro Ala Val Ala Glu Ser Ala  
195 200 205

Val Val Gly Ser Pro Asp Pro Ile Arg Gly Glu Val Val Lys Ala Phe  
210 215 220

Ile Val Leu Thr Pro Gln Phe Leu Ser His Asp Lys Asp Gln Leu Thr  
225 230 235 240

Lys Glu Leu Gln Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr  
245 250 255

Pro Arg Lys Val Glu Phe Val Ser Glu Leu Pro Lys Thr Ile Thr Gly  
260 265 270

Lys Ile Glu Arg Lys Glu Leu Arg Lys Lys Glu Thr Gly Gln Met  
275 280 285

<210> 55  
<211> 521  
<212> DNA  
<213> human organism

<400> 55  
gagagaggga ggcagaagag gaagtcagag cgatgtgctg tggaaatctac taccgttgc 60  
tggtttgaa aatggagaaa aagagtgagg aactgagaaa catggatggc cttgggaacg  
tgaaaaaggg tcactgaaat gggacgacat gaactcaagg aggctattta tgaccatgtc 120  
atggcaaca tgaagaaagc ttatctggag tgaaaagtaaa tgagaccaac agagataaga 180  
gaccggaga aatcctgggt acactgcttg aatcctgtca gtcctataact ggagtcctgt 240  
taatacaaaa taatagtaat aatccctctg tttcttatgt ttatgccaac ttcaaca 300  
agaaaacttga ctaagagaca atataagaac ttaatgtgta attaagaaaag aactctccac 360  
cacgggaaat gtgaaaggta tatgagtccc tttcacgat gcgatgtcat gtctttaaa 420  
taagccatac tttatgttca ataaaaagag aataagcagg a 480  
521

<210> 56  
<211> 34  
<212> PRT  
<213> human organism

<400> 56

Met Cys Cys Glu Ile Tyr Tyr Arg Leu Leu Val Leu Lys Met Glu Lys  
1 5 10 15

Lys Ser Glu Glu Leu Arg Asn Met Asp Gly Leu Gly Asn Val Glu Lys  
20 25 30

Gly His

<210> 57  
<211> 2064  
<212> DNA  
<213> human organism

<400> 57 atggacagtt gcctgcaaca tatgagagac ctactttacc tccttcagga gctcagggtgt 60 ttaaatccag ctacactact ccctgatcca gactccacta ctcctgttca tgactgtcag gatctgttgg aaactaccaa aactggccaa cctgatcttc aagatgtgcc cctagaaaag 120 gcaagatgcca ctgtgttcac agatggtagc agcttcctcg agcagggaga acgaaaagct 180 gtttctttc cacagccaga tctgcctgac aatcccacat actcaacaga agaagaaaa 240 ctggcttcag atgttggagc aaataaaaaat caggaaggac gtgtattcgc aaacactact 300 tggagggccg gtacctccaa ggaagtctcc tttgcagttg atttatgtgt actgttccca 360 gagccagctc gtacccatga agagcaacat aatttgcggg tcataggagc aggaagtgtc 420 gaccttgcag caggatttg acactctggg agccaaactg gatgtggaag ctccaaaggt 480 gcagaaaaag ggctccaaa ttttgacttt tacctctgtc ctggaaatca ccctgacgct 540 agctgttagag atacttacca gttttctgc cctgattgga catgtgtaac tttagccacc 600 tactctgggg gatcaactag atcttcaact cttccataa gtcgtgttcc tcatcctaaa 660 ttatgtacta gaaaaaattt taatcctctt actataactg tccatgaccc taatgcagct 720 caatggtatt atggcatgtc atggggatta agactttata tcccaggatt tgatgttggg 780 actatgttca ccatccaaa gaaaatcttg gtctcatgga gctccccaa gccaatcggg 840 cctttaactg atcttaggtga ccctatatcc cagaaacacc ctgacaaagt tgatttaact 900 gttcctctgc cattcttagt tcctagaccc cagctacaac aacaacatct tcaacccagc 960 ctaatgtcta tactaggtgg agtacaccat ctccttaacc tcacccagcc taaactagcc 1020 caagattgtt ggctatgttt aaaagcaaaa cccccttatt atgttaggatt aggagtagaa 1080 gcccacactta aacgtggccc tctatcttgt catacacgac cccgtgctct cacaatagga 1140 gatgtgtctg gaaatgttc ctgtctgatt agtaccgggt ataacttatac tgcttctcct 1200 tttcaggcta cttgtaatca gtccctgctt acttccataa gcacctcagt ctcttaccaa 1260 gcacccaaca atacctgggtt ggcctgcacc tcaggtctca ctcgctgcat taatggaact 1320 gaaccaggac ctctcctgtg cgtgttagtt catgtacttc cccaggtata tgtgtacagt 1380 1440

ggaccagaag	gacgacaact	catcgctccc	cctgagttac	atcccagggtt	gcaccaagct	1500
gtcccacttc	tggttccctt	attggctgggt	cttagcatag	ctggatcagc	agccattgggt	1560
acggctgccc	tggttcaagg	agaaaactgga	ctaataatccc	tgtctcaaca	ggtggatgct	1620
gattttagta	acctccagtc	tgccatagat	atactacatt	cccaggtaga	gtctctggct	1680
gaagtagttc	ttcaaaaactg	ccgatgctta	gatctgctat	tcctctctca	aggaggttta	1740
tgtcagctc	taggagaaag	ttgttgcttc	tatgccaatc	aatctggagt	cataaaaggt	1800
acagtaaaaaa	aagttcgaga	aaatctagat	aggcaccaac	aagaacgaga	aaataacatc	1860
ccctggtatac	aaagcatgtt	taactggaac	ccatggctaa	ctactttaat	cactgggtta	1920
gctggacctc	tcctcatcct	actattaagt	ttaattttg	ggccttgtat	attaaattcg	1980
tttcttaatt	ttataaaaca	acgcatacgct	tctgtcaaac	ttacgtatct	taagactcaa	2040
tatgacaccc	ttgttaataa	ctga				2064

<210> 58

<211> 687

<212> PRT

<213> human organism

<400> 58

Met	Asp	Ser	Cys	Leu	Gln	His	Met	Arg	Asp	Leu	Leu	Tyr	Leu	Leu	Gln
1				5					10						15

Glu	Leu	Arg	Cys	Leu	Asn	Pro	Ala	Thr	Leu	Leu	Pro	Asp	Pro	Asp	Ser
				20				25			30				

Thr	Thr	Pro	Val	His	Asp	Cys	Gln	Asp	Leu	Leu	Glu	Thr	Thr	Lys	Thr
					35			40				45			

Gly	Gln	Pro	Asp	Leu	Gln	Asp	Val	Pro	Leu	Glu	Lys	Ala	Asp	Ala	Thr
				50			55			60					

Val	Phe	Thr	Asp	Gly	Ser	Ser	Phe	Leu	Glu	Gln	Gly	Glu	Arg	Lys	Ala
					65		70		75				80		

Val	Ser	Phe	Pro	Gln	Pro	Asp	Leu	Pro	Asp	Asn	Pro	Thr	Tyr	Ser	Thr
					85			90				95			

Glu	Glu	Glu	Lys	Leu	Ala	Ser	Asp	Val	Gly	Ala	Asn	Lys	Asn	Gln	Glu
					100			105				110			

Gly Arg Val Phe Ala Asn Thr Thr Trp Arg Ala Gly Thr Ser Lys Glu  
115 120 125

Val Ser Phe Ala Val Asp Leu Cys Val Leu Phe Pro Glu Pro Ala Arg  
130 135 140

Thr His Glu Glu Gln His Asn Leu Pro Val Ile Gly Ala Gly Ser Val  
145 150 155 160

Asp Leu Ala Ala Gly Phe Gly His Ser Gly Ser Gln Thr Gly Cys Gly  
165 170 175

Ser Ser Lys Gly Ala Glu Lys Gly Leu Gln Asn Val Asp Phe Tyr Leu  
180 185 190

Cys Pro Gly Asn His Pro Asp Ala Ser Cys Arg Asp Thr Tyr Gln Phe  
195 200 205

Phe Cys Pro Asp Trp Thr Cys Val Thr Leu Ala Thr Tyr Ser Gly Gly  
210 215 220

Ser Thr Arg Ser Ser Thr Leu Ser Ile Ser Arg Val Pro His Pro Lys  
225 230 235 240

Leu Cys Thr Arg Lys Asn Cys Asn Pro Leu Thr Ile Thr Val His Asp  
245 250 255

Pro Asn Ala Ala Gln Trp Tyr Tyr Gly Met Ser Trp Gly Leu Arg Leu  
260 265 270

Tyr Ile Pro Gly Phe Asp Val Gly Thr Met Phe Thr Ile Gln Lys Lys  
275 280 285

Ile Leu Val Ser Trp Ser Ser Pro Lys Pro Ile Gly Pro Leu Thr Asp  
290 295 300

Leu Gly Asp Pro Ile Phe Gln Lys His Pro Asp Lys Val Asp Leu Thr  
305 310 315 320

Val Pro Leu Pro Phe Leu Val Pro Arg Pro Gln Leu Gln Gln His  
325 330 335

Leu Gln Pro Ser Leu Met Ser Ile Leu Gly Gly Val His His Leu Leu  
340 345 350

Asn Leu Thr Gln Pro Lys Leu Ala Gln Asp Cys Trp Leu Cys Leu Lys  
355 360 365

Ala Lys Pro Pro Tyr Tyr Val Gly Leu Gly Val Glu Ala Thr Leu Lys  
370 375 380

Arg Gly Pro Leu Ser Cys His Thr Arg Pro Arg Ala Leu Thr Ile Gly  
385 390 395 400

Asp Val Ser Gly Asn Ala Ser Cys Leu Ile Ser Thr Gly Tyr Asn Leu  
405 410 415

Ser Ala Ser Pro Phe Gln Ala Thr Cys Asn Gln Ser Leu Leu Thr Ser  
420 425 430

Ile Ser Thr Ser Val Ser Tyr Gln Ala Pro Asn Asn Thr Trp Leu Ala  
435 440 445

Cys Thr Ser Gly Leu Thr Arg Cys Ile Asn Gly Thr Glu Pro Gly Pro  
450 455 460

Leu Leu Cys Val Leu Val His Val Leu Pro Gln Val Tyr Val Tyr Ser  
465 470 475 480

Gly Pro Glu Gly Arg Gln Leu Ile Ala Pro Pro Glu Leu His Pro Arg  
485 490 495

Leu His Gln Ala Val Pro Leu Leu Val Pro Leu Leu Ala Gly Leu Ser  
500 505 510

Ile Ala Gly Ser Ala Ala Ile Gly Thr Ala Ala Leu Val Gln Gly Glu  
515 520 525

Thr Gly Leu Ile Ser Leu Ser Gln Gln Val Asp Ala Asp Phe Ser Asn  
530 535 540

Leu Gln Ser Ala Ile Asp Ile Leu His Ser Gln Val Glu Ser Leu Ala  
545 550 555 560

Glu Val Val Leu Gln Asn Cys Arg Cys Leu Asp Leu Leu Phe Leu Ser

565

570

575

Gln Gly Gly Leu Cys Ala Ala Leu Gly Glu Ser Cys Cys Phe Tyr Ala  
580 585 590

Asn Gln Ser Gly Val Ile Lys Gly Thr Val Lys Lys Val Arg Glu Asn  
595 600 605

Leu Asp Arg His Gln Gln Glu Arg Glu Asn Asn Ile Pro Trp Tyr Gln  
610 615 620

Ser Met Phe Asn Trp Asn Pro Trp Leu Thr Thr Leu Ile Thr Gly Leu  
625 630 635 640

Ala Gly Pro Leu Leu Ile Leu Leu Ser Leu Ile Phe Gly Pro Cys  
645 650 655

Ile Leu Asn Ser Phe Leu Asn Phe Ile Lys Gln Arg Ile Ala Ser Val  
660 665 670

Lys Leu Thr Tyr Leu Lys Thr Gln Tyr Asp Thr Leu Val Asn Asn  
675 680 685

<210> 59  
<211> 2960  
<212> DNA  
<213> human organism

<400> 59  
tgcgttgttggaa aattttcttga aaccgctctc gtaatttgcc acgtgctgtt gcaaatattc 60  
tggtaatgttggaa acacagaatc agcatggctt tcctttgctg agaaatcaact gatggaaagt 120  
gagacttggtt aaacttggaaa gtgaatggac ctgagtggtt cctttgtatca catcagtaaa 180  
catgagcggtt accaaacccgtt atattttatgtt ggcaccacac catgttggata gattttgtgtt 240  
gtgtgactca gaactaagtc ttatcatgtt ggaatctact gtgaatttcag aactcaaagc 300  
tggatcttta cgtttatctgtt aagactctgc agctacattttt ctgtcaataaa attcagataac 360  
acccttatatgtt aaatgtgtttt cctggtatctt taattatgtt cctgaatgtc tgctggcagt 420  
tggtacaaggca aatggtcgag ttgtacttac aagccttgggtt caagatcata actcaaagttt 480  
caaagattttt ataggaaaaag agttttgttcc aaaacatgca cgacaatgttta atacccttgc 540  
ctggaaatcca ctggatagta actggcttagc tgctgggttta gataaggcaca gagctgactt 600

ttcagtgcta atatggata tctgcagcaa atatactcct gatatagttc ccatggaaaa 660  
agtgaaactt tcagcaggtg aaactgaaaac aacattatta gtaacaaaac cactttatga 720  
gttaggacag aatgatgctt gtctgtctt ttgttgctt ccacgagacc agaaacttct 780  
ccttgctggt atgcatcgta acctagctat atttgatctt cggaatacaa gccaaaagat 840  
gttcgtaaat acaaaaagctg ttcaagggtgt gacggtagac ccatatttcc acgategtgt 900  
tgcttccttc tatgaaggtc aggttgcaat atggatctt agaaaatttg agaaggccagt 960  
tttgacattt actgagcaac caaaaacctt aacaaaagta gcatggtgcc ccaactaggac 1020  
tggtctactt gccactttaa caagggatag taatattatt agattgtatg atatgcagca 1080  
tacacccact cccattgggg atgaaaactga acccacaata attgaaagaa gtgtgcaacc 1140  
ttgtgacaat tacattgctt ccttgcgtg gcatccaaca agtcaaaaatc gaatgatagt 1200  
tgtaactccc aaccgaacaa tgtcagactt cactgtttt gaaaggatat ctcttgccctg 1260  
gagcccaatt acatcttaa tgtggcttg tggtcgcat ttatatgaat gtacggaaga 1320  
agaaaatgat aattctttag aaaaagatat agcaacgaag atgcgtcttc gggctttatc 1380  
aaggtatgga cttgatacag agcaggtgtg gaggaaccac attttagctg gaaatgaaga 1440  
tccacagctc aagtcaactt ggtatactt gcactttatg aagcaataca cagaagatat 1500  
ggatcagaaa tctccaggca acaaaggatc attggtttat gcaggaatta aatcaattgt 1560  
aaagtcatcg ttggaatgg tgaaaagcag cagacataat tggagtgggt tggataagca 1620  
aagtgatatt caaaaacttaa atgaagagag aatcttagct ttacagctt gtgggtggat 1680  
aaagaaagga acggatgttag acgtggggcc atttttgaac tcccttgtac aagaagggga 1740  
atggaaaga gctgctgctg tggcattgtt caacttggat attcgccgag caatccaaat 1800  
cctgaatgaa gggcatctt ctgaaaaagg caggagatct gaatctcaat gtggtagcaa 1860  
tggcttatacg gatgagaaga actcccttg gagagaaatg ttagcacac 1920  
tgcgattaca gctaaataac ccgtatttgcgtt tgcatttctg acaagtgaaa 1980  
caggatctt ccatggagtt ttgtatgaaa acaaagttgc agtacgtgac agagtggcat 2040  
ttgcttatacg gatgagaaga actcccttg gagagaaatg ttagcacac 2100  
gaggctggaa atttggaaagg aattttgctt acaggcctta ctaaagatgg agtggactta 2160  
atggagagtt atgttgcatac aactggagat gttcaaacag caagttactg tatgttacag 2220  
ggttcacctt tagatgttct taaagatgaa agggttcagt actggattga gaattataga 2280  
aatttatttag atgcctggag gtttggcat aaacgagctg aatttgcatac tcacaggat 2340

aagtggatc ccagttccaa gcctttagca caagtttg tgagttgcaa tttctgtggc	2400
aagtcaatct cctacagctg ttcatcgctg cctcatcagg gcagaggtt tagtcagtat	2460
ggtgtgagtg gctcaccaac gaaatctaaa gtcacaagtt gtcctggctg tcgaaaacca	2520
cttcctcgat gtgcgccttg tctcattaat atggAACAC cagttctag ctgtcctgga	2580
ggaaccaaAT cagatgaaaa agtggacttg agcaaggaca AAAAATTAGC ccaatttaac	2640
aactggTTTA catgggtca taattgcagg cacggggac atgctggaca tatgcttagt	2700
tggttcaggg accatgcaga gtgccctgtg tctgcatttgc cgtgtAAATG tatgcagttg	2760
gataacaacgg ggaatctggt acctgcagag actgtccagc cataAAATGT taccaccta	2820
agagaaccct tcaagtgtgg agctttctag taggtgtcct tcatacgctca gaaacatacc	2880
tcagaacaAG ccattcatga cttaCTGta atggaaaaAT aaatcatttct atcagaaaaAA	2940
aaaaaaaaaa aaaaaaaaaa	2960

<210> 60  
 <211> 567  
 <212> PRT  
 <213> human organism

<400> 60

Met Ser Gly Thr Lys Pro Asp Ile Leu Trp Ala Pro His His Val Asp			
1	5	10	15

Arg Phe Val Val Cys Asp Ser Glu Leu Ser Leu Tyr His Val Glu Ser			
20	25	30	

Thr Val Asn Ser Glu Leu Lys Ala Gly Ser Leu Arg Leu Ser Glu Asp			
35	40	45	

Ser Ala Ala Thr Leu Leu Ser Ile Asn Ser Asp Thr Pro Tyr Met Lys			
50	55	60	

Cys Val Ala Trp Tyr Leu Asn Tyr Asp Pro Glu Cys Leu Leu Ala Val			
65	70	75	80

Gly Gln Ala Asn Gly Arg Val Val Leu Thr Ser Leu Gly Gln Asp His			
85	90	95	

Asn Ser Lys Phe Lys Asp Leu Ile Gly Lys Glu Phe Val Pro Lys His			
100	105	110	

Ala Arg Gln Cys Asn Thr Leu Ala Trp Asn Pro Leu Asp Ser Asn Trp  
115 120 125

Leu Ala Ala Gly Leu Asp Lys His Arg Ala Asp Phe Ser Val Leu Ile  
130 135 140

Trp Asp Ile Cys Ser Lys Tyr Thr Pro Asp Ile Val Pro Met Glu Lys  
145 150 155 160

Val Lys Leu Ser Ala Gly Glu Thr Glu Thr Thr Leu Leu Val Thr Lys  
165 170 175

Pro Leu Tyr Glu Leu Gly Gln Asn Asp Ala Cys Leu Ser Leu Cys Trp  
180 185 190

Leu Pro Arg Asp Gln Lys Leu Leu Ala Gly Met His Arg Asn Leu  
195 200 205

Ala Ile Phe Asp Leu Arg Asn Thr Ser Gln Lys Met Phe Val Asn Thr  
210 215 220

Lys Ala Val Gln Gly Val Thr Val Asp Pro Tyr Phe His Asp Arg Val  
225 230 235 240

Ala Ser Phe Tyr Glu Gly Gln Val Ala Ile Trp Asp Leu Arg Lys Phe  
245 250 255

Glu Lys Pro Val Leu Thr Leu Thr Glu Gln Pro Lys Pro Leu Thr Lys  
260 265 270

Val Ala Trp Cys Pro Thr Arg Thr Gly Leu Leu Ala Thr Leu Thr Arg  
275 280 285

Asp Ser Asn Ile Ile Arg Leu Tyr Asp Met Gln His Thr Pro Thr Pro  
290 295 300

Ile Gly Asp Glu Thr Glu Pro Thr Ile Ile Glu Arg Ser Val Gln Pro  
305 310 315 320

Cys Asp Asn Tyr Ile Ala Ser Phe Ala Trp His Pro Thr Ser Gln Asn  
325 330 335

Arg Met Ile Val Val Thr Pro Asn Arg Thr Met Ser Asp Phe Thr Val  
340 345 350

Phe Glu Arg Ile Ser Leu Ala Trp Ser Pro Ile Thr Ser Leu Met Trp  
355 360 365

Ala Cys Gly Arg His Leu Tyr Glu Cys Thr Glu Glu Asn Asp Asn  
370 375 380

Ser Leu Glu Lys Asp Ile Ala Thr Lys Met Arg Leu Arg Ala Leu Ser  
385 390 395 400

Arg Tyr Gly Leu Asp Thr Glu Gln Val Trp Arg Asn His Ile Leu Ala  
405 410 415

Gly Asn Glu Asp Pro Gln Leu Lys Ser Leu Trp Tyr Thr Leu His Phe  
420 425 430

Met Lys Gln Tyr Thr Glu Asp Met Asp Gln Lys Ser Pro Gly Asn Lys  
435 440 445

Gly Ser Leu Val Tyr Ala Gly Ile Lys Ser Ile Val Lys Ser Ser Leu  
450 455 460

Gly Met Val Glu Ser Ser Arg His Asn Trp Ser Gly Leu Asp Lys Gln  
465 470 475 480

Ser Asp Ile Gln Asn Leu Asn Glu Glu Arg Ile Leu Ala Leu Gln Leu  
485 490 495

Cys Gly Trp Ile Lys Lys Gly Thr Asp Val Asp Val Gly Pro Phe Leu  
500 505 510

Asn Ser Leu Val Gln Glu Gly Glu Trp Glu Arg Ala Ala Ala Val Ala  
515 520 525

Leu Phe Asn Leu Asp Ile Arg Arg Ala Ile Gln Ile Leu Asn Glu Gly  
530 535 540

Ala Ser Ser Glu Lys Gly Arg Arg Ser Glu Ser Gln Cys Gly Ser Asn  
545 550 555 560

Gly Phe Ile Gly Leu Tyr Gly

565

<210> 61  
<211> 856  
<212> DNA  
<213> human organism

<220>  
<221> misc\_feature  
<222> (37)..(37)  
<223> n is a, c, g, or t

<220>  
<221> misc\_feature  
<222> (757)..(757)  
<223> n is a, c, g, or t

<220>  
<221> misc\_feature  
<222> (769)..(769)  
<223> n is a, c, g, or t

<400> 61  
ttgtacatct taacaacctt aagctgtaca aatagancaa taatatctaa atggtgtgat 60  
gatcagccca cagtacacat cattgatgag aatttcactg gtctcaacct ttctcatgct 120  
gagtcctggc tttgtaaaat gacttataaa ggtccaagga ttttagagatg attaagagat 180  
aagctggcat tctgtaaagg caccatcgac tatccccgtt ctatctaga taaagaatgt 240  
agtgcataat ctgtataaa tattgtacaa atggaaattc aatcttaagg attattttt 300  
ccatattgtt gtatccatt gtgggttatt ggaaagtgtat ctggactttt agtgagaaga 360  
tgtgatttgg accatggcac taaaaactc tataacctca ggcaagtctt ttaatcttct 420  
ctgagcctca gtttcctca ttttcaaat atagagagta taacatttat ctcataagac 480  
aagttgttgtt aaattactgt tttacaaatg taagataact tttaactgtg agattccata 540  
ttccagtctt acattattat gtttatctgc cacagggaga agtcctcaga taaaaatgtc 600  
taccaaaaaga ctgacacgtg gagttaatca tttgacagat gcaaattgtt ccaccccaa 660  
caaataatact ttctttaact tctgtgtggg tatcacttag ggaaaaaaaaag gcaggcaaca 720  
aaatattttt taattctatc ttagaaaaaa ttgtagncaa atctttttnt cccattaaca 780  
aataatgtaa gccttaatat tcaaggggta ataaaaatac aaagtcttcc aaacaggtaa 840  
cttacttgaa aacttt 856

<210> 62  
<211> 348  
<212> PRT  
<213> human organism

<220>  
<221> misc\_feature  
<222> (152)..(152)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> misc\_feature  
<222> (154)..(154)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> misc\_feature  
<222> (217)..(217)  
<223> Xaa can be any naturally occurring amino acid

<400> 62

Met Gly Ala Arg Gly Ala Pro Ser Arg Arg Arg Gln Ala Gly Arg Arg  
1 5 10 15

Leu Arg Tyr Leu Pro Thr Gly Ser Phe Pro Phe Leu Leu Leu Leu Leu  
20 25 30

Leu Leu Cys Ile Gln Leu Gly Gly Gln Lys Lys Lys Glu Asn Leu  
35 40 45

Leu Ala Glu Lys Val Glu Gln Leu Met Glu Trp Ser Ser Arg Arg Ser  
50 55 60

Ile Phe Arg Met Asn Gly Asp Lys Phe Arg Lys Phe Ile Lys Ala Pro  
65 70 75 80

Pro Arg Asn Tyr Ser Met Ile Val Met Phe Thr Ala Leu Gln Pro Gln  
85 90 95

Arg Gln Cys Ser Val Cys Arg Gln Ala Asn Glu Glu Tyr Gln Ile Leu  
100 105 110

Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Cys Asn Lys Leu Phe Phe  
115 120 125

Ser Met Val Asp Tyr Asp Glu Gly Thr Asp Val Phe Gln Gln Leu Asn  
130 135 140

Met Asn Ser Ala Pro Thr Phe Xaa His Xaa Pro Pro Lys Gly Arg Pro  
145 150 155 160

Lys Arg Ala Asp Thr Phe Asp Leu Gln Arg Ile Gly Phe Ala Ala Glu  
165 170 175

Gln Leu Ala Lys Trp Ile Ala Asp Arg Thr Asp Val His Ile Arg Val  
180 185 190

Phe Arg Pro Pro Asn Tyr Ser Gly Thr Ile Ala Leu Ala Leu Val  
195 200 205

Ser Leu Val Gly Gly Leu Leu Tyr Xaa Arg Arg Asn Asn Leu Glu Phe  
210 215 220

Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile Val Phe  
225 230 235 240

Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro Pro Tyr  
245 250 255

Ala His Lys Asn Pro His Asn Gly Gln Val Ser Tyr Ile His Gly Ser  
260 265 270

Ser Gln Ala Gln Phe Val Ala Glu Ser His Ile Ile Leu Val Leu Asn  
275 280 285

Ala Ala Ile Thr Met Gly Met Val Leu Leu Asn Glu Ala Ala Thr Ser  
290 295 300

Lys Gly Asp Val Gly Lys Arg Arg Ile Ile Cys Leu Val Gly Leu Gly  
305 310 315 320

Leu Val Val Phe Phe Ser Phe Leu Leu Ser Ile Phe Arg Ser Lys  
325 330 335

Tyr His Gly Tyr Pro Tyr Ser Asp Leu Asp Phe Glu  
340 345

<210> 63  
<211> 1130  
<212> DNA

<213> human organism

<400> 63  
ggtcggcgca ccggccgcct ccggccccgcc gcccgcggc gcccacccgccc 60  
ggggcgccca ccgcgtgcc agcctacccc gcggccgagc cgcccgccgccc gctgtggctg 120  
cagggcgagc cgctgcattt ctgctgccta gacttcagcc tggaggagct gcagggcgag 180  
ccgggctggc ggctgaaccg taagcccatt gagtccacgc tggtggcctg cttcatgacc 240  
ctggtcatcg tggtgtggag cgtggccgccc ctcatctggc cggtgcccat catcgccggc 300  
ttcctgcccac acggcatgga acagcgccgg accaccgcca gcaccaccgc agccacccccc 360  
gccgcagtgc ccgcaggac caccgcagcc gccgcgcgg cccgcgtgc cgccgcgc 420  
gcggccgtca cttcggggtt ggcgaccaag tgacccgctc cgctcctccc tgtgtccgtc 480  
ctgtgtccgc gcgcgcgggt gccttcccg ccggggactc ggccgggtgt cttcgtgctg 540  
tagttatcgtagttcctct tcccagatg gggccgcccga gagaccccaag cgcctttgaa 600  
aagaaggatt tgcgtgcgc ttccagttcc gaaaagcaga tgtttaagcc cttggactga 660  
gggtgggatc gcagctccga agacggagag gagggaaatg gggcccttc ccctctattg 720  
catccccctg cccgactcct tccccgcacc cacgtccct agattcatgg cagaaaatga 780  
ccaaatcctg tgtatttgc ttatataattt aataactgtt ttaaatgaaa gtttttagtaa 840  
aaaaaataca aaacaaaaaag attaaattgc tattgtgtt gtaagagaag ctctttgtat 900  
ctgaacatag ttgtatttga aatttgcgtt ttttaattt attaaaattt ggggggaggg 960  
catggaaagg atttaacacc gatataattgt taccgctgaa aatgaacttt atgaaccttt 1020  
tccaaaggatgatc tctatccagt gacgtggcct ggtggcggt tcttctgtt cttatgttgt 1080  
ttttggctt ttaatacaga catttcctc caaaaaaaaaa aaaaaaaaaagg 1130

<210> 64

<211> 150

<212> PRT

<213> human organism

<400> 64

Gly Arg Arg Thr Gly Arg Leu Arg Pro Ala Ala Ala Pro Ser Ala Ala  
1 5 10 15

Ala Ala Thr Ala Gly Ala Pro Thr Ala Leu Pro Ala Tyr Pro Ala Ala  
20 25 30

Glu Pro Pro Gly Pro Leu Trp Leu Gln Gly Glu Pro Leu His Phe Cys  
35 40 45

Cys Leu Asp Phe Ser Leu Glu Glu Leu Gln Gly Glu Pro Gly Trp Arg  
50 55 60

Leu Asn Arg Lys Pro Ile Glu Ser Thr Leu Val Ala Cys Phe Met Thr  
65 70 75 80

Leu Val Ile Val Val Trp Ser Val Ala Ala Leu Ile Trp Pro Val Pro  
85 90 95

Ile Ile Ala Gly Phe Leu Pro Asn Gly Met Glu Gln Arg Arg Thr Thr  
100 105 110

Ala Ser Thr Thr Ala Ala Thr Pro Ala Ala Val Pro Ala Gly Thr Thr  
115 120 125

Ala Val Thr  
130 135 140

Ser Gly Val Ala Thr Lys  
145 150

<210> 65  
<211> 1521  
<212> DNA  
<213> human organism

<220>  
<221> misc\_feature  
<222> (798)..(798)  
<223> n is a, c, g, or t

<400> 65  
cggccgcggc cgggtccct cgcaaagccg ctgccatccc ggaggggcca gccagcgggc 60  
tccccggggc tggccgggca ggcgtggtgc gcggtaggag ctggcgccgc acggctaccg 120  
cgcggtggagg agacactgcc ctgcccgcgt gggggcccg ggcgctcctt cacgcccgtag 180  
gcaagcgggg cggcggctgc ggtacctgcc caccgggagc tttcccttcc ttctcctgct 240  
gctgctgctc tgcatccagc tcgggggagg acagaagaaa aaggagaatc ttttagctga 300  
aaaagttagag cagctgatgg aatggagttc cagacgctca atcttccgaa tgaatggta 360  
taaattccga aaatttataa aggcaccacc tcgaaactat tccatgattg ttatgttcac 420

tgctttcag cctcagcggc agtgttctgt gtgcaggcaa gctaataaat	480
actggcgAAC tcctggcgCT attcatctgc tttttgtAAC aagctttct tcagtatggT	540
ggactatgat gaggggacAG acgttttca gcagctcaAC atgaactctG ctcctacATT	600
caygcattw cctccaaaAG gcagacctaA gagagctgat acttttgacc tccaaagaAT	660
tggatttgca gctgagcaAC tagcaaAGtG gattgtGAC agaacGGatG ttcatattcg	720
ggttttcaga ccacccaACT actctggtaC cattgtttG gccctgttag tgtcgcttGT	780
tggaggTTTg ctTTtatnGA gaaggaacAA cttggagttC atctataACA agactggTTG	840
ggccatggTG tctctgtGTa tagtcttGC tatgacttCT ggCCAGATgt ggaaccatAT	900
ccgtggacCT ccatatgCTC ataagaACCC acacaatGGA caagtGAGCT acattcatGG	960
gagcagccAG gctcagTTTg tggcagaATC acacattatt ctggtaCTG atGCCGCTat	1020
caccatgggg atggTTCTTC taaatGAAGC agcaacttCG aaaggcGATG ttggaaaaAG	1080
acgataatt tgcctagtGG gattgggcCT ggtggTCTC ttcttcAGTT ttctactttC	1140
aatatttCGT tccaagtACC acggctatCC ttatagtGAT ctggactttG agtGAGAAGA	1200
tgtgatttgg accatggcac ttAAAAACTC tataacctCA gcttttaat taaatGAAGC	1260
caagtgggat ttgcataaAG tgaatgtttA ccatGAAGAT aaactgttCC tgactttATA	1320
ctatTTGAA ttcatTCATT tcattgtGAT cagctagCTT attcttGtGt acTTTTTTA	1380
aactgtggGT ttccctAGTA aatttaATTt acagaaATCA atggtagCAT ttGtaatCT	1440
acaaaggAAA tatcaaAGtG ttTTcaAGC ctgttatATy cagtgtgtKC cacaggattG	1500
caataaaatGA caatgtAAATT A	1521

<210> 66  
 <211> 348  
 <212> PRT  
 <213> human organism

<220>  
 <221> misc\_feature  
 <222> (152)..(152)  
 <223> Xaa can be any naturally occurring amino acid

<220>  
 <221> misc\_feature  
 <222> (154)..(154)  
 <223> Xaa can be any naturally occurring amino acid

<220>

<221> misc\_feature  
<222> (217)..(217)  
<223> Xaa can be any naturally occurring amino acid

<400> 66

Met Gly Ala Arg Gly Ala Pro Ser Arg Arg Arg Gln Ala Gly Arg Arg  
1 5 10 15

Leu Arg Tyr Leu Pro Thr Gly Ser Phe Pro Phe Leu Leu Leu Leu  
20 25 30

Leu Leu Cys Ile Gln Leu Gly Gly Gln Lys Lys Lys Glu Asn Leu  
35 40 45

Leu Ala Glu Lys Val Glu Gln Leu Met Glu Trp Ser Ser Arg Arg Ser  
50 55 60

Ile Phe Arg Met Asn Gly Asp Lys Phe Arg Lys Phe Ile Lys Ala Pro  
65 70 75 80

Pro Arg Asn Tyr Ser Met Ile Val Met Phe Thr Ala Leu Gln Pro Gln  
85 90 95

Arg Gln Cys Ser Val Cys Arg Gln Ala Asn Glu Glu Tyr Gln Ile Leu  
100 105 110

Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Cys Asn Lys Leu Phe Phe  
115 120 125

Ser Met Val Asp Tyr Asp Glu Gly Thr Asp Val Phe Gln Gln Leu Asn  
130 135 140

Met Asn Ser Ala Pro Thr Phe Xaa His Xaa Pro Pro Lys Gly Arg Pro  
145 150 155 160

Lys Arg Ala Asp Thr Phe Asp Leu Gln Arg Ile Gly Phe Ala Ala Glu  
165 170 175

Gln Leu Ala Lys Trp Ile Ala Asp Arg Thr Asp Val His Ile Arg Val  
180 185 190

Phe Arg Pro Pro Asn Tyr Ser Gly Thr Ile Ala Leu Ala Leu Val  
195 200 205

Ser Leu Val Gly Gly Leu Leu Tyr Xaa Arg Arg Asn Asn Leu Glu Phe  
210 215 220

Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile Val Phe  
225 230 235 240

Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro Pro Tyr  
245 250 255

Ala His Lys Asn Pro His Asn Gly Gln Val Ser Tyr Ile His Gly Ser  
260 265 270

Ser Gln Ala Gln Phe Val Ala Glu Ser His Ile Ile Leu Val Leu Asn  
275 280 285

Ala Ala Ile Thr Met Gly Met Val Leu Leu Asn Glu Ala Ala Thr Ser  
290 295 300

Lys Gly Asp Val Gly Lys Arg Arg Ile Ile Cys Leu Val Gly Leu Gly  
305 310 315 320

Leu Val Val Phe Phe Ser Phe Leu Leu Ser Ile Phe Arg Ser Lys  
325 330 335

Tyr His Gly Tyr Pro Tyr Ser Asp Leu Asp Phe Glu  
340 345

<210> 67  
<211> 2306  
<212> DNA  
<213> human organism

<400> 67  
ggtttcatat gaactctccc gccacccggg aacagctggc tgccaccgtt tgtgtttcc 60  
gagtttgtat tcttgaggt gaccaagatg gagtttctg gaagaaaagcg gaggaagctg 120  
aggttggcag gtgaccagag gaatgcttcc tacccatt gccttcagtt ttacttgcag 180  
ccaccttctg aaaacatatac ttaaacagaa tttgaaaact tggctattga tagagttaaa 240  
ttgttaaat cagttaaaaa tcttggagtg agctatgtga aaggaactga acaataccag 300  
agtaagttgg agagttagt tcgaaagctc aagtttcct acagagagaa gctagaagat 360  
gaatatgaac cacgaagaag agatcatatt tctcattta tttgcggct tgcttattgc 420

cagtctgaag aacttagacg ctggttcatt caacaagaaa tggatctcct tcgatttaga 480  
tttagtattt tacccaagga taaaattcag gatttcttaa aggatagcca attgcagttt 540  
gaggctataa gtgatgaaga gaagactctt cgagaacagg agattgtgc ctcacccacca 600  
agtttaagtg gacttaagtt ggggttcgag tccattata agatccctt tgctgatgct 660  
ctggatttgt ttcgaggaag gaaagtctat ttgaaagatg gctttgctta cgtaccactt 720  
aaggacattg tggcaatcat cctgaatgaa tttagagcca aactgtccaa ggcttggca 780  
ttaacagcca ggtccttgcc tgctgtcag tctgatgaaa gacttcagcc tctgctcaat 840  
cacccatcgtc attcctacac tggccaaagat tacagtaccc agggaaatgt tggaaagatt 900  
tcttagatc agattgattt gctttctacc aaatccttcc caccttgcatt gcgtcagtta 960  
cataaaggcct tgcggggaaaa tcaccatctt cgtcatggag gccgaatgca gtatggccta 1020  
tttctgaagg gcattggttt aactttggaa caggcattgc agttctggaa gcaagaattt 1080  
atcaaaggaa agatggatcc agacaagttt gataaaggtt actcttacaa catccgtcac 1140  
agctttggaa aggaaggcaa gaggacagac tatacacctt tcagttgcct gaagattatt 1200  
ctgtccaatc caccaagcca aggggattat catgggtgcc cattccgtca cagtgtcc 1260  
gagctgctga agcaaaagtt gcagtcatac aagatctcctc ctggagggat aagccagatt 1320  
ttggattttag taaaggggac acattaccag gtgcctgtc aaaaatactt tgagatgata 1380  
cacaatgtgg atgattgtgg cttttctttg aatcatccta atcagttctt ttgtgagagc 1440  
caacgtattc taaatggatgg taaagacata aagaaggaac ctatccaacc agaaactcct 1500  
caacccaaac caagtgtcca gaaaaccaag gatgcattcat ctgcctggc ctctttaat 1560  
tcctctctgg aaatggatata ggaaggacta gaagattact tttagtgaaga ttcttaggca 1620  
gttttataac ctttttcctt caatagcctg tttcctgttt ttaagatttt gccttgg 1680  
ttgaaaaagg gtttcactgt caccaaggct tagtcagtg acacaattac agctgattgc 1740  
agccttgacc ttcccagctc aagtgtatcct cctacccatcg cctcccaagt agttaggaca 1800  
cacaggtgtg cacctcatat ccagataatt ttttcaatt ttttttggta gaggtggggg 1860  
gtctccctat gttgcccagg cagatctcag actcctggc tcaagcgatc ctcacaccc 1920  
agcgtcccag agtgcgtggaa ttacagttgt gagccactgt gcctggcctt tttttttttt 1980  
taaccttttc gtttaacttc tctcttcaact gcatccaaat ccatctacag gcatgcacac 2040  
ttatttaggaa aggaggtttg aggttacaac agagacttcc actatatttt gctttgacag 2100  
aaggaaagag gaggagtttc tattaaaatc tgtcacttga gtgtatgtcat ttaagtccta 2160

ttttaggaga taaaaacagc tttggggact ggttaaagtc ccccgagaaac tacaataaag 2220  
aacaactttt gtttaactc ttaatcactt tgtaatttg actcaatcct tttctggacc 2280  
attttgtta ataaatatca aagtgt 2306

<210> 68  
<211> 509  
<212> PRT  
<213> human organism

<400> 68

Met Glu Phe Ser Gly Arg Lys Arg Arg Lys Leu Arg Leu Ala Gly Asp  
1 5 10 15

Gln Arg Asn Ala Ser Tyr Pro His Cys Leu Gln Phe Tyr Leu Gln Pro  
20 25 30

Pro Ser Glu Asn Ile Ser Leu Thr Glu Phe Glu Asn Leu Ala Ile Asp  
35 40 45

Arg Val Lys Leu Leu Lys Ser Val Glu Asn Leu Gly Val Ser Tyr Val  
50 55 60

Lys Gly Thr Glu Gln Tyr Gln Ser Lys Leu Glu Ser Glu Leu Arg Lys  
65 70 75 80

Leu Lys Phe Ser Tyr Arg Glu Lys Leu Glu Asp Glu Tyr Glu Pro Arg  
85 90 95

Arg Arg Asp His Ile Ser His Phe Ile Leu Arg Leu Ala Tyr Cys Gln  
100 105 110

Ser Glu Glu Leu Arg Arg Trp Phe Ile Gln Gln Glu Met Asp Leu Leu  
115 120 125

Arg Phe Arg Phe Ser Ile Leu Pro Lys Asp Lys Ile Gln Asp Phe Leu  
130 135 140

Lys Asp Ser Gln Leu Gln Phe Glu Ala Ile Ser Asp Glu Glu Lys Thr  
145 150 155 160

Leu Arg Glu Gln Glu Ile Val Ala Ser Ser Pro Ser Leu Ser Gly Leu  
165 170 175

Lys Leu Gly Phe Glu Ser Ile Tyr Lys Ile Pro Phe Ala Asp Ala Leu  
180 185 190

Asp Leu Phe Arg Gly Arg Lys Val Tyr Leu Glu Asp Gly Phe Ala Tyr  
195 200 205

Val Pro Leu Lys Asp Ile Val Ala Ile Ile Leu Asn Glu Phe Arg Ala  
210 215 220

Lys Leu Ser Lys Ala Leu Ala Leu Thr Ala Arg Ser Leu Pro Ala Val  
225 230 235 240

Gln Ser Asp Glu Arg Leu Gln Pro Leu Leu Asn His Leu Ser His Ser  
245 250 255

Tyr Thr Gly Gln Asp Tyr Ser Thr Gln Gly Asn Val Gly Lys Ile Ser  
260 265 270

Leu Asp Gln Ile Asp Leu Leu Ser Thr Lys Ser Phe Pro Pro Cys Met  
275 280 285

Arg Gln Leu His Lys Ala Leu Arg Glu Asn His His Leu Arg His Gly  
290 295 300

Gly Arg Met Gln Tyr Gly Leu Phe Leu Lys Gly Ile Gly Leu Thr Leu  
305 310 315 320

Glu Gln Ala Leu Gln Phe Trp Lys Gln Glu Phe Ile Lys Gly Lys Met  
325 330 335

Asp Pro Asp Lys Phe Asp Lys Gly Tyr Ser Tyr Asn Ile Arg His Ser  
340 345 350

Phe Gly Lys Glu Gly Lys Arg Thr Asp Tyr Thr Pro Phe Ser Cys Leu  
355 360 365

Lys Ile Ile Leu Ser Asn Pro Pro Ser Gln Gly Asp Tyr His Gly Cys  
370 375 380

Pro Phe Arg His Ser Asp Pro Glu Leu Leu Lys Gln Lys Leu Gln Ser  
385 390 395 400

Tyr Lys Ile Ser Pro Gly Gly Ile Ser Gln Ile Leu Asp Leu Val Lys  
405 410 415

Gly Thr His Tyr Gln Val Ala Cys Gln Lys Tyr Phe Glu Met Ile His  
420 425 430

Asn Val Asp Asp Cys Gly Phe Ser Leu Asn His Pro Asn Gln Phe Phe  
435 440 445

Cys Glu Ser Gln Arg Ile Leu Asn Gly Gly Lys Asp Ile Lys Lys Glu  
450 455 460

Pro Ile Gln Pro Glu Thr Pro Gln Pro Lys Pro Ser Val Gln Lys Thr  
465 470 475 480

Lys Asp Ala Ser Ser Ala Leu Ala Ser Leu Asn Ser Ser Leu Glu Met  
485 490 495

Asp Met Glu Gly Leu Glu Asp Tyr Phe Ser Glu Asp Ser  
500 505

<210> 69  
<211> 1901  
<212> DNA  
<213> human organism

<400> 69  
aattcataca ggagagaagt catatatatg cagtgattgt ggaaaaggct tcatacgaa 60  
gtctcggctc attaatcatc agagagttca tacaggagag aaaccacatg gatgcagcct 120  
gtgtggaaag gccttctcca aaaggtccag gtcactgaa caccagagaa ctcatacagg 180  
agagaagccc tatgaatgca ctgaatgtga caaagcattc cgctggaaat cacagctcaa 240  
tgcacatcg aaagctcaca caggagagaa gtcatatata tgccgtgatt gtggaaaagg 300  
cttcattcag aaggaaatc tcattgtaca tcagcgaatt catactggag aaaaacccta 360  
tatatgcaat gaatgtggaa aaggcttcat ccaaaaggcc aacccctta ttcatcgacg 420  
tactcacact ggagagaaac cctatgaatg caatgaatgt gggaaaggct tcagccagaa 480  
gacatgttta atatccatc agagattca cacaggaaag acacccttg tatgtactga 540  
gtgtggaaaa tcctgctcac acaagtcagg tctcattaac caccagagaa ttcacacagg 600  
agagaaaccc tatacatgca gtgactgtgg gaaagcttc agagataaat catgtctcaa 660

cagacatcg	agaactcata	cagggagag	accgtatgga	tgctctgatt	gtggaaagc	720
tttctccac	ttgtcatgcc	ttgttatca	taagggaatg	ctgcatgcaa	gagagaaatg	780
tgttagttca	gtcaaattgg	aaaatcctt	ctcagagagt	catagcttat	cacatacacg	840
tgatctcata	caggataaaag	actctgttaa	catggtact	ctgcagatgc	cttctgtggc	900
agctcagacc	tcattaacta	acagtgcgtt	ccaagcagag	agcaaagtag	ccattgtgag	960
ccagcctgtt	gccagaagtt	cagtctcagc	agatagtaga	atttgcacag	aataaaaacc	1020
atatgaatgc	agtgaatgtg	gtagtgc	cagtgatcaa	ttacatcata	tgtcacaaaa	1080
aacacagagg	aacaaactga	tatattcaag	gtggaaagcc	cttgaataaa	accttatggc	1140
taataagcat	atactcagag	aaaaatagta	tgaagtggag	actggaaat	tctttatgg	1200
gaagatagat	cttctcatca	gtgaccatag	atcacatctt	cagtgagctt	atagttggta	1260
gaaatataat	gatcatggaa	aagtccttgt	tcagaaacag	tacgccagta	ggtatcaggg	1320
ggtttacaca	ggagagaaac	tttggaaga	ccttgaagg	ctatgaatgt	ggcagggttg	1380
ctagttgtac	attctgcctt	atcctcagag	ggaatcatat	agaaataaaa	ctatgaaaat	1440
gtaactagaa	catcttcatc	aaaatatgaa	agaacacacg	aagcaaataa	gccctgtgaa	1500
aaggagtatt	ttagagattt	cgatcagaaa	tctaacatca	ttatatggca	gataatatac	1560
aggatgtgta	ttttaggaca	atatacctt	aatcaactgt	tgatatgtca	atgactaatt	1620
aaaaggggtt	gtcagtgtt	cacatcattt	gttaaattt	tagcacaatg	tacctttcc	1680
cccttttt	ataagagtct	tctattccca	accaagatca	ttatatgatt	agctttgt	1740
tttctttgat	tccaaattt	ttcacttgtt	atttcagact	actgaagctc	ttcaaaagga	1800
aaaatgtatt	taatttaata	atgtAACACA	acaagttgg	atgtgtttaa	ctttataaaat	1860
aatcacccca	gaggaatgaa	gttcaaaact	tgtgaataac	c		1901

<210> 70  
 <211> 127  
 <212> PRT  
 <213> human organism

<400> 70

Met	Asp	Ala	Ala	Cys	Val	Gly	Arg	Pro	Ser	Pro	Lys	Gly	Pro	Gly	Ser
1					5				10				15		

Leu	Asn	Thr	Arg	Glu	Leu	Ile	Gln	Glu	Arg	Ser	Pro	Met	Asn	Ala	Leu
					20			25				30			

Asn Val Thr Lys His Ser Ala Gly Asn His Ser Ser Met His Ile Arg  
35 40 45

Lys Leu Thr Gln Glu Arg Ser His Ile Tyr Ala Val Ile Val Glu Lys  
50 55 60

Ala Ser Phe Arg Arg Glu Ile Ser Leu Tyr Ile Ser Glu Phe Ile Leu  
65 70 75 80

Glu Lys Asn Pro Ile Tyr Ala Met Asn Val Glu Lys Ala Ser Ser Lys  
85 90 95

Arg Ala Thr Ser Leu Phe Ile Asp Val Leu Thr Leu Glu Arg Asn Pro  
100 105 110

Met Asn Ala Met Asn Val Gly Lys Ala Ser Ala Arg Arg His Val  
115 120 125

<210> 71  
<211> 1005  
<212> DNA  
<213> human organism

<400> 71	
aatttcggca cgggggggag gcacagttag tccactgggg cacggcagcg tctaagccac	60
aagccgactg acataagcca ggtcctaacg gagcctatgt gtaagtccac tactggtgca	120
aggttgcaca cttctaagaa gagcggcgtg gggggctcg cgaccttcgc ttcagtcgct	180
ccccctgtca gtccccctgtc cccaagacac agcctgatgc ttgtgctccg gtggggcggac	240
ttggaggcgg cgggaactgc aatttggtggc tttgaagggc ggcgagcggg aacagcttt	300
gaggagttag actgcaggag atgtggcccg tgccaaagag atggatgaga ctgttgctga	360
gttcatcaag aggaccatct tgaaaatccc catgaatgaa ctgacaacaa tcctgaaggc	420
ctgggatttt ttgtctgaaa atcaactgca gactgtaaat ttccgacaga gaaaggaatc	480
tgtagttcag cacttgatcc atctgtgtga ggaaaagcgt gcaagtatca gtgatgctgc	540
cctgttagac atcatttata tgcaatttca tcagcaccag aaagtttggg atgttttca	600
gatgagtaaa ggaccaggtg aagatgttgat ccttttgat atgaaacaat ttaaaaattc	660
ttcaagaaaa attcttcaga gagcattaaa aaatgtgaca gtcagcttca gagaaactga	720
ggagaatgca gtctggattc gaattgcctg gggAACACAG tacacaaAGC caaaccagta	780

caaacctacc tacgtggtgt actactccca gactccgtac gccttcacgt ctcctccat 840  
gctgaggcgc aatacaccgc ttctgggtca ggagtttagaa gctactggga aaatctacct 900  
ccgacaagag gagatcattt tagatattac cgaaatgaag aaagcttgca attagtgaac 960  
atgaaaggaa aataaaaatt cctcacagtc aaaaaaaaaa aaaaa 1005

<210> 72  
<211> 204  
<212> PRT  
<213> human organism

<400> 72

Met Asp Glu Thr Val Ala Glu Phe Ile Lys Arg Thr Ile Leu Lys Ile  
1 5 10 15

Pro Met Asn Glu Leu Thr Thr Ile Leu Lys Ala Trp Asp Phe Leu Ser  
20 25 30

Glu Asn Gln Leu Gln Thr Val Asn Phe Arg Gln Arg Lys Glu Ser Val  
35 40 45

Val Gln His Leu Ile His Leu Cys Glu Glu Lys Arg Ala Ser Ile Ser  
50 55 60

Asp Ala Ala Leu Leu Asp Ile Ile Tyr Met Gln Phe His Gln His Gln  
65 70 75 80

Lys Val Trp Asp Val Phe Gln Met Ser Lys Gly Pro Gly Glu Asp Val  
85 90 95

Asp Leu Phe Asp Met Lys Gln Phe Lys Asn Ser Phe Lys Ile Leu  
100 105 110

Gln Arg Ala Leu Lys Asn Val Thr Val Ser Phe Arg Glu Thr Glu Glu  
115 120 125

Asn Ala Val Trp Ile Arg Ile Ala Trp Gly Thr Gln Tyr Thr Lys Pro  
130 135 140

Asn Gln Tyr Lys Pro Thr Tyr Val Val Tyr Ser Gln Thr Pro Tyr  
145 150 155 160

Ala Phe Thr Ser Ser Ser Met Leu Arg Arg Asn Thr Pro Leu Leu Gly

165

170

175

Gln Glu Leu Glu Ala Thr Gly Lys Ile Tyr Leu Arg Gln Glu Glu Ile  
 180                            185                            190

Ile Leu Asp Ile Thr Glu Met Lys Lys Ala Cys Asn  
 195                            200

<210> 73  
<211> 1125  
<212> DNA  
<213> human organism

<400> 73						
atggtgctgt	gggagtcccc	gcggcagtgc	agcagctgga	cactttgcga	gggctttgc	60
tggctgctgc	tgctgccgt	catgctactc	atcgtagccc	gcccggtgaa	gctcgctgct	120
ttccctacct	ccttaagtga	ctgccaaacg	cccaccggct	ggaattgctc	tggttatgat	180
gacagagaaa	atgatctt	cctctgtgac	accaacacct	gtaaatttga	tggggaatgt	240
ttaagaattg	gagacactgt	gacttgcgtc	tgtcagttca	agtcaacaa	tgactatgt	300
cctgtgtgt	gctccaatgg	ggagagctac	cagaatgagt	gttacctgct	acaggctgca	360
tgcaaacagc	agagtgagat	acttgtggtg	tcagaaggat	catgtgccac	agatgcagga	420
tcaggatctg	gagatggagt	ccatgaaggc	tctggagaaa	ctagtcaaaa	ggagacatcc	480
acctgtgata	tttgcagtt	tggtcagaa	tgtgacgaa	atgcccggaa	tgtctgggt	540
gtgtgtata	ttgactgttc	tcaaaccaac	ttcaatcccc	tctgcgttcc	tgtatggaaa	600
tcttatgata	atgcatgcca	aatcaaagaa	gcatcgtgtc	agaaacagga	gaaaattgaa	660
gtcatgtctt	tgggtcgatg	tcaagataac	acaactacaa	ctactaagtc	tgaagatggg	720
cattatgcaa	gaacagatta	tgcagagaat	gctaacaat	tagaagaaa	tgccagagaa	780
caccacatac	cttgtccgga	acattacaat	ggcttctgca	tgcatggaa	gtgtgagcat	840
tctatcaata	tgcaggagcc	atcttgcagg	tgtgatgctg	gttatactgg	acaacactgt	900
aaaaaaaaagg	actacagtgt	tctatacggt	gttccggtc	ctgtacgatt	tcagtatgtc	960
ttaatcgag	ctgtgattgg	aacaattcag	attgctgtca	tctgtgtggt	ggtcctctgc	1020
atcacaagga	aatgccccag	aagcaacaga	attcacagac	agaagcaaaa	tacagggcac	1080
tacagttcag	acaatacaac	aagagcgtcc	acgaggtaa	tctga		1125

&lt;210&gt; 74

<211> 374

<212> PRT

<213> human organism

<400> 74

Met Val Leu Trp Glu Ser Pro Arg Gln Cys Ser Ser Trp Thr Leu Cys  
1 5 10 15

Glu Gly Phe Cys Trp Leu Leu Leu Pro Val Met Leu Leu Ile Val  
20 25 30

Ala Arg Pro Val Lys Leu Ala Ala Phe Pro Thr Ser Leu Ser Asp Cys  
35 40 45

Gln Thr Pro Thr Gly Trp Asn Cys Ser Gly Tyr Asp Asp Arg Glu Asn  
50 55 60

Asp Leu Phe Leu Cys Asp Thr Asn Thr Cys Lys Phe Asp Gly Glu Cys  
65 70 75 80

Leu Arg Ile Gly Asp Thr Val Thr Cys Val Cys Gln Phe Lys Cys Asn  
85 90 95

Asn Asp Tyr Val Pro Val Cys Gly Ser Asn Gly Glu Ser Tyr Gln Asn  
100 105 110

Glu Cys Tyr Leu Arg Gln Ala Ala Cys Lys Gln Gln Ser Glu Ile Leu  
115 120 125

Val Val Ser Glu Gly Ser Cys Ala Thr Asp Ala Gly Ser Gly Ser Gly  
130 135 140

Asp Gly Val His Glu Gly Ser Gly Glu Thr Ser Gln Lys Glu Thr Ser  
145 150 155 160

Thr Cys Asp Ile Cys Gln Phe Gly Ala Glu Cys Asp Glu Asp Ala Glu  
165 170 175

Asp Val Trp Cys Val Cys Asn Ile Asp Cys Ser Gln Thr Asn Phe Asn  
180 185 190

Pro Leu Cys Ala Ser Asp Gly Lys Ser Tyr Asp Asn Ala Cys Gln Ile  
195 200 205

Lys Glu Ala Ser Cys Gln Lys Gln Glu Lys Ile Glu Val Met Ser Leu  
210 215 220

Gly Arg Cys Gln Asp Asn Thr Thr Thr Thr Lys Ser Glu Asp Gly  
225 230 235 240

His Tyr Ala Arg Thr Asp Tyr Ala Glu Asn Ala Asn Lys Leu Glu Glu  
245 250 255

Ser Ala Arg Glu His His Ile Pro Cys Pro Glu His Tyr Asn Gly Phe  
260 265 270

Cys Met His Gly Lys Cys Glu His Ser Ile Asn Met Gln Glu Pro Ser  
275 280 285

Cys Arg Cys Asp Ala Gly Tyr Thr Gly Gln His Cys Glu Lys Lys Asp  
290 295 300

Tyr Ser Val Leu Tyr Val Val Pro Gly Pro Val Arg Phe Gln Tyr Val  
305 310 315 320

Leu Ile Ala Ala Val Ile Gly Thr Ile Gln Ile Ala Val Ile Cys Val  
325 330 335

Val Val Leu Cys Ile Thr Arg Lys Cys Pro Arg Ser Asn Arg Ile His  
340 345 350

Arg Gln Lys Gln Asn Thr Gly His Tyr Ser Ser Asp Asn Thr Thr Arg  
355 360 365

Ala Ser Thr Arg Leu Ile  
370

<210> 75  
<211> 2068  
<212> DNA  
<213> human organism

<220>  
<221> misc\_feature  
<222> (143)..(143)  
<223> n is a, c, g, or t

<400> 75

ggcgccggga ttgggagggc ttcttcagg ctgctggct ggggctaagg gctgctcagt 60  
ttccttcagc ggggcactgg gaagcgccat ggcactgcag ggcacatctcg tcgtggagct 120  
gtccggcctg gccccgggcc gtntctgtgc tatggcctg gctgacttcg gggcgctgt 180  
ggtacgcgtg gaccggcccg gctcccgtca cgacgtgagc cgcttgggcc gggcaagcg 240  
ctcgcttagtg ctggacctga agcagccgcg ggagccgcgt gctgcccgt ctgtgcaagc 300  
ggtcggatgt gctgctggag cccttcggcc gcgggtgtcat ggagaaaactc cagctggcc 360  
cagagattct gcagcggaa aatccaaggc ttatttatgc caggctgagt ggatttggcc 420  
agttcaggaa agcttctgcc ggttagctgg ccacgataatc aactatttgg ctttgcagg 480  
tgttctctca aaaattggca gaagtggta gaatccgtat gccccgtga atctcggtgc 540  
tgactttgct ggtgggtggcc ttatgtgtgc actggcatt ataatggctc ttttgcaccg 600  
cacacgcact gacaagggtc aggtcattga tgcaaataatg gtggaaggaa cagcatat 660  
aagttctttt ctgtggaaaa ctcagaaatc gagtctgtgg gaagcacctc gaggacagaa 720  
catgttggat ggtggagcac ctttctatac gacttacagg acagcagatg ggaaattcat 780  
ggctgttggaa gcaatagaac cccagttcta cgagctgctg atcaaaggac ttggactaaa 840  
gtctgatgaa cttcccaatc agatgagcac ggatgattgg ccagaaatga agaagaagtt 900  
tgcaagatgta tttgcaaaaga agacgaaggc agagtggtgt caaatctttg acggcacaga 960  
tgccctgtgtg actccggttc tgactttga ggaggttgtt catcatgatc acaacaagga 1020  
acggggctcg tttatcacca gtgaggagca ggacgtgagc ccccgcccttg cacctctgct 1080  
gttaaacacc ccagccatcc cttttccaa aggggatcct ttcataaggag aacacactga 1140  
ggagatactt gaagaatttg gattcagccg agaagagatt tatcagctta actcagataa 1200  
aatcattgaa agtaataagg taaaagctag tctctaactt ccaggcccac ggctcaagt 1260  
aatttgaata ctgcatttac agttagttagt aacacataac attgtatgca tggaaacatg 1320  
gaggaacagt attacagtgt cctaccactc taatcaagaa aagaattaca gactctgatt 1380  
ctacagtgtat gattgaattc taaaaatggt tatcattagg gctttgatt tataaaactt 1440  
tgggtactta tactaaatta tggtagttat tctgccttcc agtttgcctt atatattgt 1500  
tgatattaag attcttgact tatatttga atgggttcta gtaaaaagg aatgatatat 1560  
tcttgaagac atcgatatac atttatttac actcttgatt ctacaatgta gaaaatgagg 1620  
aaatgccaca aattgtatgg tgataaaaagt cacgtgaaac agagtgattt gttgcaccca 1680  
ggcctttgtt cttgggtgttc atgatctccc tctaagcaca ttccaaactt tagcaacagt 1740

tatcacactt tgtaatttgc aaagaaaaagt ttcacctgta ttgaatcaga atgccttcaa 1800  
ctgaaaaaaaa catatccaaa ataatgagga aatgtgttgg ctcactacgt agagtccaga 1860  
gggacagtca gtttagggt tgcctgtatc cagtaactcg gggcctgttt cccctgggt 1920  
ctctgggctg tcagcttcc tttctccatg tgtttgattt ctccctcaggc tggttagcaag 1980  
ttctggatct tatacccaac acacagcaac atccagaaat aaagatctca ggacccccc 2040  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 2068

<210> 76  
<211> 382  
<212> PRT  
<213> human organism

<220>  
<221> misc\_feature  
<222> (19)..(19)  
<223> Xaa can be any naturally occurring amino acid

<400> 76

Met Ala Leu Gln Gly Ile Ser Val Val Glu Leu Ser Gly Leu Ala Pro  
1 5 10 15

Gly Arg Xaa Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val  
20 25 30

Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg  
35 40 45

Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Glu Pro Arg  
50 55 60

Ala Ala Ala Ser Val Gln Ala Val Gly Cys Ala Ala Gly Ala Leu Pro  
65 70 75 80

Pro Arg Cys His Gly Glu Thr Pro Ala Gly Pro Arg Asp Ser Ala Ala  
85 90 95

Gly Lys Ser Lys Ala Tyr Leu Cys Gln Ala Glu Trp Ile Trp Pro Val  
100 105 110

Gln Glu Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala  
115 120 125

Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr  
130 135 140

Ala Pro Leu Asn Leu Val Ala Asp Phe Ala Gly Gly Gly Leu Met Cys  
145 150 155 160

Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys  
165 170 175

Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser  
180 185 190

Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg  
195 200 205

Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg  
210 215 220

Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe  
225 230 235 240

Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro  
245 250 255

Asn Gln Met Ser Thr Asp Asp Trp Pro Glu Met Lys Lys Phe Ala  
260 265 270

Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp  
275 280 285

Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val  
290 295 300

His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu  
305 310 315 320

Gln Asp Val Ser Pro Arg Leu Ala Pro Leu Leu Leu Asn Thr Pro Ala  
325 330 335

Ile Pro Ser Ser Lys Gly Asp Pro Phe Ile Gly Glu His Thr Glu Glu  
340 345 350

Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn  
355 360 365

Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu  
370 375 380

<210> 77  
<211> 5685  
<212> DNA  
<213> human organism

<400> 77  
gttaaatcct tacttacca gattcttgat ggtatccatt acctccatgc aaattgggtg 60  
cttcacagag acttgaaacc agcaaatac ctagtaatgg gagaaggccc tgagaggggg 120  
agagtcaaaa tagctgacat gggtttgcc agattattca attctcctct aaagccacta 180  
gcagatttgg atccagtagt tgtgacattt tggtatcggg ctccagaact tttgcttgg 240  
gcaaggcatt atacaaggc cattgatata tggcaatag gttgtatatt tgctgaattg 300  
ttgacttcgg aacctatccc tcactgtcgt caggaagata taaaaacaag caatccctt 360  
catcatgatc aactggatcg gatatttagt gtcatgggtt ttcctgcaga taaagactgg 420  
gaagatatta gaaagatgcc agaatatccc acacttcaa aagactttag aagaacaacg 480  
tatgccaaca gtagcctcat aaagtacatg gagaaacaca aggtcaagcc tgacagcaaa 540  
gtgttcctct tgcttcagaa actcctgacc atggatccaa ccaagagaat tacctcgag 600  
caagctctgc aggtcccta tttcaggag gacccttgc caacattaga tgtatttgc 660  
ggctgccaga ttccataccc caaacgagaa ttccttaatg aagatgatcc tgaagaaaa 720  
ggtgacaaga atcagcaaca gcagcagaac cagcatcagc agccccacagc ccctccacag 780  
caggcagcag cccctccaca ggcgcggccca ccacagcaga acagcacccca gaccaacggg 840  
accgcaggtg gggctgggc cggggtcggg ggcaccggag cagggttgc gcacagccag 900  
gactccagcc tgaaccaggt gcctccaaac aagaagccac ggctagggcc ttcaggcgca 960  
aactcaggtg gacctgtgat gccctcgat tatcagcact ccagttctcg cctgaattac 1020  
caaaggcagcg ttcaaggatc ctctcagtcc cagagcacac ttggctactc ttcctcgat 1080  
cagcagagct cacagtacca cccatctcac caggcccacc ggtactgacc agctcccggt 1140  
gggccaggcc agccccagccc agagcacagg ctccagcaat atgtctgcat taaaaagaac 1200  
caaaaaaaaaatg caaactatga tgccattaa aactcataca catgggagga aaacccatata 1260

tactgagcat tgtgcaggac tgatagctct tctttattga cttaaagaag attcttgtga 1320  
agtttccccca gcaccccttc cctgcattgtg ttccattgtg acttctctga taaagcgtct 1380  
gatctaattcc cagcacattct gtaaccttca gcatttctt gaaggatttc ctgggcacc 1440  
tttctcatgc tgttagcaatc actatggttt atctttcaa agctcttttta ataggatttt 1500  
aatgttttag aaacaggatt ccagtgggtgt atagtttat acttcatgaa ctgatttagc 1560  
aacacaggtta aaaatgcacc ttttaaagca ctacgtttc acagacaata actgttctgc 1620  
tcatttgcgtt cttaaacaga aactgttact gtcccaaagt actttactat tacgttcgta 1680  
tttatctagt ttcaaggaaag gtctaataaa aagacaagcg gtgggacaga gggAACCTAC 1740  
aaccaaaaac tgccttagatc ttgcagttt tttttttttt gcccacgaaga actgaagtat 1800  
gtggtaattt ttatagaatc attcatatgg aactgagttc ccagcatcat cttattctga 1860  
atagcattca gtaattaaga attacaattt taaccttcat gtagctaagt ctaccttaaa 1920  
aagggtttca agagctttgt acagtctcgta tggcccacac caaaacgctg aagagagtaa 1980  
caactgcact aggatttctg taaggagtaa ttttgcataa aagacgtgtt acttcccttt 2040  
gaaggaaaaag ttttttagtgt gtattgtaca taaagtcggc ttctctaaag aaccattgg 2100  
ttcttcacat ctgggtctgc gtgagtaact ttcttgata atcaagggtta ctcaagttaga 2160  
agcctgaaaaa ttaatctgct tttaaaataa agagcagtgt tctccattcg tattttgtatt 2220  
agatatacgat tgactatTTT taaagcatgt taaaattta gtttttattc atgtttaaag 2280  
tatgtattat gtatgcataa ttttgcgtt gttactgaaa cttttttctta tcaagaatct 2340  
ttttcattgc actgaatgtat ttctttgcctt cctaggagaa aacttaataa ttgtgcctaa 2400  
aaactatggg cggatagttat aagactatac tagacaaagt gaatattgc atttccattta 2460  
tctatgaatt agtggctgag ttctttctta gctgctttaa ggagccccctc actccccaga 2520  
gtcaaaagga aatgtaaaaaa cttagagctc ccattgtat gtaaggggca agaaattttgt 2580  
gttcttctga atgctactag cagcaccagc cttgttttaa atgttttctt gagctagaag 2640  
aaatagctga ttattgtata tgcaaaattac atgcattttt aaaaactatt ctgttctgaac 2700  
ttatctacct ggttatgata ctgtgggtcc atacacaagt aaaataagat tagacagaag 2760  
ccagtataca ttttgcacta ttgtatgtat actgttagcca gccaggaccc tactgatctc 2820  
agcataataa tgctcaactaa taatgaagtc tgcatagtga cactcatcaa gactgaagat 2880  
gaagcagggtt acgtgctcca ttggaaaggag tttctgtatag tctcctgctg ttttacccct 2940  
tccatTTTTT aaaataagaa attagcagcc ctctgcataa tttttttttt tatatgcagt 3000

tttatcctgt gccctaaagc ctcactgtcc agagctgttgc gtcatcagat gcttattgca 3060  
ccctcaccat gtgcctggtg ccctgctggg tagagaacac agaggacagg gcatacttct 3120  
tgtccttaag gagcttgtga tctgtgacag taagccctcc tggatgtct gtgccatgtg 3180  
attgacttac aagtgaaaact gtcttataat atgaaggtct tttgtttac ttctaaaccc 3240  
acttggtag ttactatccc caaatctgtt ctgtaaataa tattatggaa gggtttctat 3300  
gtcagtctac ctttagagaaa gccagtgatt caatatcaca aaaggcattt acgtatctt 3360  
gaaatgttca cagcagcctt ttaacaacaa ctgggtggtc cttgtaggca gaacatactc 3420  
tcctaagtgg ttgttaggaaa ttgcaaggaa aatagaaggt ctgttcttgc tctcaaggag 3480  
gttaccttta ataaaagaag acaaaccagg atagatatgt aaaccaaaat actatgcccc 3540  
ttaatacttt ataaggcagca ttgttaaata gttcttacgc ttatacattt acagaactac 3600  
cctgtttcc ttgtatataa tgactttgc tggcagaact gaaatataaa ctgtaagggg 3660  
atttcgtcag ttgctcccag tatacaatat cctccaggac atagccagaa atctccattt 3720  
cacacatgac tgagttccta tccctgcact ggtactggct ctttctcct cttccttgc 3780  
ctcagggttc gtgctaccca ctgattccct ttacccttag taataattt ggatcattt 3840  
cttccttta aaggggaaaca aagcctttt tttttttag acggagtgtt gctctgtcac 3900  
ccaagctgga gtgcagtggc acgatcttgg ctcactccaa cctccaccc ttccatccaa 3960  
gtgattctcc tgccctcagcc tcccgagtag ctggactac gggcacgcac caccacgtct 4020  
ggctaatttt tgtatttta gttagagatgg ggttccaccc tattggtcag gctggtctt 4080  
aattcctcac ctcaggtcat ccgcctgtct cggcctcccg aagtgtggg attataggtg 4140  
tgagccaccc cacccagttt ggaacaaagc ctttttaaca cacgtaaaggg ccctcaaacc 4200  
gtgggacctc taaggagacc tttgaagctt tttgagggca aactttaccc ttgtggtccc 4260  
caaatgatgg catttctt cttttttat tagatactgt tatgtcccc aagggtacag 4320  
gaggggcattc ctcagccta tggAACACC CAAACTAGGA GGGTTATTG ACAGGAAGGA 4380  
atgaatccaa gtgaaggctt tctgctttc gtgttacaaa ccagtttccat agttagctt 4440  
ctggggaggt gtgtgtttgt gaaaggaatt caagtgttgc aggacagatg agctcaaggt 4500  
aaggtagctt tggcagcagg gctgatacta tgaggctgaa acaatccttgc tgatgaagta 4560  
gatcatgcag tgacatacaa agaccaagga ttatgtatat ttttatatct ctgtggttt 4620  
gaaacttttag tacttagaat tttggccttc tgcactactc ttttgcctt acgaacataa 4680

tggactctta agaatggaaa gggatgacat ttacctatgt gtgctgcctc attcctggtg	4740
aagcaactgc tacttgttct ctatgcctct aaaatgatgc tgccccctct gctaaaggta	4800
aaagaaaaaga aaaaaatagt tggaaaataa gacatgcaac ttgatgtgct tttgagtaaa	4860
tttatgcagc agaaaactata caatgaagga agaattctat ggaaattaca aatccaaaac	4920
tctatgatga tgtcttccta gggagtagag aaaggcagt aaatggcagt tagaccaaca	4980
gaggcgtgaa ggattcaagt acaagtaata ttttgtataa aacatagcag ttttaggtccc	5040
cataatcctc aaaaatagtc acaaataataa caaagttcat tgccccctggg ttttaaaaaa	5100
acgtgttgta cctaaggcca tacttactct tctatgctat cactgcaaag gggtgatatg	5160
tatgtattat ataaaaaaaaaa aaacccttaa tgcactgtta tctcctaaat atttagtaaa	5220
ttaatactat ttaattttt taaagatttg tctgtgtaga cactaaaagt attacacaaa	5280
atctggactg aaggtgtcct ttttaacaac aatttaaagt actttttata tatgttatgt	5340
agtatatcct ttctaaactg cctagttgt atattcctat aattcctatt tgtgaagtgt	5400
acctgttctt gtctctttt tcagtcattt tctgcacgca tccccctta tatggttata	5460
gagatgactg tagctttcg tgctccactg cgaggttgt gctcagagcc gctgcacccc	5520
agcgaggcct gctccatgga gtgcaggacg agctactgct ttggagcggag ggtttcctgc	5580
ttttgagttg acctgacttc cttcttgaaa tgactgttaa aactaaaata aattacattg	5640
catttatattt atattcttgg ttgaaataaa atttaattga cttttgc	5685

<210> 78  
<211> 375  
<212> PRT  
<213> human organism

<400> 78

Val Lys Ser Leu Leu Tyr Gln Ile Leu Asp Gly Ile His Tyr Leu His  
1 5 10 15

Ala Asn Trp Val Leu His Arg Asp Leu Lys Pro Ala Asn Ile Leu Val  
20 25 30

Met Gly Glu Gly Pro Glu Arg Gly Arg Val Lys Ile Ala Asp Met Gly  
35 40 45

Phe Ala Arg Leu Phe Asn Ser Pro Leu Lys Pro Leu Ala Asp Leu Asp  
50 55 60

Pro Val Val Val Thr Phe Trp Tyr Arg Ala Pro Glu Leu Leu Leu Gly  
65 70 75 80

Ala Arg His Tyr Thr Lys Ala Ile Asp Ile Trp Ala Ile Gly Cys Ile  
85 90 95

Phe Ala Glu Leu Leu Thr Ser Glu Pro Ile Phe His Cys Arg Gln Glu  
100 105 110

Asp Ile Lys Thr Ser Asn Pro Phe His His Asp Gln Leu Asp Arg Ile  
115 120 125

Phe Ser Val Met Gly Phe Pro Ala Asp Lys Asp Trp Glu Asp Ile Arg  
130 135 140

Lys Met Pro Glu Tyr Pro Thr Leu Gln Lys Asp Phe Arg Arg Thr Thr  
145 150 155 160

Tyr Ala Asn Ser Ser Leu Ile Lys Tyr Met Glu Lys His Lys Val Lys  
165 170 175

Pro Asp Ser Lys Val Phe Leu Leu Leu Gln Lys Leu Leu Thr Met Asp  
180 185 190

Pro Thr Lys Arg Ile Thr Ser Glu Gln Ala Leu Gln Asp Pro Tyr Phe  
195 200 205

Gln Glu Asp Pro Leu Pro Thr Leu Asp Val Phe Ala Gly Cys Gln Ile  
210 215 220

Pro Tyr Pro Lys Arg Glu Phe Leu Asn Glu Asp Asp Pro Glu Glu Lys  
225 230 235 240

Gly Asp Lys Asn Gln Gln Gln Gln Asn Gln His Gln Gln Pro Thr  
245 250 255

Ala Pro Pro Gln Gln Ala Ala Ala Pro Pro Gln Ala Pro Pro Pro Gln  
260 265 270

Gln Asn Ser Thr Gln Thr Asn Gly Thr Ala Gly Gly Ala Gly Ala Gly  
275 280 285

Val Gly Gly Thr Gly Ala Gly Leu Gln His Ser Gln Asp Ser Ser Leu  
290 295 300

Asn Gln Val Pro Pro Asn Lys Lys Pro Arg Leu Gly Pro Ser Gly Ala  
305 310 315 320

Asn Ser Gly Gly Pro Val Met Pro Ser Asp Tyr Gln His Ser Ser Ser  
325 330 335

Arg Leu Asn Tyr Gln Ser Ser Val Gln Gly Ser Ser Gln Ser Gln Ser  
340 345 350

Thr Leu Gly Tyr Ser Ser Ser Gln Gln Ser Ser Gln Tyr His Pro  
355 360 365

Ser His Gln Ala His Arg Tyr  
370 375

<210> 79  
<211> 2190  
<212> DNA  
<213> human organism

<400> 79  
atgaatcctt tccagaaaaa tgagtccaag gaaactcttt tttcacctgt ctccattgaa 60  
gaggtaccac ctcgaccacc tagccctcca aagaagccat ctccgacaat ctgtggctcc 120  
aactatccac tgagcattgc cttcattgtg gtgaatgaat tctgcgagcg ctttcctat 180  
tatggaatga aagctgtgct gatcctgtat ttcctgtatt tcctgcactg gaatgaagat 240  
acacctccacat ctatatacca tgccttcagg agcctctgtt attttactcc catcctggga 300  
gcagccattt ctgactcgtg gttggaaaa ttcaagacaa tcatctatct ctccctggtg 360  
tatgtgcttgc gccatgtgat caagtccctt ggtgccttac caatactggg aggacaagt 420  
gtacacacag tcctatcatt gatcggcctg agtctaatacg ctttggggac aggaggcatc 480  
aaaccctgtt tggcagctt tggggagac cagtttgaag aaaaacatgc agaggaacgg 540  
actagataact tctcagtctt ctacctgtcc atcaatgcag ggagcttgc ttctacattt 600  
atcacaccca tgctgagagg agatgtgcaa tggggag aagactgcta tgcattggct 660  
tttggagttc caggactgct catggtaatt gcacttggttt tggttgcattt gggaaagcaa 720  
atatacaata aaccaccccc tgaaggaaac atagtggctc aagtttcaa atgtatctgg 780  
tttgctattt ccaatcgttt caagaaccgt tctggagaca ttccaaagcg acagcactgg 840

ctagactggg cagctgagaa atatccaaag cagtcatta tggatgtaaa ggcactgacc	900
agggtactat tccttataat cccattgccc atgttctggg ctctttgga tcagcagggt	960
tcacgatgga ctttgcaagc catcaggatg aataggaatt tggggtttt tgtgcttcag	1020
ccggaccaga tgcaggttct aaatccctt ctggttctta tcttcatccc gttgtttgac	1080
tttgtcattt atcgtctggc ctccaagtgt ggaattaact tctcatcact taggaaaaatg	1140
gctgttgta tgatcctagc gtgcctggca tttgcagttg cggcagctgt agagataaaa	1200
ataaatgaaa tggccccagc ccagtcaggt ccccaggagg ttttcctaca agtcttgaat	1260
ctggcagatg atgaggtgaa ggtgacagtg gtggaaatg aaaacaattc tctgttata	1320
gagtccatca aatccttca gaaaacacca cactattcca aactgcacct gaaaacaaaa	1380
agccaggatt ttcacttcca cctgaaatat cacaatttgc ctctctacac tgagcattct	1440
gtgcaggaga agaactggta cagtcttgc attcgtgaag atggaaacag tatctccagc	1500
atgatggtaa aggatacaga aagcaaaaca accaatggga tgacaaccgt gaggttgg	1560
aacactttgc ataaagatgt caacatctcc ctgagttacag atacctctct caatgttgg	1620
gaagactatg gtgtgtctgc ttatagaact gtgcaaagag gagaataccc tgcagtgcac	1680
tgtagaacag aagataagaa cttttctctg aatttgggtc ttctagactt tggcagca	1740
tatctgtttt ttattactaa taacaccaat cagggcttc aggccctggaa gattgaagac	1800
attccagcca acaaaatgtc cattgcgtgg cagctaccac aatatgcctt ggtagcagct	1860
ggggaggtca tttttctgt cacaggtctt gagtttctt attctcaggc tccctctagc	1920
atgaaatctg tgctccaggc agcttggcta ttgacaattt cagttggaa tatcatcg	1980
cttgggttgg cacagttcag tggcctggta cagtgcccg aattcatttt gttttctgc	2040
ctcctgtgg tgatctgcct gatcttctcc atcatggct actactatgt tcctgtaaag	2100
acagaggata tgcggggtcc agcagataag cacattcctc acatccaggg gaacatgatc	2160
aaactagaga ccaagaagac aaaactctga	2190

<210> 80  
 <211> 729  
 <212> PRT  
 <213> human organism

<400> 80

Met	Asn	Pro	Phe	Gln	Lys	Asn	Glu	Ser	Lys	Glu	Thr	Leu	Phe	Ser	Pro
1				5			10						15		

Val Ser Ile Glu Glu Val Pro Pro Arg Pro Pro Ser Pro Pro Lys Lys  
20 25 30

Pro Ser Pro Thr Ile Cys Gly Ser Asn Tyr Pro Leu Ser Ile Ala Phe  
35 40 45

Ile Val Val Asn Glu Phe Cys Glu Arg Phe Ser Tyr Tyr Gly Met Lys  
50 55 60

Ala Val Leu Ile Leu Tyr Phe Leu Tyr Phe Leu His Trp Asn Glu Asp  
65 70 75 80

Thr Ser Thr Ser Ile Tyr His Ala Phe Ser Ser Leu Cys Tyr Phe Thr  
85 90 95

Pro Ile Leu Gly Ala Ala Ile Ala Asp Ser Trp Leu Gly Lys Phe Lys  
100 105 110

Thr Ile Ile Tyr Leu Ser Leu Val Tyr Val Leu Gly His Val Ile Lys  
115 120 125

Ser Leu Gly Ala Leu Pro Ile Leu Gly Gly Gln Val Val His Thr Val  
130 135 140

Leu Ser Leu Ile Gly Leu Ser Leu Ile Ala Leu Gly Thr Gly Gly Ile  
145 150 155 160

Lys Pro Cys Val Ala Ala Phe Gly Asp Gln Phe Glu Glu Lys His  
165 170 175

Ala Glu Glu Arg Thr Arg Tyr Phe Ser Val Phe Tyr Leu Ser Ile Asn  
180 185 190

Ala Gly Ser Leu Ile Ser Thr Phe Ile Thr Pro Met Leu Arg Gly Asp  
195 200 205

Val Gln Cys Phe Gly Glu Asp Cys Tyr Ala Leu Ala Phe Gly Val Pro  
210 215 220

Gly Leu Leu Met Val Ile Ala Leu Val Val Phe Ala Met Gly Ser Lys  
225 230 235 240

Ile Tyr Asn Lys Pro Pro Pro Glu Gly Asn Ile Val Ala Gln Val Phe  
245 250 255

Lys Cys Ile Trp Phe Ala Ile Ser Asn Arg Phe Lys Asn Arg Ser Gly  
260 265 270

Asp Ile Pro Lys Arg Gln His Trp Leu Asp Trp Ala Ala Glu Lys Tyr  
275 280 285

Pro Lys Gln Leu Ile Met Asp Val Lys Ala Leu Thr Arg Val Leu Phe  
290 295 300

Leu Tyr Ile Pro Leu Pro Met Phe Trp Ala Leu Leu Asp Gln Gln Gly  
305 310 315 320

Ser Arg Trp Thr Leu Gln Ala Ile Arg Met Asn Arg Asn Leu Gly Phe  
325 330 335

Phe Val Leu Gln Pro Asp Gln Met Gln Val Leu Asn Pro Phe Leu Val  
340 345 350

Leu Ile Phe Ile Pro Leu Phe Asp Phe Val Ile Tyr Arg Leu Val Ser  
355 360 365

Lys Cys Gly Ile Asn Phe Ser Ser Leu Arg Lys Met Ala Val Gly Met  
370 375 380

Ile Leu Ala Cys Leu Ala Phe Ala Val Ala Ala Val Glu Ile Lys  
385 390 395 400

Ile Asn Glu Met Ala Pro Ala Gln Ser Gly Pro Gln Glu Val Phe Leu  
405 410 415

Gln Val Leu Asn Leu Ala Asp Asp Glu Val Lys Val Thr Val Val Gly  
420 425 430

Asn Glu Asn Asn Ser Leu Leu Ile Glu Ser Ile Lys Ser Phe Gln Lys  
435 440 445

Thr Pro His Tyr Ser Lys Leu His Leu Lys Thr Lys Ser Gln Asp Phe  
450 455 460

His Phe His Leu Lys Tyr His Asn Leu Ser Leu Tyr Thr Glu His Ser  
465                          470                          475                          480

Val Gln Glu Lys Asn Trp Tyr Ser Leu Val Ile Arg Glu Asp Gly Asn  
485                          490                          495

Ser Ile Ser Ser Met Met Val Lys Asp Thr Glu Ser Lys Thr Thr Asn  
500                          505                          510

Gly Met Thr Thr Val Arg Phe Val Asn Thr Leu His Lys Asp Val Asn  
515                          520                          525

Ile Ser Leu Ser Thr Asp Thr Ser Leu Asn Val Gly Glu Asp Tyr Gly  
530                          535                          540

Val Ser Ala Tyr Arg Thr Val Gln Arg Gly Glu Tyr Pro Ala Val His  
545                          550                          555                          560

Cys Arg Thr Glu Asp Lys Asn Phe Ser Leu Asn Leu Gly Leu Leu Asp  
565                          570                          575

Phe Gly Ala Ala Tyr Leu Phe Val Ile Thr Asn Asn Thr Asn Gln Gly  
580                          585                          590

Leu Gln Ala Trp Lys Ile Glu Asp Ile Pro Ala Asn Lys Met Ser Ile  
595                          600                          605

Ala Trp Gln Leu Pro Gln Tyr Ala Leu Val Thr Ala Gly Glu Val Met  
610                          615                          620

Phe Ser Val Thr Gly Leu Glu Phe Ser Tyr Ser Gln Ala Pro Ser Ser  
625                          630                          635                          640

Met Lys Ser Val Leu Gln Ala Ala Trp Leu Leu Thr Ile Ala Val Gly  
645                          650                          655

Asn Ile Ile Val Leu Val Val Ala Gln Phe Ser Gly Leu Val Gln Trp  
660                          665                          670

Ala Glu Phe Ile Leu Phe Ser Cys Leu Leu Leu Val Ile Cys Leu Ile  
675                          680                          685

Phe Ser Ile Met Gly Tyr Tyr Val Pro Val Lys Thr Glu Asp Met

690

695

700

Arg Gly Pro Ala Asp Lys His Ile Pro His Ile Gln Gly Asn Met Ile  
 705 710 715 720

Lys Leu Glu Thr Lys Lys Thr Lys Leu  
 725

<210> 81  
<211> 1221  
<212> DNA  
<213> human organism

<400> 81		
atggacggat cccacagcgc agccctgaag ctgcagcagc tgcctcccac aagttagctcc	60	
agcgccgtaa gcgaggcctc cttctcctac aaggaaaacc tgattggcgc cctcttggcg	120	
atcttcgggc acctcgttgt cagcattgca cttAACCTCC agaagtactg ccacatccgc	180	
ctggcaggct ccaaggatcc ccgggcctat ttcaagacca agacatggtg gctgggcctg	240	
ttcctgatgc ttctggcga gctgggtgtg ttgcctcct acgccttcgc gccgctgtca	300	
ctcatcgtgc ccctcagcgc agtttctgtg atagcttagt ccatcatagg aatcatattc	360	
atcaaggaaa agtggaaacc gaaagacttt ctgaggcgct acgtcttgc ctttggc	420	
tgcggtttgg ctgtcgtgg tacctacctg ctggtgacat tcgcacccaa cagtcacgag	480	
aagatgacag gcgagaatgt caccaggcac ctcgtgagct ggcccttcct tttgtacatg	540	
ctggtgaga tcattctgtt ctgcttgctg ctctacttct acaaggagaa gaacgccaac	600	
aacattgtcg tgattcttct cttggggcg ttacttgc ccatgacagt ggtgacagtc	660	
aaggccgtgg ctgggatgct tgtcttgcc attcaaggga acctgcagct tgactacccc	720	
atcttctacg tcatgttgtt gtgcgttgt gcaaccggcg tctatcaggc tgcgttttg	780	
agtcaaggct cacagatgta cgactcctct ttgattgcca gtgtggctt cattctgtcc	840	
acaaccattg ctatcacagc aggtgcaata ttttacctgg acttcatcgg ggaggacgtg	900	
ctgcacatct gcatgtttgc actggggtgc ctcattgcat tcttggcgct ttcttaatc	960	
acgcgttaaca ggaagaagcc cattccattt gagccctata tttccatgga tgccatgcca	1020	
ggtatgcaga acatgcacga taaagggatg actgtccagc ctgaacttaa agcttcttt	1080	
tcctatgggg ctctggaaaa caatgacaac atttctgaga tctacgctcc tgccacccctg	1140	
ccagtcatgc aagaagagca cggctccaga agtgcctctg gggtccccta ccgagtccta	1200	

gagcacacca agaaggaatg a

1221

<210> 82  
<211> 406  
<212> PRT  
<213> human organism

<400> 82

Met Asp Gly Ser His Ser Ala Ala Leu Lys Leu Gln Gln Leu Pro Pro  
1 5 10 15

Thr Ser Ser Ser Ser Ala Val Ser Glu Ala Ser Phe Ser Tyr Lys Glu  
20 25 30

Asn Leu Ile Gly Ala Leu Leu Ala Ile Phe Gly His Leu Val Val Ser  
35 40 45

Ile Ala Leu Asn Leu Gln Lys Tyr Cys His Ile Arg Leu Ala Gly Ser  
50 55 60

Lys Asp Pro Arg Ala Tyr Phe Lys Thr Lys Thr Trp Trp Leu Gly Leu  
65 70 75 80

Phe Leu Met Leu Leu Gly Glu Leu Gly Val Phe Ala Ser Tyr Ala Phe  
85 90 95

Ala Pro Leu Ser Leu Ile Val Pro Leu Ser Ala Val Ser Val Ile Ala  
100 105 110

Ser Ala Ile Ile Gly Ile Ile Phe Ile Lys Glu Lys Trp Lys Pro Lys  
115 120 125

Asp Phe Leu Arg Arg Tyr Val Leu Ser Phe Val Gly Cys Gly Leu Ala  
130 135 140

Val Val Gly Thr Tyr Leu Leu Val Thr Phe Ala Pro Asn Ser His Glu  
145 150 155 160

Lys Met Thr Gly Glu Asn Val Thr Arg His Leu Val Ser Trp Pro Phe  
165 170 175

Leu Leu Tyr Met Leu Val Glu Ile Ile Leu Phe Cys Leu Leu Tyr  
180 185 190

Phe Tyr Lys Glu Lys Asn Ala Asn Asn Ile Val Val Ile Leu Leu Leu  
195 200 205

Val Ala Leu Leu Gly Ser Met Thr Val Val Thr Val Lys Ala Val Ala  
210 215 220

Gly Met Leu Val Leu Ser Ile Gln Gly Asn Leu Gln Leu Asp Tyr Pro  
225 230 235 240

Ile Phe Tyr Val Met Phe Val Cys Met Val Ala Thr Ala Val Tyr Gln  
245 250 255

Ala Ala Phe Leu Ser Gln Ala Ser Gln Met Tyr Asp Ser Ser Leu Ile  
260 265 270

Ala Ser Val Gly Tyr Ile Leu Ser Thr Thr Ile Ala Ile Thr Ala Gly  
275 280 285

Ala Ile Phe Tyr Leu Asp Phe Ile Gly Glu Asp Val Leu His Ile Cys  
290 295 300

Met Phe Ala Leu Gly Cys Leu Ile Ala Phe Leu Gly Val Phe Leu Ile  
305 310 315 320

Thr Arg Asn Arg Lys Lys Pro Ile Pro Phe Glu Pro Tyr Ile Ser Met  
325 330 335

Asp Ala Met Pro Gly Met Gln Asn Met His Asp Lys Gly Met Thr Val  
340 345 350

Gln Pro Glu Leu Lys Ala Ser Phe Ser Tyr Gly Ala Leu Glu Asn Asn  
355 360 365

Asp Asn Ile Ser Glu Ile Tyr Ala Pro Ala Thr Leu Pro Val Met Gln  
370 375 380

Glu Glu His Gly Ser Arg Ser Ala Ser Gly Val Pro Tyr Arg Val Leu  
385 390 395 400

Glu His Thr Lys Lys Glu  
405

<210> 83  
 <211> 1316  
 <212> DNA  
 <213> human organism

<400> 83  
 cactcattaa gaacagagga ggctgcctgt tactcctgggt gttgcataccc tccagacact 60  
 ctgctgttcc ctgccttaggc gtggctgcag ccatggctag gaaaaggcgctg ccaccacccc  
 acctggggcca gagctgggttc tgctcctgct gcagggacac tgagctggct atctcggcgc 120  
 ttccggcaag aactgcaaca ggctctcctg ggtcctgcag gtgtacagcc gggccccctgc 180  
 cttgtgcctc agctctcgag agctgctgct gccgggtgac ctgatccaac ctgataaggt 240  
 gccatcttca gctaccactg caaggccctg agggcaacag cagcacggca ctgcccacccc 300  
 ggctgctgat ggctgggtgc cagctggag tcctccggc acttcgaggc cactgagcca 420  
 cccttccagc cccagccac catggacagg ggtatccagc ttccctcctca acctcgctcct 480  
 ctgccccctga gccagtgacg cccaggaca tgcctgttac ccaggtcctg taccagcact 540  
 agctggtaaa gggcatgaca gtgctggagg ccgtcttgaa gatccaggcc atcaactggca 600  
 gcaggctgct ctccatggtg ccagggcccg ccaggccacc aggctcatgc tgggacccaa 660  
 cccagtgcac aaggacttgg ctgctgagcc acacacccag gagaagggtgg ataagtggc 720  
 taccaagggc ttccctgcagg cttagggagg agccacccccc gcttcccttat tgtgaccagg 780  
 cctatgggga ggagctgtcc atacgccacc gtgagacctg ggctggctc tcaaggacag 840  
 acacccgcctg gcctgggtgc ccaggggtga agcaggccag aatcctgggg gagctgctcc 900  
 tggtttgagc tgcattcagg aagtgcggga catggtaggg gaggcaaaaaa gccttggca 960  
 ctacccctccc tgtggagctg ttccgggtgc gtcgagctag ccacacccctg acaccatgtt 1020  
 caagggtacc ggaagagaag ggtgtctgcc cccaacctcc cctgtgggtg tcactggca 1080  
 gatgtcatga gggaaagcagg ccttgtgagt ggacactgac catgagtccc tggggggagt 1140  
 gatccccccag gcacatcgatgc ccatgttgca cttctgccc ggcagcaggg tgggtggta 1200  
 ccatgggtgc ccacccctcc accacatggg gccccaaagc actgcaggcc aagcagggca 1260  
 accccacacc cttgacataa aagcatctt aagctttaa aaaaaaaaaa aaaaaaa . 1316

<210> 84  
 <211> 117  
 <212> PRT  
 <213> human organism

<400> 84

Met Thr Val Leu Glu Ala Val Leu Glu Ile Gln Ala Ile Thr Gly Ser  
1 5 10 15

Arg Leu Leu Ser Met Val Pro Gly Pro Ala Arg Pro Pro Gly Ser Cys  
20 25 30

Trp Asp Pro Thr Gln Cys Thr Arg Thr Trp Leu Leu Ser His Thr Pro  
35 40 45

Arg Arg Arg Trp Ile Ser Gly Leu Pro Arg Ala Ser Cys Arg Leu Gly  
50 55 60

Glu Glu Pro Pro Pro Leu Pro Tyr Cys Asp Gln Ala Tyr Gly Glu Glu  
65 70 75 80

Leu Ser Ile Arg His Arg Glu Thr Trp Ala Trp Leu Ser Arg Thr Asp  
85 90 95

Thr Ala Trp Pro Gly Ala Pro Gly Val Lys Gln Ala Arg Ile Leu Gly  
100 105 110

Glu Leu Leu Leu Val  
115

<210> 85  
<211> 3442  
<212> DNA  
<213> human organism

<400> 85  
agccgggtgcg ccgcagacta gggcgccctcg ggccaggag cgcggaggag ccatggccac 60  
cgctaacggg gccgtggaaa acgggcagcc ggacggaaag cgcggggccc tgccgcgcc 120  
catccgcaac ctggagggtca agttcaccaa gatatttatac aacaatgaat ggcacgaatc 180  
caagagtggg aaaaagtttgc ctacatgtaa cccttcaact cgggagcaaa tatgtgaagt 240  
ggaagaagga gataagcccg acgtggacaa ggctgtggag gctgcacagg ttgccttcca 300  
gaggggctcg ccatggcgcc ggctggatgc cctgagtcgt gggcggctgc tgcaccagct 360  
ggctgacctg gtggagaggg accgcgccac cttggccgcc ctggagacga tggatacagg 420  
gaagccattt cttcatgctt ttttcatcga cctggaggc tgtattagaa ccctcagata 480  
ctttgcaggg tgggcagaca aaatccaggg caagaccatc cccacagatg acaacgtcgt 540

atgttcacc aggcatgagc ccattggtgt ctgtgggcc atcaactccat ggaacttccc 600  
cctgctgatg ctggtgtgga agctggcacc cgccctctgc tgtggaaaca ccatggtcct 660  
gaaggctgcg gaggcagacac ctctcaccgc ccttatctc ggctctctga tcaaagaggc 720  
cggttccct ccaggagtgg tgaacattgt gccaggattc gggcccacag tgggagcagc 780  
aatttcttct caccctcaga tcaacaagat cgccttcacc ggctccacag aggttgaaa 840  
actggtaaa gaagctgcgt cccggagcaa tctgaagcgg gtgacgctgg agctgggggg 900  
gaagaacccc tgcacatcggt gtgcggacgc tgacttggac ttggcagtgg agtgtgccc 960  
tcagggagtg ttcttcaacc aaggccagtg ttgcacggca gcctccaggg tgttcgtgga 1020  
ggagcaggc tactctgagt ttgtcaggcg gagcgtggag tatgccaaga aacggccgt 1080  
gggagacccc ttcgatgtca aaacagaaca ggggcctcag attgatcaaa agcagttcga 1140  
caaaatctta gagctgatcg agagtggaa gaaggaaggg gccaagctgg aatgcggggg 1200  
ctcagccatg gaagacaagg ggcttctcat caaacccact gtcttctcag aagtcacaga 1260  
caacatgcgg attgccaaag aggagattt cgggcccagtg caaccaatac tgaagttcaa 1320  
aagtatcgaa gaagtgataa aaagagcgaa tagcaccgac tatggactca cagcagccgt 1380  
gttcacaaaa aatctcgaca aagccctgaa gttggcttct gccttagagt ctggAACGGT 1440  
ctggatcaac tgctacaacg ccctctatgc acaggctcca tttgggtggct taaaaatgtc 1500  
aggaaatggc agagaactag gtgaatacgc tttggccgaa tacacagaag tgaaaactgt 1560  
caccatcaaa cttggcgaca agaaccctg aaggaaaggc ggggctcctt cctcaaacat 1620  
cgacggcgg aatgtggcag atgaaatgtg ctggagggaa aaaatgacat ttctgacctt 1680  
cccgacac attcttctgg aggcttaca tctactggag ttgaatgatt gctgtttcc 1740  
tctcaactctc ctgttattc accagactgg ggatgcctat aggttgtctg tgaaatcgca 1800  
gtcctgcctg gggagggagc tttggccat ttctgtgtt ccctttaaac cagatcctgg 1860  
agacagttag atactcaggg cgttgttaac agggagtggt atttgaagtg tccagcagtt 1920  
gctgaaatg ctttgcgaa tctgactcca gtaagaatgt gggaaaaccc cctgtgtgtt 1980  
ctgcaaggcag ggctctgca ccagcggctc cctcagggtg gacctgctta cagagcaagc 2040  
cacgcctctt tccgaggtga aggtgggacc attccttggg aaaggattca cagtaaggtt 2100  
ttttggtttt tgtttttgtt ttcttgggtt taaaaaaag gatttcacag tgagaaagtt 2160  
ttggtagtg cataccgtgg aaggcgcaca gggtcttgc ggattgcattt ttgacattga 2220  
ccgtgagatt cggcttcaaa ccaatactgc ctttggataa tgacagaatc aatagccag 2280

agagcttagt caaagacgt atcacggtct accttaacca aggcaacttc ttaagcagaa	2340
aatattgttg aggttacctt tgctgctaaa gatccaatct tctaacgcca caacagcata	2400
gcaaatccta ggataattca ctcctcatt tgacaaatca gagctgtaat tcactttaac	2460
aaattacgca tttctatcac gttcaactaac agcttatgtat aagtctgtgt agtcttcctt	2520
ttctccagtt ctgttaccca atttagatta gtaaagcgta cacaactgga aagactgctg	2580
taataacaca gccttgttat ttttaagtcc tatTTTgata ttaatttctg attagtttagt	2640
aaataacacc tggattctat ggaggacctc ggtcttcattt caagtggcct gagtatttca	2700
ctggcagggtt gtgaattttt ctttcctct ttgggaatcc aaatgatgtat gtgcatttc	2760
atgttttaac ttgggaaact gaaagtgttc ccatatagtt tcaaaaacaa aaacaaatgt	2820
gttatccgac ggatactttt atggtaacta actagttactt tcctaattgg gaaagtagtg	2880
cttaagtttgc caaattaagt tggggagggc aataataaaa tgagggcccg taacagaacc	2940
agtgtgtgtta taacgaaaac catgtataaa atgggcctat cacccttgtc agagatataa	3000
attaccacat ttggcttccc ttcatcagct aacacttatac acttataacta ccaataactt	3060
gtttaatcag gatttggctt catacaactga attttcagta ttttatctca agtagatata	3120
gacactaacc ttgatagtga tacgttagag gtttcctatt cttccattgt acgataatgt	3180
ctttaatatg aaatgctaca ttatttataa ttggtagagt tattgtatct ttttatagtt	3240
gtaagtacac agaggtggta tatttaact tctgtatatac actgtattta gaaatggaaa	3300
tatataatgt gttaggtttc acttctttta aggtttaccc ctgtgggtgtg gtttaaaaat	3360
ctataggcct gggaaattccg atccttagctg cagatcgcattt cccacaatgc gagaatgata	3420
aaataaaaatt ggatatttga ga	3442

<210> 86  
<211> 512  
<212> PRT  
<213> human organism

<400> 86

```

Met Ala Thr Ala Asn Gly Ala Val Glu Asn Gly Gln Pro Asp Gly Lys
1          5          10          15

```

Pro Pro Ala Leu Pro Arg Pro Ile Arg Asn Leu Glu Val Lys Phe Thr  
 20 25 30

Lys Ile Phe Ile Asn Asn Glu Trp His Glu Ser Lys Ser Gly Lys Lys  
35 40 45

Phe Ala Thr Cys Asn Pro Ser Thr Arg Glu Gln Ile Cys Glu Val Glu  
50 55 60

Glu Gly Asp Lys Pro Asp Val Asp Lys Ala Val Glu Ala Ala Gln Val  
65 70 75 80

Ala Phe Gln Arg Gly Ser Pro Trp Arg Arg Leu Asp Ala Leu Ser Arg  
85 90 95

Gly Arg Leu Leu His Gln Leu Ala Asp Leu Val Glu Arg Asp Arg Ala  
100 105 110

Thr Leu Ala Ala Leu Glu Thr Met Asp Thr Gly Lys Pro Phe Leu His  
115 120 125

Ala Phe Phe Ile Asp Leu Glu Gly Cys Ile Arg Thr Leu Arg Tyr Phe  
130 135 140

Ala Gly Trp Ala Asp Lys Ile Gln Gly Lys Thr Ile Pro Thr Asp Asp  
145 150 155 160

Asn Val Val Cys Phe Thr Arg His Glu Pro Ile Gly Val Cys Gly Ala  
165 170 175

Ile Thr Pro Trp Asn Phe Pro Leu Leu Met Leu Val Trp Lys Leu Ala  
180 185 190

Pro Ala Leu Cys Cys Gly Asn Thr Met Val Leu Lys Pro Ala Glu Gln  
195 200 205

Thr Pro Leu Thr Ala Leu Tyr Leu Gly Ser Leu Ile Lys Glu Ala Gly  
210 215 220

Phe Pro Pro Gly Val Val Asn Ile Val Pro Gly Phe Gly Pro Thr Val  
225 230 235 240

Gly Ala Ala Ile Ser Ser His Pro Gln Ile Asn Lys Ile Ala Phe Thr  
245 250 255

Gly Ser Thr Glu Val Gly Lys Leu Val Lys Glu Ala Ala Ser Arg Ser

260

265

270

Asn Leu Lys Arg Val Thr Leu Glu Leu Gly Gly Lys Asn Pro Cys Ile  
275 280 285

Val Cys Ala Asp Ala Asp Leu Asp Leu Ala Val Glu Cys Ala His Gln  
290 295 300

Gly Val Phe Phe Asn Gln Gly Gln Cys Cys Thr Ala Ala Ser Arg Val  
305 310 315 320

Phe Val Glu Glu Gln Val Tyr Ser Glu Phe Val Arg Arg Ser Val Glu  
325 330 335

Tyr Ala Lys Lys Arg Pro Val Gly Asp Pro Phe Asp Val Lys Thr Glu  
340 345 350

Gln Gly Pro Gln Ile Asp Gln Lys Gln Phe Asp Lys Ile Leu Glu Leu  
355 360 365

Ile Glu Ser Gly Lys Glu Gly Ala Lys Leu Glu Cys Gly Gly Ser  
370 375 380

Ala Met Glu Asp Lys Gly Leu Phe Ile Lys Pro Thr Val Phe Ser Glu  
385 390 395 400

Val Thr Asp Asn Met Arg Ile Ala Lys Glu Glu Ile Phe Gly Pro Val  
405 410 415

Gln Pro Ile Leu Lys Phe Lys Ser Ile Glu Glu Val Ile Lys Arg Ala  
420 425 430

Asn Ser Thr Asp Tyr Gly Leu Thr Ala Ala Val Phe Thr Lys Asn Leu  
435 440 445

Asp Lys Ala Leu Lys Leu Ala Ser Ala Leu Glu Ser Gly Thr Val Trp  
450 455 460

Ile Asn Cys Tyr Asn Ala Leu Tyr Ala Gln Ala Pro Phe Gly Gly Phe  
465 470 475 480

Lys Met Ser Gly Asn Gly Arg Glu Leu Gly Glu Tyr Ala Leu Ala Glu  
485 490 495

Tyr Thr Glu Val Lys Thr Val Thr Ile Lys Leu Gly Asp Lys Asn Pro  
500 505 510

<210> 87  
<211> 2252  
<212> DNA  
<213> human organism

<400> 87  
gaccattagc aggacccag gcctgtctt ggctcgaaa cggtgcccc caatgttagcc 60  
tagtttgaac ctaggaactg caggaccaga gagattccac tggagcctga tggacgggtg 120  
acagagggaa ccctactctg gaaactgtca gtcccaggc actggggagg gctgaggccg 180  
accatgccca gcctgctgct gctgttcacg gctgctctgc tgtccagctg ggctcagctt 240  
ctgacagacg ccaactcctg gtggtcatta gcttgaacc cggtgcagag acccgagatg 300  
tttatcatcg gtgcccagcc cgtgtgcagt cagttcccg ggctctcccc tggccagagg 360  
aagctgtgcc aattgtacca ggagcacatg gcctacatag gggagggagc caagactggc 420  
atcaaggaat gccagcacca gttccggcag cggcggtgga attgcagcac agcggacaac 480  
gcatactgtct ttgggagagt catgcagata ggcagccgag agaccgcctt cacccacgcg 540  
gtgagcgccg cgggcgtggt caacgccatc agccgggcct gccgcgaggg cgagotctcc 600  
acctgcggct gcagccggac ggcgcggccc aaggacctgc cccggactg gctgtggggc 660  
ggctgtgggg acaacgtgga gtacggctac cgcttcgcca aggagttgt ggatgccegg 720  
gagcgagaga agaactttgc caaaggatca gaggagcagg gccgggtgct catgaacctg 780  
caaaaacaacg aggccggctcg cagggctgtg tataagatgg cagacgtac ctgcaaatgc 840  
cacggcgtct cggggtcctg cagcctcaag acctgctggc tgcagctggc cgagttccgc 900  
aaggtcgggg accggctgaa ggagaagtac gacagcgcgg ccgcgcgcg cgtcacccgc 960  
aaggggccggc tggagctggt caacagccgc ttcacccagc ccaccccgga ggacctggtc 1020  
tatgtggacc ccagccccga ctactgcctg cgcaacgaga gcacgggctc cctgggcacg 1080  
cagggccggc tctgcaacaa gacctcggag ggcattggatg gctgtgagct catgtctgc 1140  
gggcgtggct acaaccagtt caagagcgtg caggtggagc gctgccactg caagttccac 1200  
tggtgctgct tcgtcaggtg taagaagtgc acggagatcg tggaccagta catctgtaaa 1260  
tagccccggag ggcctgctcc cggccccccc tgcactctgc ctcacaaagg tctatattat 1320  
ataaaatctat ataaatctat tttatatttg tataagtaaa tgggtgggtg ctataacaatg 1380

gaaagatgaa	aatggaaagg	aagagcttat	ttaagagacg	ctggagatct	ctgaggagtg	1440
gactttgctg	gttcttcct	cttgggggt	gggagacagg	gcttttctc	tccctctggc	1500
gaggactctc	aggatgttagg	gacttgaaa	tatttactgt	ctgtccacca	cggcctggag	1560
gagggagggtt	gtgggtggat	ggaggagatg	atcttgtctg	gaagtctaga	gtctttgttg	1620
gttagaggac	tgcctgtgat	cctggccact	aggccaagag	gccstatgaa	ggtggcggga	1680
actcagcttc	aacctcgatg	tcttcagggt	cttgcacccaga	atgttagatgg	gttccgttaag	1740
aggcctggtg	ctctcttact	ctttcatcca	cgtgcacttg	tgcggcatct	gcagtttaca	1800
ggaacggctc	cttccctaaa	atgagaagtc	caaggtcatc	tctggcccag	tgaccacaga	1860
gagatctgca	cctccggac	ttcaggcctg	cctttccagc	gagaattctt	catcctccac	1920
ggttcaactag	ctcctacctg	aagaggaaag	ggggccattt	gacctgacat	gtcaggaaag	1980
ccctaaactg	aatgtttgcg	cctggctgc	agaagccagg	gtgcatgacc	aggctgcgtg	2040
gacgttatac	tgtctttccc	cacccccggg	gaggggaagc	tttagctgct	gctgtcaactc	2100
ctccaccgag	ggaggcctca	caaaccacag	gacgctgcaa	cgggtcaggc	tggcgggccc	2160
ggcgtgctca	tcatctctgc	cccaggtgta	cggttctct	ctgacattaa	atgccttca	2220
tggaaaaaaaaa	aaaaagaaaa	aaaaaaaaaa	aaaaaa	aa		2252

<210> 88  
 <211> 359  
 <212> PRT  
 <213> human organism

<400> 88

Met	Pro	Ser	Leu	Leu	Leu	Leu	Phe	Thr	Ala	Ala	Leu	Leu	Ser	Ser	Trp
1									10						15

Ala	Gln	Leu	Leu	Thr	Asp	Ala	Asn	Ser	Trp	Trp	Ser	Leu	Ala	Leu	Asn
								20			25			30	

Pro	Val	Gln	Arg	Pro	Glu	Met	Phe	Ile	Ile	Gly	Ala	Gln	Pro	Val	Cys
						35				40				45	

Ser	Gln	Leu	Pro	Gly	Leu	Ser	Pro	Gly	Gln	Arg	Lys	Leu	Cys	Gln	Leu
						50			55			60			

Tyr	Gln	Glu	His	Met	Ala	Tyr	Ile	Gly	Glu	Gly	Ala	Lys	Thr	Gly	Ile
						65			70			75			80

Lys Glu Cys Gln His Gln Phe Arg Gln Arg Arg Trp Asn Cys Ser Thr  
85 90 95

Ala Asp Asn Ala Ser Val Phe Gly Arg Val Met Gln Ile Gly Ser Arg  
100 105 110

Glu Thr Ala Phe Thr His Ala Val Ser Ala Ala Gly Val Val Asn Ala  
115 120 125

Ile Ser Arg Ala Cys Arg Glu Gly Glu Leu Ser Thr Cys Gly Cys Ser  
130 135 140

Arg Thr Ala Arg Pro Lys Asp Leu Pro Arg Asp Trp Leu Trp Gly Gly  
145 150 155 160

Cys Gly Asp Asn Val Glu Tyr Gly Tyr Arg Phe Ala Lys Glu Phe Val  
165 170 175

Asp Ala Arg Glu Arg Glu Lys Asn Phe Ala Lys Gly Ser Glu Glu Gln  
180 185 190

Gly Arg Val Leu Met Asn Leu Gln Asn Asn Glu Ala Gly Arg Arg Ala  
195 200 205

Val Tyr Lys Met Ala Asp Val Ala Cys Lys Cys His Gly Val Ser Gly  
210 215 220

Ser Cys Ser Leu Lys Thr Cys Trp Leu Gln Leu Ala Glu Phe Arg Lys  
225 230 235 240

Val Gly Asp Arg Leu Lys Glu Lys Tyr Asp Ser Ala Ala Ala Met Arg  
245 250 255

Val Thr Arg Lys Gly Arg Leu Glu Leu Val Asn Ser Arg Phe Thr Gln  
260 265 270

Pro Thr Pro Glu Asp Leu Val Tyr Val Asp Pro Ser Pro Asp Tyr Cys  
275 280 285

Leu Arg Asn Glu Ser Thr Gly Ser Leu Gly Thr Gln Gly Arg Leu Cys  
290 295 300

Asn Lys Thr Ser Glu Gly Met Asp Gly Cys Glu Leu Met Cys Cys Gly  
305 310 315 320

Arg Gly Tyr Asn Gln Phe Lys Ser Val Gln Val Glu Arg Cys His Cys  
325 330 335

Lys Phe His Trp Cys Cys Phe Val Arg Cys Lys Lys Cys Thr Glu Ile  
340 345 350

Val Asp Gln Tyr Ile Cys Lys  
355

<210> 89

<211> 794

<212> DNA

<213> human organism

<400> 89

ggcagccgtc	tgtgccaccc	agagccggcg	ggccgcctagg	tccccggaga	ccctgctatg	60
gtgcgtgcgg	gcgcgcgtggg	ggctcatctc	cccgcgccg	gcttggatat	cttcggggac	120
ctgaagaaga	tgaacaagcg	ccagctctat	taccaggttt	taaaacttcgc	catgatcgtg	180
tcttctgcac	tcatgatatg	gaaaggcttg	atcgtgctca	caggcagtga	gagccccatc	240
gtggtgtgc	ttagtggcag	tatggagccg	gccttcaca	gaggagacct	cctgttcctc	300
acaaaattcc	gggaagaccc	aatcagagct	ggtgaaatag	ttgtttttaa	agttgaagga	360
cgagacattc	caatagttca	cagagtaatc	aaagttcatg	aaaaagataa	tggagacatc	420
aaatttctga	ctaaaggaga	taataatgaa	gttgatgata	gaggcttgta	caaagaaggc	480
cagaactggc	tggaaaagaa	ggacgtggtg	ggaagagcaa	gagggtttt	accatatgtt	540
ggtatggtca	ccataataat	aatgactat	ccaaaattca	agtatgctct	tttggctgta	600
atgggtgcat	atgtgttact	aaaacgtgaa	tcctaaaatg	agaagcagtt	cctgggacca	660
gattgaaatg	aattctgttg	aaaaagagaa	aaactaatat	atttgagatg	ttccattttc	720
tgtataaaag	ggaacagtgt	ggagatgtt	ttgtcttgta	caaataaaag	attcaccagt	780
aaaaaaaaaa	aaaa					794

<210> 90

<211> 192

<212> PRT

<213> human organism

<400> 90

Met Val Arg Ala Gly Ala Val Gly Ala His Leu Pro Ala Ser Gly Leu  
1 5 10 15

Asp Ile Phe Gly Asp Leu Lys Lys Met Asn Lys Arg Gln Leu Tyr Tyr  
20 25 30

Gln Val Leu Asn Phe Ala Met Ile Val Ser Ser Ala Leu Met Ile Trp  
35 40 45

Lys Gly Leu Ile Val Leu Thr Gly Ser Glu Ser Pro Ile Val Val Val  
50 55 60

Leu Ser Gly Ser Met Glu Pro Ala Phe His Arg Gly Asp Leu Leu Phe  
65 70 75 80

Leu Thr Asn Phe Arg Glu Asp Pro Ile Arg Ala Gly Glu Ile Val Val  
85 90 95

Phe Lys Val Glu Gly Arg Asp Ile Pro Ile Val His Arg Val Ile Lys  
100 105 110

Val His Glu Lys Asp Asn Gly Asp Ile Lys Phe Leu Thr Lys Gly Asp  
115 120 125

Asn Asn Glu Val Asp Asp Arg Gly Leu Tyr Lys Glu Gly Gln Asn Trp  
130 135 140

Leu Glu Lys Asp Val Val Gly Arg Ala Arg Gly Phe Leu Pro Tyr  
145 150 155 160

Val Gly Met Val Thr Ile Ile Met Asn Asp Tyr Pro Lys Phe Lys Tyr  
165 170 175

Ala Leu Leu Ala Val Met Gly Ala Tyr Val Leu Leu Lys Arg Glu Ser  
180 185 190

<210> 91  
<211> 2108  
<212> DNA  
<213> human organism

<400> 91  
gattactcac acagtcttga agatgcaatg tcagctattt aggacagaaa catccaaggc 60

cgtgtcagaa ctcaattacg actacatatg cattaaggca ggaactggca ggcctcaggg 120  
tacGCCAact ataggactcg tgcttctcg acgctggct ataatctatg aaactgagct 180  
ccagagccag ccaatcactt agctcctcat aacaagtcta actggctctg gaaagctgaa 240  
aggctgcac tggAACACA cagatgagat attctacaca ttaatctact tatctggaat 300  
cactttgcct ctaaaggcca gagaaaaatc acagttcct tgtcggaggg gaaaaggaca 360  
ggtgatctgg ggAAAACGCA gctacacctg gagcaaggtc tcttcccggc ttggcaatct 420  
cagctgtgcc ggcgctacgg gacCCGAGCC gtcccagaaa ccaaAGGGCA ggcacggcag 480  
caaACGCCTG agtgctgctg cttcggtga ctatATGAGA atggAAACTT ctaAGGAAGC 540  
caggttgtta gaattgttac cccctttact cagagataac atagattatc caggctgaga 600  
tggAAAACAA GCCCTTTATT gaattttcaa cacagactcc ctgcttctca totccttaat 660  
aaaatttcat taaaatcccc ttGAactccc atgttcaaAT ctccatttGT tgacagacaa 720  
agCCAACAAAT actctAAACT gaggcctgca agtcatttca tttgtatTT tgcAGGAA 780  
tttcccataG gaagacttca ctcctacAA ctccGAAGAA aacccttact gtccaaGACC 840  
gtcaccAGCA accatccgca gtcattcaag tggAGCTT cacAGCTTt gtacatttC 900  
tgtgtcaata tacaactgag ttacAGACTG tcccctggct ccctgaccct tacaAAACACT 960  
aaaAGTTTG ttGACTCAA CTCAGCTG CTCATCTGTT agtaAGTgat gttcactcca 1020  
gaacacATTc atGATGAGAA CTTCTAAAA gaccAGCAct gctttcccc tcctataatc 1080  
ataATAATCA tgataACCTG aaACATGTT ctggactcg acatTTTCT ggggattgaa 1140  
atCTTtagTC CTTGGAGCTG tcACATAGCA ggggcaACCT cacACTgAAA caaAGGAAGT 1200  
gatgtcccAt tattatccAC cctgAGGCCAc cataATATGc tgTTTACATT tattttCTTC 1260  
agcctgtgca aaACAAAGCA atggAAAAGG aaACTAAAAA atatacatac tagtaccatt 1320  
atcttctttt gcctAAATT actaatgcAC cacgtcAGTC tgcttcCTTC aggcatcatt 1380  
ctcaattcat caggacttGT attAGCAGGT tctggCTAGA gagactatCT cctgtcatca 1440  
cgatcaatta atgtttctg gtgatcacat caggCCCTAT ctaAGAAGCT catggTatac 1500  
aagggtcAcc caaatAGCTG agtgcAGTCC ttgctCATAT ttccTTcATC ttaACCCGc 1560  
aaacaAGAAAT taAGATGATC ccaataAAAG AAAAATTGCT caggAAACTG AACCTTTTC 1620  
tgaACCAAGC actgtcAGCA aatctcAGGT attAGAGCAA ctatggTTGA ttgAAAAGTG 1680  
tctcaAAATC tggGCCAAGA atgattGCTA ggtccataAG ctaattGTC tggcTTGCC 1740

atttacgtaa	gccaaagaaa	gtcactcatg	agtaaactat	agaaaaacgtt	cagacccatc	1800
ctgttagtat	gtcaaatcaa	ctaagactgg	cagggtatta	actccattcc	aggtgacatg	1860
gataaagagc	cccattattt	tcacagtgcc	agcctctacc	taaggaaacc	ctagaccttg	1920
gaaccagttt	cctggtaggg	aactgctgac	agtttcaatg	ctgacagttg	gagccaatgc	1980
ctcatagtgt	aaactgaaaag	aaaaatagtt	gcttttaaa	atgtcagcaa	gaaggcctgc	2040
ctcatcttaa	caaagcaaaa	aaaaatgctt	taattcaaat	taaaaatcat	gatactaaaa	2100
aaaaaaaaa						2108

<210> 92  
<211> 59  
<212> PRT  
<213> human organism

<400> 92

Met	Gln	Cys	Gln	Leu	Phe	Arg	Thr	Glu	Thr	Ser	Lys	Ala	Val	Ser	Glu
1				5				10			15				

Leu	Asn	Tyr	Asp	Tyr	Ile	Cys	Ile	Lys	Ala	Gly	Thr	Gly	Arg	Pro	Gln
				20				25				30			

Gly	Thr	Pro	Thr	Ile	Gly	Leu	Val	Leu	Leu	Val	Arg	Trp	Ala	Ile	Ile
				35			40			45					

Tyr	Glu	Thr	Glu	Leu	Gln	Ser	Gln	Pro	Ile	Thr					
				50		55									

<210> 93  
<211> 1991  
<212> DNA  
<213> human organism

<400> 93

cgcggcggct	ggcgtcggga	aagtacagta	aaaagtccga	gtgcagccgc	cgggcgcagg	60
atgggatccg	gctcctccag	ctaccggccc	aaggccatct	acctggacat	cgatggacgc	120
attcagaagg	taatcttcag	caagtactgc	aactccagcg	acatcatgga	cctgttctgc	180
atcgccaccg	gcctgcctcg	gaacacgacc	atctccctgc	tgaccaccga	cgacgccatg	240
gtctccatcg	accccaccat	gcccgcgaat	tcagaacgca	ctccgtacaa	agtgagacct	300
gtggccatca	agcaactctc	cgctggtgtc	gaggacaaga	gaaccacaag	ccgtggccag	360
tctgctgaga	gaccactgag	ggacagacgg	gttgtggcc	tggagcagcc	ccggagggaa	420

ggagcattt	aaagtggaca	ggttagagccc	aggcccagag	agccccaggg	ctgctaccag	480
gaaggccagc	gcatccctcc	agagagagaa	gaattaatcc	agagcgtgct	ggcgaggtt	540
gcagagcagt	tctcaagagc	attcaaaaatc	aatgaactga	aagctgaagt	tgcaaataac	600
ttggctgtcc	tagagaaacg	cgtggaaattt	gaaggactaa	aagtggtgg	gattgagaaa	660
tgcaagagtg	acattaagaa	gatgagggag	gagctggcgg	ccagaagcag	caggaccaac	720
tgccctgtta	agtacagttt	tttggataac	cacaagaagt	tgactcctcg	acgcgatgtt	780
cccaacttacc	ccaagtacct	gctctctcca	gagaccatcg	aggccctg	gaagccgacc	840
tttgacgtct	ggctttggga	gcccaatgag	atgctgagct	gcctggagca	catgtaccac	900
gacctcgggc	tggtcaggg	cttcagcatc	aaccctgtca	ccctcaggag	gtggctgttc	960
tgtgtccacg	acaactacag	aaacaacccc	ttccacaact	tccggactg	cttctgcgtg	1020
gcccagatga	tgtacagcat	ggtctggctc	tgcagtctcc	aggagaagtt	ctcacaaacg	1080
gatatcctga	tcctaattgac	agcggccatc	tgccacgatc	tggaccatcc	cggttacaac	1140
aacacgtacc	agatcaatgc	ccgcacagag	ctggcggtcc	gctacaatga	catctcaccg	1200
ctggagaacc	accactgcgc	cgtggccttc	cagatcctcg	ccgagcctga	gtgcaacatc	1260
ttctccaaca	tcccacctga	tgggttcaag	cagatccgac	aggaaatgtat	cacattaatc	1320
ttggccactg	acatggcaag	acatgcagaa	attatggatt	ctttcaaaga	aaaaatggag	1380
aattttgact	acagcaacga	ggagcacatg	accctgctga	agatgatttt	gataaaatgc	1440
tgtgatatct	ctaacgaggt	ccgtccaatg	gaagtcgcag	agccttgggt	ggactgttta	1500
ttagaggaat	attttatgca	gagcgaccgt	gagaagtcag	aaggccttcc	tgtggcaccc	1560
ttcatggacc	gagacaaagt	gaccaaggcc	acagcccaga	ttgggttcat	caagtttgtc	1620
ctgatcccaa	tgtttgaaac	agtgaccaag	ctttccccca	tgggttggaa	gatcatgctg	1680
cagccactt	ggaaatcccg	agatcgctac	gaggagctga	agcggataga	tgacgccatg	1740
aaagagttac	agaagaagac	tgacagctt	acgtctgggg	ccaccgagaa	gtccagagag	1800
agaagcagag	atgtgaaaaaa	cagtgaagga	gactgtgcct	gaggaaagcg	ggggcgtgg	1860
ctgcagttct	ggacgggctg	gccgagctgc	gcgggatcct	tgtgcaggga	agagctgccc	1920
tgggcacctg	gcaccacaag	accatgtttt	ctaagaacca	tttggcac	tgataaaaaa	1980
aaaaaaaaaa	a					1991

<211> 593

<212> PRT

<213> human organism

<400> 94

Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp  
1 5 10 15

Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser  
20 25 30

Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn  
35 40 45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp  
50 55 60

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro  
65 70 75 80

Val Ala Ile Lys Gln Leu Ser Ala Gly Val Glu Asp Lys Arg Thr Thr  
85 90 95

Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg Arg Val Val  
100 105 110

Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser Gly Gln Val  
115 120 125

Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu Gly Gln Arg  
130 135 140

Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val  
145 150 155 160

Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu  
165 170 175

Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly  
180 185 190

Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys Met  
195 200 205

Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys  
210 215 220

Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val  
225 230 235 240

Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu  
245 250 255

Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu  
260 265 270

Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe  
275 280 285

Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp  
290 295 300

Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val  
305 310 315 320

Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys  
325 330 335

Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His  
340 345 350

Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg  
355 360 365

Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His  
370 375 380

His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile  
385 390 395 400

Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met  
405 410 415

Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met  
420 425 430

Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu  
435 440 445

His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser  
450 455 460

Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu  
465 470 475 480

Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu  
485 490 495

Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala  
500 505 510

Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val  
515 520 525

Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp  
530 535 540

Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met  
545 550 555 560

Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu  
565 570 575

Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys  
580 585 590

Ala

<210> 95  
<211> 691  
<212> DNA  
<213> human organism

<400> 95  
cagtcacagg cgagagccyt gggatgcacc ggccagaggc atgctgctgc tgctcacgct 60  
tgccctcctg gggggccccca cctgggcagg gaagatgtat ggccctggag gaggcaagta 120  
tttcagcacc actgaagact acgaccatga aatcacaggg ctgcgggtgt ctgttaggtct 180  
tctcctggtg aaaagtgtcc aggtgaaaact tggagactcc tggacgtga aactgggagc 240

cttaggtggg aatacccagg aagtcaccct gcagccaggc gaatacatca caaaagtctt	300
tgtcgcccttc caagcttcc tccgggtat ggtcatgtac accagcaagg accgctattt	360
ctatttggg aagcttgatg gccagatctc ctctgcctac cccagccaag aggggcaggt	420
gctggtgggc atctatggcc agtatcaact cttggcattc aagagcattg gctttgaatg	480
gaattatcca ctagaggagc cgaccactga gccaccagtt aatctcacat actcagcaaa	540
ctcacccgtg ggtcgctagg gtgggtatg gggccatccg agctgaggcc atctgtgtgg	600
tggtggctga tggtaactgga gtaactgagt cgggacgctg aatctgaatc caccaataaa	660
taaaagcttct gcagaatcag tgaaaaaaaaa a	691

<210> 96  
<211> 172  
<212> PRT  
<213> human organism

<400> 96

Met Leu Leu Leu Leu Thr Leu Ala Leu Leu Gly Gly Pro Thr Trp Ala			
1	5	10	15

Gly Lys Met Tyr Gly Pro Gly Gly Lys Tyr Phe Ser Thr Thr Glu		
20	25	30

Asp Tyr Asp His Glu Ile Thr Gly Leu Arg Val Ser Val Gly Leu Leu		
35	40	45

Leu Val Lys Ser Val Gln Val Lys Leu Gly Asp Ser Trp Asp Val Lys		
50	55	60

Leu Gly Ala Leu Gly Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly			
65	70	75	80

Glu Tyr Ile Thr Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly		
85	90	95

Met Val Met Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu		
100	105	110

Asp Gly Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu		
115	120	125

Val Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly  
130 135 140

Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro Val  
145 150 155 160

Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg  
165 170

<210> 97  
<211> 1059  
<212> DNA  
<213> human organism

<400> 97  
ccgttccgcg ctctggcgcc tcctcccggg cgatgcctcc gctctgggcc ctgctggccc 60  
tcggctgcct gcgggttcggc tcggctgtga acctgcagcc ccaactggcc agtgtgactt  
tcgccaccaa caacccaca cttaccactg tggccttgga aaagcctctc tgcatgtttg 120  
acagcaaaga ggccctcact ggcacccacg aggtctacct gtatgtcctg gtcgactcag  
ccatttccag gaatgcctca gtgcaagaca gcaccaacac cccactgggc tcaacgttcc 180  
tacaaacaga gggtgggagg acaggtccct acaaagctgt ggccttgac ctgatcccc 240  
gcagtgaccc gcccagcctg gatgccattt gggatgtgtc caaggcctca cagatcctga  
atgcctaccc ggtcagggtg ggtgccaacg ggacctgcct gtgggatccc aacttccagg 420  
gcctctgtaa cgcacccctg tcggcagcca cggagtagac gttcaagtat gtcctggta 540  
atatgtccac gggcttgta gaggaccaga ccctgtggc ggacccatc cgcaccaacc 600  
agtcacccca atactcgacg atcgacacgt ggccaggccg gcccggccgaa ggcattatcg  
tcatcacttc catcctggc tccctgcct tcttttact tgtgggtttt gctggcgcca 660  
ttgccctcag cctcgtggac atggggagtt ctgatgggaa aacgactcac gactccaaa 720  
tcactcagga ggctgtttcc aagtcgctgg gggcctcgga gtcttcctac acgtccgtga 780  
accgggggccc gccactggac agggctgagg tgtattccag caagctccaa gactgagccc 840  
agcaccaccc ctgggcagca gcatcctcct ctctggcctt gccccaggcc ctgcagcggt 900  
ggttgtcaca ccctgacttc agggaaagggtg aaacagggtt tgtccctcca actgcaggaa 960  
aaccccttaat aaaatcttct gatgagttct aaaaaaaaaa 1020  
1059

<210> 98  
<211> 287

<212> PRT

<213> human organism

<400> 98

Met Pro Pro Leu Trp Ala Leu Leu Ala Leu Gly Cys Leu Arg Phe Gly  
1 5 10 15

Ser Ala Val Asn Leu Gln Pro Gln Leu Ala Ser Val Thr Phe Ala Thr  
20 25 30

Asn Asn Pro Thr Leu Thr Val Ala Leu Glu Lys Pro Leu Cys Met  
35 40 45

Phe Asp Ser Lys Glu Ala Leu Thr Gly Thr His Glu Val Tyr Leu Tyr  
50 55 60

Val Leu Val Asp Ser Ala Ile Ser Arg Asn Ala Ser Val Gln Asp Ser  
65 70 75 80

Thr Asn Thr Pro Leu Gly Ser Thr Phe Leu Gln Thr Glu Gly Gly Arg  
85 90 95

Thr Gly Pro Tyr Lys Ala Val Ala Phe Asp Leu Ile Pro Cys Ser Asp  
100 105 110

Leu Pro Ser Leu Asp Ala Ile Gly Asp Val Ser Lys Ala Ser Gln Ile  
115 120 125

Leu Asn Ala Tyr Leu Val Arg Val Gly Ala Asn Gly Thr Cys Leu Trp  
130 135 140

Asp Pro Asn Phe Gln Gly Leu Cys Asn Ala Pro Leu Ser Ala Ala Thr  
145 150 155 160

Glu Tyr Arg Phe Lys Tyr Val Leu Val Asn Met Ser Thr Gly Leu Val  
165 170 175

Glu Asp Gln Thr Leu Trp Ser Asp Pro Ile Arg Thr Asn Gln Leu Thr  
180 185 190

Pro Tyr Ser Thr Ile Asp Thr Trp Pro Gly Arg Arg Ser Gly Gly Met  
195 200 205

Ile Val Ile Thr Ser Ile Leu Gly Ser Leu Pro Phe Phe Leu Leu Val  
210 215 220

Gly Phe Ala Gly Ala Ile Ala Leu Ser Leu Val Asp Met Gly Ser Ser  
225 230 235 - 240

Asp Gly Glu Thr Thr His Asp Ser Gln Ile Thr Gln Glu Ala Val Pro  
245 250 255

Lys Ser Leu Gly Ala Ser Glu Ser Ser Tyr Thr Ser Val Asn Arg Gly  
260 265 270

Pro Pro Leu Asp Arg Ala Glu Val Tyr Ser Ser Lys Leu Gln Asp  
275 280 285

<210> 99  
<211> 1894  
<212> DNA  
<213> human organism

<400> 99  
gtctgacttc ctcccagcac attcctgcac tctgccgtgt ccacactgcc ccacagaccc 60  
agtccctccaa gcctgctgcc agctccctgc aagcccccta gggtgggcct tgccacgggt 120  
ccaggcaggca gccctggct gggggtaggg gactccctac aggcacgcag ccctgagacc 180  
tcagagggcc acccctttagg ggtggccagg ccccccagtgg ccaaccttagg tgctgcctct 240  
gccaccagcc ctgctggccc ctggttccgc tggcccccca gatgcctggc tgagacacgc 300  
cagtggcctc agctgcccac acctcttccc ggccccctgaa gttggcactg cagcagacag 360  
ctccctgggc accaggcagc taacagacac agccgccagc ccaaacagca gggcatggg 420  
cagcgccagc ccgggtctga gcagcgtatc ccccaagccac ctccctgctgc ccccccacac 480  
ggtgtcgccgg acaggcttgg agaaggccggc agcgggggca gtgggtctcg agagacggga 540  
ctggagtccttcc agtccaccccg ccacgcccga gcagggcctg tccgccttctt acctcttccta 600  
ctttgacatg ctgtaccctg aggacagcag ctgggcagcc aaggccccctg gggccagcag 660  
tcggggaggag ccacctgagg agcctgagca gtgcccggtc attgacagcc aagccccagc 720  
gggcagcctg gacttggtgc cggcgggct gaccttgag gagcactcgc tggagcaggt 780  
gcagtcctatg gtggggggcg aagtgctcaa ggacatcgag acggcctgca agctgctcaa 840  
catcaccgca gatcccatgg actggagccc cagcaatgtg cagaagtggc tcctgtggac 900  
agagcaccaa taccggctgc ccccccattgg caaggccttc caggagctgg cgggcaaqqa 960

gctgtgcgcc	atgtcgagg	agcagttccg	ccagcgctcg	cccctgggtg	gggatgtgct	1020
gcacgcccac	ctggacatct	ggaagtcagc	ggcctggatg	aaagagcgg	cttcacctgg	1080
ggcgattcac	tactgtgcct	cgaccagtga	ggagagctgg	accgacagcg	aggtggactc	1140
atcatgctcc	gggcagccca	tccacctgtg	gcagttcctc	aaggagttgc	tactcaagcc	1200
ccacagctat	ggccgcttca	ttaggtggct	caacaaggag	aagggcatct	tcaaaaattga	1260
ggactcagcc	caggtggccc	ggctgtgggg	catccgcaag	aaccgtcccc	ccatgaacta	1320
cgacaagctg	agccgctcca	tccgccagta	ttacaagaag	ggcatcatcc	ggaagccaga	1380
catctcccag	cgcctcgct	accagttcgt	gcacccatc	tgagtgcctg	gcccaggggcc	1440
tgaaacccgc	cctcaggggc	ctctctcctg	cctgcctgc	ctcagccagg	ccctgagatg	1500
ggggaaaaacg	ggcagttctgc	tctgctgctc	tgaccttcca	gagcccaagg	tcagggaggg	1560
gcaaccaact	gccccagggg	gatatgggtc	ctctggggcc	ttcgggacca	tggggcaggg	1620
gtgcttcctc	ctcagggcca	gctgctcccc	tggaggacag	agggagacag	ggctgctccc	1680
caacacctgc	ctctgacccc	agcatttcca	gagcagagcc	tacagaaggg	cagtgactcg	1740
acaaggcca	caggcagtcc	aggcctctct	ctgctccatc	cccctgcctc	ccattctgca	1800
ccacacctgg	catggtgcag	ggagacatct	gcacccctga	gttgggcagc	caggagtgcc	1860
cccggaatg	gataataaag	atactagaga	actg			1894

<210> 100

<211> 335

<212> PRT

<213> human organism

<400> 100

Met	Gly	Ser	Ala	Ser	Pro	Gly	Leu	Ser	Ser	Val	Ser	Pro	Ser	His	Leu
1				5				10				15			

Leu	Leu	Pro	Pro	Asp	Thr	Val	Ser	Arg	Thr	Gly	Leu	Glu	Lys	Ala	Ala
					20			25				30			

Ala	Gly	Ala	Val	Gly	Leu	Glu	Arg	Arg	Asp	Trp	Ser	Pro	Ser	Pro	Pro
					35			40			45				

Ala	Thr	Pro	Glu	Gln	Gly	Leu	Ser	Ala	Phe	Tyr	Leu	Ser	Tyr	Phe	Asp
					50			55			60				

Met Leu Tyr Pro Glu Asp Ser Ser Trp Ala Ala Lys Ala Pro Gly Ala  
65 70 75 80

Ser Ser Arg Glu Glu Pro Pro Glu Glu Pro Glu Gln Cys Pro Val Ile  
85 90 95

Asp Ser Gln Ala Pro Ala Gly Ser Leu Asp Leu Val Pro Gly Gly Leu  
100 105 110

Thr Leu Glu Glu His Ser Leu Glu Gln Val Gln Ser Met Val Val Gly  
115 120 125

Glu Val Leu Lys Asp Ile Glu Thr Ala Cys Lys Leu Leu Asn Ile Thr  
130 135 140

Ala Asp Pro Met Asp Trp Ser Pro Ser Asn Val Gln Lys Trp Leu Leu  
145 150 155 160

Trp Thr Glu His Gln Tyr Arg Leu Pro Pro Met Gly Lys Ala Phe Gln  
165 170 175

Glu Leu Ala Gly Lys Glu Leu Cys Ala Met Ser Glu Glu Gln Phe Arg  
180 185 190

Gln Arg Ser Pro Leu Gly Gly Asp Val Leu His Ala His Leu Asp Ile  
195 200 205

Trp Lys Ser Ala Ala Trp Met Lys Glu Arg Thr Ser Pro Gly Ala Ile  
210 215 220

His Tyr Cys Ala Ser Thr Ser Glu Glu Ser Trp Thr Asp Ser Glu Val  
225 230 235 240

Asp Ser Ser Cys Ser Gly Gln Pro Ile His Leu Trp Gln Phe Leu Lys  
245 250 255

Glu Leu Leu Leu Lys Pro His Ser Tyr Gly Arg Phe Ile Arg Trp Leu  
260 265 270

Asn Lys Glu Lys Gly Ile Phe Lys Ile Glu Asp Ser Ala Gln Val Ala  
275 280 285

Arg Leu Trp Gly Ile Arg Lys Asn Arg Pro Ala Met Asn Tyr Asp Lys

290

295

300

Leu Ser Arg Ser Ile Arg Gln Tyr Tyr Lys Lys Gly Ile Ile Arg Lys  
305 310 315 320

Pro Asp Ile Ser Gln Arg Leu Val Tyr Gln Phe Val His Pro Ile  
325 330 335

<210> 101  
<211> 2664  
<212> DNA  
<213> human organism

<400> 101  
gagagaacag cgtgagcctg tgtgcttgtg tgctgagccc tcatccctc ctggggccag 60  
gcttgggttt cacctgcaga atcgcttgtg ctgggctgcc tgggctgtcc tcagtggcac  
ctgcatgaag ccgttctggc tgccagagct ggacagcccc agaaaaaccc acctctctgc 120  
agagcttgcc cagctgtccc cgaaaagcca aatgcctctc atgtaagtct tctgctcgac  
ggggtgtctc ctaaaccctc actcttcagc ctctgtttga ccatgaaatg aagtgactga 180  
gctctattct gtacctgcca ctctatttct ggggtgactt ttgtcagctg cccagaatct  
ccaagccagg ctggttctct gcattcatttc aatgacctgt tttcttctgt aaccacaggt 240  
tcggtggtga gaggaagcct cgcagaatcc agcagaatcc tcacagaatc cagcagcagc  
tctgctgggg acatggtcca tggtgcaacc cacagcaaag ccctgacctg acctcctgat 300  
gctcaggaga agccatgggc ccctcctgtc ctgtgttctt gtccttcaca aagctcagcc  
tgtggtggtct ccttctgacc ccagcaggtg gagaggaagc taagcgccca cctcccaagg 360  
ctcctggaga cccactctcc tctcccagtc ccacggcatt gccgcaggga ggctcgata  
ccgagactga ggaccggctc ttcaaaccacc tcttccgggg ctacaaccgc tgggcgcgcc 420  
cggtgcccaa cacttcagac gtggtgattt tgccctttgg actgtccatc gctcagctca  
tcgatgtgga tgagaagaac caaatgatga ccaccaacgt ctggctaaaa caggagtgg 480  
gchgactacaa actgcgctgg aaccccgctg attttggcaa catcacatct ctcagggtcc  
cttctgagat gatctggatc cccgacattt ttctctacaa caatgcagat ggggagttt 540  
cagtgacccca catgaccaag gcccacctct tctccacggg cactgtgcac tgggtgcccc  
cgcccatcta caagagctcc tgcagcatcg acgtcacctt cttcccttc gaccagcaga 600  
actgcaagat gaagtttggc tcctggactt atgacaaggc caagatgcac ctqqaqcqa 660  
actgcaagat gaagtttggc tcctggactt atgacaaggc caagatgcac ctqqaqcqa 720  
actgcaagat gaagtttggc tcctggactt atgacaaggc caagatgcac ctqqaqcqa 780  
actgcaagat gaagtttggc tcctggactt atgacaaggc caagatgcac ctqqaqcqa 840  
actgcaagat gaagtttggc tcctggactt atgacaaggc caagatgcac ctqqaqcqa 900  
actgcaagat gaagtttggc tcctggactt atgacaaggc caagatgcac ctqqaqcqa 960  
actgcaagat gaagtttggc tcctggactt atgacaaggc caagatgcac ctqqaqcqa 1020  
actgcaagat gaagtttggc tcctggactt atgacaaggc caagatgcac ctqqaqcqa 1080  
actgcaagat gaagtttggc tcctggactt atgacaaggc caagatgcac ctqqaqcqa 1140  
actgcaagat gaagtttggc tcctggactt atgacaaggc caagatgcac ctqqaqcqa 1200

tggagcagac tgtggacctg aaggactact	1260
gggagagcgg cgagtgggcc atcgtaatg	
ccacgggcac ctacaacagc aagaagtacg actgctgcgc	1320
cgagatctac cccgacgtca	
cctacgcctt cgtcatccgg cggtgtccgc ttttacac	1380
catcaacctc atcatccc	
gcctgctcat ctccctgcctc actgtgctgg ttttacac	1440
gccctccgac tgccggcaga	
agatcacgct gtgcatttcg gtgctgctgt cactaccgt	1500
cttcctgctg ctcatcactg	
agatcatccc gtccacctcg ctggtcatcc cgctcatcg	1560
cgagtacctg ctgttacca	
tgtatcttcgt caccctgtcc atcgcatca ccgtttcgt	1620
gctcaatgtg caccaccgct	
cccccagcac ccacaccatg ccccactggg tgccgggggc	1680
ccttctgggc tgtgtcccc	
ggtgtggcttct gatgaaccgg ccccccaccac ccgtggagct	1740
ctgccaccccc ctacgcctga	
agctcagccc ctcttatcac tggctggaga gcaacgtgga	1800
tgccgaggag agggaggtgg	
ttggtgagga ggaggacaga tggcatgtg caggtcatgt	1860
ggccccctct gtgggcaccc	
tctgcagcca cggccacctg cactctgggg cctcaggtcc	1920
caaggctgag gctctgctgc	
ttcaccacaca tgcagaaggc actggaaggt gtgcactaca	1980
ttgccgacca cctgcgtct gaggatgctg actcttcgtt	2040
gaaggaggac tggaagtatg	
ttgccatggt catcgacagg atcttcctct ggctgtttat	2100
catcgctgc ttccctggga	
ccatcggcct ctttctgcct ccgttcctag ctggaatgat	2160
ctgactgcac ctccctcgag	
ctggctccca gggcaaaggg gaggttctt ggatgtggaa	2220
gggcttgaa caatgtttag	
atttggagat gagcccaaag tgcaggaggag aacagccagg	2280
tgaggtggga gttggagag	
ccaggtgagg tctctctaag tcaggctggg gttgaagttt	2340
ggagtctgtc cgagtttgca	
gggtgctgag ctgtatggtc cagcaggggta gtaataaggg	2400
ctcttcggaa agggaggaa	
gcgggaggca ggcctgcacc tcatgtggag gtacaggcag	2460
atcttcctta ccggggagg	
atggatggtt ggatacaggt ggctggcata ttccatccat	2520
ctggaaagcac atttggcct	
ccaggcttct ctttgacgtc attcctctcc ttccctgctg	2580
caaaatggct ctgcaccagc	
cggcccccag gaggtctggc agagctgaga gcatggcct	2640
gcaggggctc catatgtccc	
tacgcgtgca gcaggcaaac aaga	2664

<210> 102  
<211> 529  
<212> PRT  
<213> human organism

<400> 102

Met Gly Pro Ser Cys Pro Val Phe Leu Ser Phe Thr Lys Leu Ser Leu  
1 5 10 15

Trp Trp Leu Leu Leu Thr Pro Ala Gly Gly Glu Ala Lys Arg Pro  
20 25 30

Pro Pro Arg Ala Pro Gly Asp Pro Leu Ser Ser Pro Ser Pro Thr Ala  
35 40 45

Leu Pro Gln Gly Gly Ser His Thr Glu Thr Glu Asp Arg Leu Phe Lys  
50 55 60

His Leu Phe Arg Gly Tyr Asn Arg Trp Ala Arg Pro Val Pro Asn Thr  
65 70 75 80

Ser Asp Val Val Ile Val Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile  
85 90 95

Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr Asn Val Trp Leu Lys  
100 105 110

Gln Glu Trp Ser Asp Tyr Lys Leu Arg Trp Asn Pro Ala Asp Phe Gly  
115 120 125

Asn Ile Thr Ser Leu Arg Val Pro Ser Glu Met Ile Trp Ile Pro Asp  
130 135 140

Ile Val Leu Tyr Asn Asn Ala Asp Gly Glu Phe Ala Val Thr His Met  
145 150 155 160

Thr Lys Ala His Leu Phe Ser Thr Gly Thr Val His Trp Val Pro Pro  
165 170 175

Ala Ile Tyr Lys Ser Ser Cys Ser Ilè Asp Val Thr Phe Phe Pro Phe  
180 185 190

Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser Trp Thr Tyr Asp Lys  
195 200 205

Ala Lys Ile Asp Leu Glu Gln Met Glu Gln Thr Val Asp Leu Lys Asp  
210 215 220

Tyr Trp Glu Ser Gly Glu Trp Ala Ile Val Asn Ala Thr Gly Thr Tyr  
225 230 235 240

Asn Ser Lys Lys Tyr Asp Cys Cys Ala Glu Ile Tyr Pro Asp Val Thr  
245 250 255

Tyr Ala Phe Val Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu  
260 265 270

Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr Val Leu Val Phe Tyr  
275 280 285

Leu Pro Ser Asp Cys Gly Glu Lys Ile Thr Leu Cys Ile Ser Val Leu  
290 295 300

Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser  
305 310 315 320

Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met  
325 330 335

Ile Phe Val Thr Leu Ser Ile Val Ile Thr Val Phe Val Leu Asn Val  
340 345 350

His His Arg Ser Pro Ser Thr His Thr Met Pro His Trp Val Arg Gly  
355 360 365

Ala Leu Leu Gly Cys Val Pro Arg Trp Leu Leu Met Asn Arg Pro Pro  
370 375 380

Pro Pro Val Glu Leu Cys His Pro Leu Arg Leu Lys Leu Ser Pro Ser  
385 390 395 400

Tyr His Trp Leu Glu Ser Asn Val Asp Ala Glu Glu Arg Glu Val Val  
405 410 415

Val Glu Glu Glu Asp Arg Trp Ala Cys Ala Gly His Val Ala Pro Ser  
420 425 430

Val Gly Thr Leu Cys Ser His Gly His Leu His Ser Gly Ala Ser Gly  
435 440 445

Pro Lys Ala Glu Ala Leu Leu Gln Glu Gly Glu Leu Leu Ser Pro

450

455

460

His Met Gln Lys Ala Leu Glu Gly Val His Tyr Ile Ala Asp His Leu  
465 470 475 480

Arg Ser Glu Asp Ala Asp Ser Ser Val Lys Glu Asp Trp Lys Tyr Val  
485 490 495

Ala Met Val Ile Asp Arg Ile Phe Leu Trp Leu Phe Ile Ile Val Cys  
500 505 510

Phe Leu Gly Thr Ile Gly Leu Phe Leu Pro Pro Phe Leu Ala Gly Met  
515 520 525

Ile

<210> 103  
<211> 1181  
<212> DNA  
<213> human organism

<400> 103  
cacaggctg gaaggggcca cttcacacct cgggctcgcc ataaagcggc cgccggccgc 60  
cggcccccag acgcgcgcgc gctgccatgg cccagccccgt gtgcccgcgc ctctccgagt 120  
cctggatgct ctctgcggcc tggggcccaa ctcggcggcc gccgcctcc gacaaggact 180  
gcggccgctc cctcgctcg tccccagact catggggcag cacccagcc gacagccccg 240  
tggcgagccc cgcgccgcca ggcaccctcc gggaccccccgcgccccctcc gtaggttaggc 300  
gcggcgccgcg cagcagccgc ctgggcagcg ggcagaggca gagcgccagt gagcgggaga 360  
aactgcgcat gcgcacgctg gcccgcgcgc tgacacgact ggcgcgcctt ctaccggcgt 420  
ccgtggcgcc cgcggggccag agcctgacca agatcgagac gctgcgcctg gctatccgct 480  
atatcgccca cctgtcgccgc gtgctaggcc tcagcgagga gagtctccag cgccggtgcc 540  
ggcagcgcgg tgacgcgggg tccccctcggt gctgccccgt gtgccccgac gactgccccg 600  
cgcagatgca gacacggacg caggctgagg ggcaggggca ggggcgcggg ctgggcctgg 660  
tatccggcgt ccgcgcgggg gctgcctggg gatccccgc tgccctgcccc ggagccccgag 720  
ctgcacccga gccgcgcgcac ccgcctgcgc tggtcgccga ggccggcgtgc ccggaaagggc 780  
aggcgatgga gccaagccca ccgtccccgc tccttccggg cgacgtgctg gctctgttgg 840

agacctggat gcccctctcg cctctggagt ggctgcctga ggagcccaag tgacaaggga	900
caactgacgc cgtctctgtg agcaccgagg cttttggcc tcagcacctt cgaagtggtt	960
ccttggcaga ctgccttcc tggaaagaggg cacgggcgat cccgacgggg gcattcctgc	1020
gggtgagagc cgtccccacc gcggcggccc ttctcagccc ctccctccat ggagggaccc	1080
atagggctag acactttgag gcaagcagga ggctctgcct aatgtgaatt tatttatttg	1140
tgaataaact gtactggtgt caaaaaaaaaaaaaaaa a	1181

<210> 104

<211> 268

<212> PRT

<213> human organism

<400> 104

Met Ala Gln Pro Leu Cys Pro Pro Leu Ser Glu Ser Trp Met Leu Ser			
1	5	10	15

Ala Ala Trp Gly Pro Thr Arg Arg Pro Pro Pro Ser Asp Lys Asp Cys			
20	25	30	

Gly Arg Ser Leu Val Ser Ser Pro Asp Ser Trp Gly Ser Thr Pro Ala			
35	40	45	

Asp Ser Pro Val Ala Ser Pro Ala Arg Pro Gly Thr Leu Arg Asp Pro			
50	55	60	

Arg Ala Pro Ser Val Gly Arg Arg Gly Ala Arg Ser Ser Arg Leu Gly			
65	70	75	80

Ser Gly Gln Arg Gln Ser Ala Ser Glu Arg Glu Lys Leu Arg Met Arg			
85	90	95	

Thr Leu Ala Arg Ala Leu His Glu Leu Arg Arg Phe Leu Pro Pro Ser			
100	105	110	

Val Ala Pro Ala Gly Gln Ser Leu Thr Lys Ile Glu Thr Leu Arg Leu			
115	120	125	

Ala Ile Arg Tyr Ile Gly His Leu Ser Ala Val Leu Gly Leu Ser Glu			
130	135	140	

Glu Ser Leu Gln Arg Arg Cys Arg Gln Arg Gly Asp Ala Gly Ser Pro

145                    150                    155                    160

Arg Gly Cys Pro Leu Cys Pro Asp Asp Cys Pro Ala Gln Met Gln Thr  
165                    170                    175

Arg Thr Gln Ala Glu Gly Gln Gly Arg Gly Leu Gly Leu Val  
180                    185                    190

Ser Ala Val Arg Ala Gly Ala Ser Trp Gly Ser Pro Pro Ala Cys Pro  
195                    200                    205

Gly Ala Arg Ala Ala Pro Glu Pro Arg Asp Pro Pro Ala Leu Phe Ala  
210                    215                    220

Glu Ala Ala Cys Pro Glu Gly Gln Ala Met Glu Pro Ser Pro Pro Ser  
225                    230                    235                    240

Pro Leu Leu Pro Gly Asp Val Leu Ala Leu Leu Glu Thr Trp Met Pro  
245                    250                    255

Leu Ser Pro Leu Glu Trp Leu Pro Glu Glu Pro Lys  
260                    265

<210> 105

<211> 3810

<212> DNA

<213> human organism

<400> 105

ccacggagaa	gcccaccgat	gcctacggag	agctggactt	cacgggggcc	ggccgcaagc	60
acagcaattt	cctccggctc	tctgaccgaa	cggatccagc	tgcagtttat	agtctggtca	120
cacgcacatg	gggcttccgt	gccccgaacc	tggtggtgtc	agtgctgggg	ggatcggggg	180
gccccgtcct	ccagacctgg	ctgcaggacc	tgctgcgtcg	tgggctggtg	cgggctgccc	240
agagcacagg	agcctggatt	gtcactgggg	gtctgcacac	gggcacgcgc	cggcatgttg	300
gtgtggctgt	acgggaccat	cagatggcca	gcactggggg	caccaaggtg	gtggccatgg	360
gtgtggcccc	ctggggtgtg	gtccggaata	gagacaccct	catcaacccc	aagggctcgt	420
tccctgcgag	gtaccggtgg	cgcggtgacc	cggaggacgg	ggtccagttt	cccctggact	480
acaactactc	ggccttcttc	ctggtgacg	acggcacaca	cggctgcctg	ggggggcgaga	540
accgcttccg	cttgcgcctg	gagtcctaca	tctcacagca	gaagacgggc	gtgggagggaa	600

ctggaattga catccctgtc ctgctcctcc tgattgatgg tcatgagaag atgttgacgc 660  
gaatagagaa cgccacccag gctcagctcc catgtctcct cgtggctggc tcagggggag 720  
ctgcggactg cctggcgag acccttggaa acactctggc cccaggaggt gggggagcca 780  
ggcaaggcga agcccggagat cgaatcaggc gtttcttcc caaaggggac cttgaggtcc 840  
tgcaggccca ggtggagagg attatgaccc ggaaggagct cctgacagtc tattttctg 900  
aggatgggtc tgaggaattc gagaccatag ttttgaaggc ctttgtgaag gcctgtggga 960  
gctcgaggc ctcagcc tac ctggatgagc tgcgttggc tgtggcttgg aaccgcgtgg 1020  
acattgccc a ggtgaactc ttccgggggg acatccaatg gcggtccttc catctcgaag 1080  
cttccctcat ggacgccc tg ctgaatgacc ggcctgagtt cgtgcgc ttg ctcatttccc 1140  
acggcctcag cctggccac ttccctgaccc c gatgcgc ct ggcccaactc tacagcgcgg 1200  
cgccctccaa ctcgctcatc cgcaaccttt tggaccaggc gtcccacagc gcaggcacca 1260  
aagccccagc cctaaaaggg ggagctgcgg agctccggcc ccctgacgtg gggcatgtgc 1320  
tgaggatgct gctggggaa atgtgcgcgc cgaggtaccc ctccgggggc gcctgggacc 1380  
ctcaccagg ccaggccttc gggagagca tgtatctgct ctcggacaag gccacctcgc 1440  
cgctctcgct g gatgctggc ctcggcagg cccctggag cgacctgctt cttgggcac 1500  
tttgctgaa cagggcacag atggccatgt acttctggaa gatgggttcc aatgcagtt 1560  
cctcagctct tggggcctgt ttgctgctcc gggtgatggc acgcctggag cctgacgctg 1620  
aggaggcagc acggaggaaa gacctggcgt tcaagttga gggatgggc gttgacctct 1680  
ttggcgagtg ctatcgacgc agtgagggtga gggctgccc ctcctcctc cgtgcgtgcc 1740  
cgctctgggg g gatgccact tgcctccagc tggccatgca agctgacgcc cgtgccttct 1800  
ttgcccagga tggggtacag tctctgctga cacagaagtg gtggggagat atggccagca 1860  
ctacacccat ctggccctg gttctcgct tctttgccc tccactcatc tacacccgcc 1920  
tcatcacctt cagaaatca gaagaggagc ccacacggga ggagcttagag tttgacatgg 1980  
atagtgtcat taatggggaa gggcctgtcg ggacggcgg a cccagccgag aagacgccgc 2040  
tgggggtccc ggcgcagtcg ggcgtccgg gttgctgcgg gggccgtgc gggggcgcc 2100  
gggcctacg cgcctggttc cacttctggg ggcgcggcgt gaccatcttc atggcaacg 2160  
tggtcagcta cctgctgttc ttgctgcttt tctcgccgg gctgctcgtg gatttccagc 2220  
cgccgcggcc cggccctg gagctgctgc tctatttctg ggcttcacg ctgctgtgcg 2280  
aggaactgcg ccagggcctg agcggaggcg gggcagccct cgccagcggg ggccccgggc 2340

ctggccatgc ctcactgagc cagcgccgc gcctctaccc cgccgacagg tggaaccagt 2400  
gcgacctagt ggctctcacc tgcttccccc tggcggtgg ctgccggctg accccgggtt 2460  
tgtaccacct gggccgcact gtcctctgca tcgacttcat gttttcacg gtgcggctgc 2520  
ttcacatctt cacggtaaac aaacagctgg ggcccaagat cgtcatcgtg agcaagatga 2580  
tgaaggacgt gtttttttc ctcttccccc tcggcggttg gctggtagcc tatggcggtgg 2640  
ccacggaggg gtcctgagg ccacggaca gtgacttccc aagtatcctg cgccgcgtct 2700  
tctaccgtcc ctacctgcag atcttcgggc agattccccaa ggaggacatg gacgtggccc 2760  
tcatggagca cagcaactgc tcgtcgagc ccggcttctg ggcacacccct cctggggccc 2820  
aggcgggcac ctgcgtctcc cagtatgcca actggctggt ggtgctgctc ctcgtcatct 2880  
tcctgctcgt ggccaacatc ctgctggta acttgctcat tgccatgttc agttacacat 2940  
tcggcaaagt acagggcaac agcgatctct actggaaggc gcagcggtac cgccctcatcc 3000  
ggaaattcca ctctcgcccc ggcgtggccc cgccctttat cgtcatctcc cacttgcgcc 3060  
tcctgctcag gcaattgtgc aggcgacccc ggagccccca gccgtctcc cggccctcg 3120  
agcatttccg gtttacctt tctaaggaag ccgagcggaa gctgctaacg tggaatcgg 3180  
tgcataagga gaactttctg ctggcacgac ctagggacaa gcgggagagc gactccgagc 3240  
gtctggagcg cacgtcccag aaggtggact tggcactgaa acagctggga cacatccgac 3300  
agtacgaaca gcgcctgaaa gtgctggagc gggaggtcca gcagtgtac cgccgtctgg 3360  
ggtgggtgac gtaggccgtt agcagctctg ccatgttgcc ctcaggtggg ccgcacccccc 3420  
ttgacctgca tgggtccaaa gagtgagcca tgctggcgga ttttaaggag aagcccccac 3480  
agggatttt gctcttagag taaggctcat gtgggcctcg gccccgcac ctgggtggcct 3540  
tgtcctttag gtagccccca tgtccatctg ggccactgtc aggaccaccc ttgggagtgt 3600  
catccttaca aaccacagca tgcccggtc ctcggcagaac cagtcggcagc ctgggaggat 3660  
caaggcctgg atccccggcc gttatccatc tggaggctgc agggtccttg gggtaacagg 3720  
gaccacagac ccctcaccac tcacagattc ctcacactgg ggaaataaaag ccatttcaga 3780  
ggaaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaa 3810

<210> 106  
<211> 1016  
<212> PRT  
<213> human organism

<400> 106

Met Ala Ser Thr Gly Gly Thr Lys Val Val Ala Met Gly Val Ala Pro  
1 5 10 15

Trp Gly Val Val Arg Asn Arg Asp Thr Leu Ile Asn Pro Lys Gly Ser  
20 25 30

Phe Pro Ala Arg Tyr Arg Trp Arg Gly Asp Pro Glu Asp Gly Val Gln  
35 40 45

Phe Pro Leu Asp Tyr Asn Tyr Ser Ala Phe Phe Leu Val Asp Asp Gly  
50 55 60

Thr His Gly Cys Leu Gly Gly Glu Asn Arg Phe Arg Leu Arg Leu Glu  
65 70 75 80

Ser Tyr Ile Ser Gln Gln Lys Thr Gly Val Gly Gly Thr Gly Ile Asp  
85 90 95

Ile Pro Val Leu Leu Leu Ile Asp Gly Asp Glu Lys Met Leu Thr  
100 105 110

Arg Ile Glu Asn Ala Thr Gln Ala Gln Leu Pro Cys Leu Leu Val Ala  
115 120 125

Gly Ser Gly Gly Ala Ala Asp Cys Leu Ala Glu Thr Leu Glu Asp Thr  
130 135 140

Leu Ala Pro Gly Ser Gly Gly Ala Arg Gln Gly Glu Ala Arg Asp Arg  
145 150 155 160

Ile Arg Arg Phe Phe Pro Lys Gly Asp Leu Glu Val Leu Gln Ala Gln  
165 170 175

Val Glu Arg Ile Met Thr Arg Lys Glu Leu Leu Thr Val Tyr Ser Ser  
180 185 190

Glu Asp Gly Ser Glu Glu Phe Glu Thr Ile Val Leu Lys Ala Leu Val  
195 200 205

Lys Ala Cys Gly Ser Ser Glu Ala Ser Ala Tyr Leu Asp Glu Leu Arg  
210 215 220

Leu Ala Val Ala Trp Asn Arg Val Asp Ile Ala Gln Ser Glu Leu Phe  
225                   230                   235                   240

Arg Gly Asp Ile Gln Trp Arg Ser Phe His Leu Glu Ala Ser Leu Met  
245                   250                   255

Asp Ala Leu Leu Asn Asp Arg Pro Glu Phe Val Arg Leu Leu Ile Ser  
260                   265                   270

His Gly Leu Ser Leu Gly His Phe Leu Thr Pro Met Arg Leu Ala Gln  
275                   280                   285

Leu Tyr Ser Ala Ala Pro Ser Asn Ser Leu Ile Arg Asn Leu Leu Asp  
290                   295                   300

Gln Ala Ser His Ser Ala Gly Thr Lys Ala Pro Ala Leu Lys Gly Gly  
305                   310                   315                   320

Ala Ala Glu Leu Arg Pro Pro Asp Val Gly His Val Leu Arg Met Leu  
325                   330                   335

Leu Gly Lys Met Cys Ala Pro Arg Tyr Pro Ser Gly Gly Ala Trp Asp  
340                   345                   350

Pro His Pro Gly Gln Gly Phe Gly Glu Ser Met Tyr Leu Leu Ser Asp  
355                   360                   365

Lys Ala Thr Ser Pro Leu Ser Leu Asp Ala Gly Leu Gly Gln Ala Pro  
370                   375                   380

Trp Ser Asp Leu Leu Trp Ala Leu Leu Leu Asn Arg Ala Gln Met  
385                   390                   395                   400

Ala Met Tyr Phe Trp Glu Met Gly Ser Asn Ala Val Ser Ser Ala Leu  
405                   410                   415

Gly Ala Cys Leu Leu Leu Arg Val Met Ala Arg Leu Glu Pro Asp Ala  
420                   425                   430

Glu Glu Ala Ala Arg Arg Lys Asp Leu Ala Phe Lys Phe Glu Gly Met  
435                   440                   445

Gly Val Asp Leu Phe Gly Glu Cys Tyr Arg Ser Ser Glu Val Arg Ala  
450 455 460

Ala Arg Leu Leu Leu Arg Arg Cys Pro Leu Trp Gly Asp Ala Thr Cys  
465 470 475 480

Leu Gln Leu Ala Met Gln Ala Asp Ala Arg Ala Phe Phe Ala Gln Asp  
485 490 495

Gly Val Gln Ser Leu Leu Thr Gln Lys Trp Trp Gly Asp Met Ala Ser  
500 505 510

Thr Thr Pro Ile Trp Ala Leu Val Leu Ala Phe Phe Cys Pro Pro Leu  
515 520 525

Ile Tyr Thr Arg Leu Ile Thr Phe Arg Lys Ser Glu Glu Glu Pro Thr  
530 535 540

Arg Glu Glu Leu Glu Phe Asp Met Asp Ser Val Ile Asn Gly Glu Gly  
545 550 555 560

Pro Val Gly Thr Ala Asp Pro Ala Glu Lys Thr Pro Leu Gly Val Pro  
565 570 575

Arg Gln Ser Gly Arg Pro Gly Cys Cys Gly Gly Arg Cys Gly Gly Arg  
580 585 590

Arg Cys Leu Arg Arg Trp Phe His Phe Trp Gly Ala Pro Val Thr Ile  
595 600 605

Phe Met Gly Asn Val Val Ser Tyr Leu Leu Phe Leu Leu Leu Phe Ser  
610 615 620

Arg Val Leu Leu Val Asp Phe Gln Pro Ala Pro Pro Gly Ser Leu Glu  
625 630 635 640

Leu Leu Leu Tyr Phe Trp Ala Phe Thr Leu Leu Cys Glu Glu Leu Arg  
645 650 655

Gln Gly Leu Ser Gly Gly Ser Leu Ala Ser Gly Gly Pro Gly  
660 665 670

Pro Gly His Ala Ser Leu Ser Gln Arg Leu Arg Leu Tyr Leu Ala Asp

675

680

685

Ser Trp Asn Gln Cys Asp Leu Val Ala Leu Thr Cys Phe Leu Leu Gly  
690 695 700

Val Gly Cys Arg Leu Thr Pro Gly Leu Tyr His Leu Gly Arg Thr Val  
705 710 715 720

Leu Cys Ile Asp Phe Met Val Phe Thr Val Arg Leu Leu His Ile Phe  
725 730 735

Thr Val Asn Lys Gln Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met  
740 745 750

Met Lys Asp Val Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val  
755 760 765

Ala Tyr Gly Val Ala Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp  
770 775 780

Phe Pro Ser Ile Leu Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile  
785 790 795 800

Phe Gly Gln Ile Pro Gln Glu Asp Met Asp Val Ala Leu Met Glu His  
805 810 815

Ser Asn Cys Ser Ser Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala  
820 825 830

Gln Ala Gly Thr Cys Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu  
835 840 845

Leu Leu Val Ile Phe Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu  
850 855 860

Leu Ile Ala Met Phe Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser  
865 870 875 880

Asp Leu Tyr Trp Lys Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His  
885 890 895

Ser Arg Pro Ala Leu Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg  
900 905 910

Leu Leu Leu Arg Gln Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser  
915 920 925

Ser Pro Ala Leu Glu His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu  
930 935 940

Arg Lys Leu Leu Thr Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu  
945 950 955 960

Ala Arg Ala Arg Asp Lys Arg Glu Ser Asp Ser Glu Arg Leu Glu Arg  
965 970 975

Thr Ser Gln Lys Val Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg  
980 985 990

Glu Tyr Glu Gln Arg Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys  
995 1000 1005

Ser Arg Val Leu Gly Trp Val Thr  
1010 1015

<210> 107  
<211> 1378  
<212> DNA  
<213> human organism

<400> 107  
ggtagcagca tccaccgggc gggagggtcg aggcaagaa gccttaaagg ctactgagtg 60  
cgccggccgt tccgtgtcca gaacctcccc tactcctccg ctttctttc cttggccgcc 120  
cacccgccaag ttccgactcc ggttttcgccc tttgcaaagc ctaaggagga gtttaggaac 180  
agcccgccccc ccctccctgc ggccgccc ccctgcctct cggctctgct ccctgcccgc 240  
tgccgcctggg ccgtgcgcggc cggcaggcgc cagccatgtc gatgctgccc tcgtttggct 300  
ttacgcagga gcaagtggcg tgcgtgtcg aggttctgca gcaaggcgga aacctggagc 360  
gcctgggcag gttcctgtgg tcaactgcccc cctgcacca cctgcacaag aacgagagcg 420  
tactcaaggc caaggcggtg gtcgccttcc accgcggcaa cttccgtgag ctctacaaga 480  
tcctggagag ccaccagttc tcgcctcaca accacccaa actgcagcaa ctgtggctga 540  
aggcgcattt cgtggaggcc gagaagctgc gcggccgacc cctgggcgcc gtgggcaaat 600  
atcgggtgcg ccgaaaattt ccactgcccgc gcaccatctg ggacggcgag gagaccagct 660

actgcttcaa ggagaagtcg aggggtgtcc tgcgggagtg gtacgcgcac aatccctacc	720
catcgccgca tgagaagcgg gagctggccg aggccaccgg cctcaccacc acccaggta	780
gcaactggtt taagaaccgg aggcaaagag accggggccgc ggaggccaag gaaagggaga	840
acaccgaaaa caataactcc tcctccaaca agcagaacca actctctcct ctggaagggg	900
gcaagccgct catgtccagc tcagaagagg aattctcacc tccccaaagt ccagaccaga	960
actcggtcct tctgctgcag ggcaatatgg gccacgccag gagctcaaac tattctctcc	1020
cgggcttaac agcctcgca gcccagtcacg gcctgcagac ccaccagcat cagctccaag	1080
actctctgct cggcccccctc acctccagtc tgggtggactt ggggtcctaa gtggggaggg	1140
actggggcct cgaaggatt cctggagcag caaccactgc agcgactagg gacacttgta	1200
aatagaaaatc aggaacattt ttgcagctt tttctggagt ttttgcgca taaaggaatg	1260
gtggactttc acaaataatct tttaaaaat caaaaccaac agcgatctca agcttaatct	1320
cctcttctt ccaactttt ccacttttgc attttccttc ccaatgcaga gatcaggg	1378

<210> 108  
<211> 284  
<212> PRT  
<213> human organism

<400> 108

Met	Ser	Met	Leu	Pro	Ser	Phe	Gly	Phe	Thr	Gln	Glu	Gln	Val	Ala	Cys
1					5	.				10					15

Val Cys Glu Val Leu Gln Gln Gly Gly Asn Leu Glu Arg Leu Gly Arg  
20 25 30

Phe Leu Trp Ser Leu Pro Ala Cys Asp His Leu His Lys Asn Glu Ser  
35 40 45

Val Leu Lys Ala Lys Ala Val Val Ala Phe His Arg Gly Asn Phe Arg  
50 55 60

Glu Leu Tyr Lys Ile Leu Glu Ser His Gln Phe Ser Pro His Asn His  
 65              70              75              80

Pro Lys Leu Gln Gln Leu Trp Leu Lys Ala His Tyr Val Glu Ala Glu  
85 90 95

Lys Leu Arg Gly Arg Pro Leu Gly Ala Val Gly Lys Tyr Arg Val Arg  
100 105 110

Arg Lys Phe Pro Leu Pro Arg Thr Ile Trp Asp Gly Glu Glu Thr Ser  
115 120 125

Tyr Cys Phe Lys Glu Lys Ser Arg Gly Val Leu Arg Glu Trp Tyr Ala  
130 135 140

His Asn Pro Tyr Pro Ser Pro Arg Glu Lys Arg Glu Leu Ala Glu Ala  
145 150 155 160

Thr Gly Leu Thr Thr Gln Val Ser Asn Trp Phe Lys Asn Arg Arg  
165 170 175

Gln Arg Asp Arg Ala Ala Glu Ala Lys Glu Arg Glu Asn Thr Glu Asn  
180 185 190

Asn Asn Ser Ser Ser Asn Lys Gln Asn Gln Leu Ser Pro Leu Glu Gly  
195 200 205

Gly Lys Pro Leu Met Ser Ser Ser Glu Glu Glu Phe Ser Pro Pro Gln  
210 215 220

Ser Pro Asp Gln Asn Ser Val Leu Leu Gln Gly Asn Met Gly His  
225 230 235 240

Ala Arg Ser Ser Asn Tyr Ser Leu Pro Gly Leu Thr Ala Ser Gln Pro  
245 250 255

Ser His Gly Leu Gln Thr His Gln His Gln Leu Gln Asp Ser Leu Leu  
260 265 270

Gly Pro Leu Thr Ser Ser Leu Val Asp Leu Gly Ser  
275 280

<210> 109  
<211> 3885  
<212> DNA  
<213> human organism

<400> 109  
ggggctccgc gggcctggag cacggccggg tctaatatgc ccggagccga ggcgcgatga 60  
aggagaagtc caagaatgct gcacaagacca ggagggagaa ggaaaatggc gagtttacg 120

agttgccaa gctgctcccg ctgccgtcg ccatacttc gcagctggac aaagcgtcca 180  
tcatccgcct caccacgagc tacctgaaga tgcgcgcccgt cttccccgaa ggtttaggag 240  
acgcgtgggg acagccgagc cgccgcgggc ccctggacgg cgtcgccaag gagctggat 300  
cgcaacttgct gcagactttg gatggatttg tttttgttgt agcatctgat ggcaaaatca 360  
tgtatatatc cgagaccgct tctgtccatt taggcttatac ccaggtggag ctcacggca 420  
acagtattta tgaatacatc catccttctg accacgatga gatgaccgct gtcctcacgg 480  
cccaccagcc gctgcaccac cacctgctcc aagagtatga gatagagagg tcgttcttc 540  
ttcgaatgaa atgtgtcttg gcaaagggaa acgcgggcct gacctgcagc ggataacaagg 600  
tcatccactg cagtggtctac ttgaagatca ggcagtatatac gctggacatg tccctgtacg 660  
actcctgcta ccagatgtg gggctgggtgg ccgtgggcca gtcgctgcca cccagtgcca 720  
tcaccgagat caagctgtac agtaacatgt tcatgttcag ggccagcctt gacctgaagc 780  
tgatattcct ggattccagg gtgaccgagg tgacgggtta cgagccgcag gacctgatcg 840  
agaagaccct ataccatcac gtgcacggct gcgacgtgtt ccaccccgac tacgcacacc 900  
acccctgtt ggtgaaggc caggtcacca ccaagatac ccggctgctg tccaagcggg 960  
gcggctgggt gtgggtgcag agctacgcca ccgtgggtca caacagccgc tcgtccggc 1020  
cccactgcat cgtgagtgta aattatgtac tcacggagat tgaatacaag gaacctcagc 1080  
tgtccctgga gcaggtgtcc actgccaagt cccaggactc ctggaggacc gccttgc 1140  
cctcacaaga aactaggaaa ttagtgaaac ccaaaaatac caagatgaag acaaagctga 1200  
gaacaaaccc ttaccccca cagcaataca gtcgttcca aatggacaaa ctggaatgcg 1260  
gccagctcgaa aaactggaga gccagtcggcc ctgcaagcgc tgctgctcct ccagaactgc 1320  
agccccactc agaaagcagt gacccctgt acacccatc ctacagcctg cccttctcct 1380  
accattacgg acacttcct ctggactctc acgtttcag cagaaaaag ccaatgtgc 1440  
cgcccaagtt cgggcagccc caaggatccc cttgtgaggt ggcacgctt ttccctgagca 1500  
cactgccagc cagcggtgaa tgccagtggc attatgccaa cccctagtg cctagcagct 1560  
cgtctccagc taaaaatcct ccagagccac cggcgaacac tgctaggcac agcctggc 1620  
caagctacga agcgcccgcc gccgcccgtgc gcaggttcgg cgaggacacc ggcggccg 1680  
gctccccgag ctgcggccac taccgcgagg agcccgct gggcccgcc aaagccgccc 1740  
gccaggccgc ccgggacggg ggcggcgtgg cgctggcccg cgccgcaccc gagtgctgcg 1800

cgcccccggac ccccgaggcc cggggcgccg cggcgcagct gcccttcgtg ctgctcaact 1860  
accaccgcgt gctggccccg cgccggaccgc tggggggcgcc cgccacccgccc gcctccggcc 1920  
tggcctgcgc tcccgccggc cccgaggccg cgaccggcgcc gctgcggctc cggcacccga 1980  
gccccgcccgc cacctccccg cccggcgccgc ccctgcccga ctacctgggc gcctcggtca 2040  
tcatcaccaa cgggagggtga cccgctggcc gcccggccca ggagcctggaa cccggcctcc 2100  
cgccccgtcg gcgccaccga gcccggcaaa tgcgcacgac ctacattaat ttatgcagag 2160  
acagctgttt gaattggacc cccggccgaa cttgcggatt tccaccgcgg aggccccgcg 2220  
cgccggtgcc gagggcccgag gagcggccgg gtccggcag gtgaccgccc gcctctgtcc 2280  
tgcgagggcc ggtgcgaccc agttgctggg ggcttggtt cctcaccttg aaatcgggct 2340  
tcacgcgtct tgccttgcc ccaacgttcc acaacagtcc cgtggggga ttgaagcggt 2400  
ttcactccgc aaatatcctc cacttcagg agggaaaacc caccctacca cagtccgctc 2460  
ttccaagtgg acggcagacc tgggagggga cgcctgtgtc acgagccctt ttagatgctt 2520  
aggtgaaggc agaagtgtatg attgttaagtc ccatgaatac acaactccac tgtctttaaa 2580  
agtcattcaa gagtctcatt attttggtt ttatctaacc ctttcttcaa tacaaaaagc 2640  
caacaaacca agactaaggg ggtgaccatg caattccatt ttgtgtctgt gaacataggt 2700  
gtgcttccca aatacattaa caagctctta cttcccccta acccctatga actcttgata 2760  
acaccaagag tagcacccctc agaatatatt gaataggcat taaatgc当地 aatatatatg 2820  
tagccagaca gtttatgaga atgaccctgt caagcttcat tattacgtgg caaaatccct 2880  
ctggcccaca cagatctgtt attcaactagg ctcgtgtttt ctacaaatag tgctaataaa 2940  
gttaaattgc acgtgcaata cggAACACTG tcaatggact gcaccttgg aaggaaaaac 3000  
atgcttaagg ggggtgtatg aaaatgtatg agacattttt acacagcgag 3060  
aaaacttcgt aagaacatgt tacgtgtca acaggtaaac agaaatcctt tcataaagca 3120  
ccagcagtgt ttaaaaaatg agcttccatt aattttact ttttatgggt tttgcttaaa 3180  
gatctcaaca tggaaaaatc ctgtcatggc tctgaactgc acaatgcatt gaaccggcgt 3240  
ccttcaattt tcttcacact atcaacactg cagcattttt ctgctttatc aaaatggttt 3300  
attttaggaa acttttcca ctttctgaa tggaaagagg ttttcacaaa tgttttaaac 3360  
tcatcggtct aaaatcaagt gcacccacac caactgctct caaaatgtga actgacttt 3420  
ttttttttt ttttgccaaac cctgtgtcac ttagtgagga cctgacaccaa tccctacagg 3480  
gtgtctgtca gtggggcctca tggtaagagt cacaatttgc aaatttagga ccgtgggtca 3540



tgcagcgaag gggctggatg gtaggaaggg atgtccccgc ctctccacgc actcagctat 3600  
acccattca cagctccttg tgagtgtgtg cacaggaaat aagccgaggg tattatttt 3660  
ttatgttcat gagtcttgta attaaaccgt gattctgaa aggtgttaggt ttgattacta 3720  
ggagatacca ccgacattt tcaataaaagt actgcaaataat gctttgtgt ctaccttgtt 3780  
attaactttt ggggctgtat ttagtaaaaaa taaatcaagg ctatcgagc agttcaataa 3840  
caaaggttac tggtagaaaaa aaagacccta tcatacattt acaag 3885

<210> 110  
<211> 667  
<212> PRT  
<213> human organism

<400> 110

Met Lys Glu Lys Ser Lys Asn Ala Ala Lys Thr Arg Arg Glu Lys Glu  
1 5 10 15

Asn Gly Glu Phe Tyr Glu Leu Ala Lys Leu Leu Pro Leu Pro Ser Ala  
20 25 30

Ile Thr Ser Gln Leu Asp Lys Ala Ser Ile Ile Arg Leu Thr Thr Ser  
35 40 45

Tyr Leu Lys Met Arg Ala Val Phe Pro Glu Gly Leu Gly Asp Ala Trp  
50 55 60

Gly Gln Pro Ser Arg Ala Gly Pro Leu Asp Gly Val Ala Lys Glu Leu  
65 70 75 80

Gly Ser His Leu Leu Gln Thr Leu Asp Gly Phe Val Phe Val Val Ala  
85 90 95

Ser Asp Gly Lys Ile Met Tyr Ile Ser Glu Thr Ala Ser Val His Leu  
100 105 110

Gly Leu Ser Gln Val Glu Leu Thr Gly Asn Ser Ile Tyr Glu Tyr Ile  
115 120 125

His Pro Ser Asp His Asp Glu Met Thr Ala Val Leu Thr Ala His Gln  
130 135 140

Pro Leu His His His Leu Leu Gln Glu Tyr Glu Ile Glu Arg Ser Phe  
145 150 155 160

Phe Leu Arg Met Lys Cys Val Leu Ala Lys Arg Asn Ala Gly Leu Thr  
165 170 175

Cys Ser Gly Tyr Lys Val Ile His Cys Ser Gly Tyr Leu Lys Ile Arg  
180 185 190

Gln Tyr Met Leu Asp Met Ser Leu Tyr Asp Ser Cys Tyr Gln Ile Val  
195 200 205

Gly Leu Val Ala Val Gly Gln Ser Leu Pro Pro Ser Ala Ile Thr Glu  
210 215 220

Ile Lys Leu Tyr Ser Asn Met Phe Met Phe Arg Ala Ser Leu Asp Leu  
225 230 235 240

Lys Leu Ile Phe Leu Asp Ser Arg Val Thr Glu Val Thr Gly Tyr Glu  
245 250 255

Pro Gln Asp Leu Ile Glu Lys Thr Leu Tyr His His Val His Gly Cys  
260 265 270

Asp Val Phe His Leu Arg Tyr Ala His His Leu Leu Leu Val Lys Gly  
275 280 285

Gln Val Thr Thr Lys Tyr Tyr Arg Leu Leu Ser Lys Arg Gly Gly Trp  
290 295 300

Val Trp Val Gln Ser Tyr Ala Thr Val Val His Asn Ser Arg Ser Ser  
305 310 315 320

Arg Pro His Cys Ile Val Ser Val Asn Tyr Val Leu Thr Glu Ile Glu  
325 330 335

Tyr Lys Glu Leu Gln Leu Ser Leu Glu Gln Val Ser Thr Ala Lys Ser  
340 345 350

Gln Asp Ser Trp Arg Thr Ala Leu Ser Thr Ser Gln Glu Thr Arg Lys  
355 360 365

Leu Val Lys Pro Lys Asn Thr Lys Met Lys Thr Lys Leu Arg Thr Asn

	375		380
Pro Tyr Pro Pro Gln Gln Tyr Ser Ser Phe Gln Met Asp Lys Leu Glu			
385	390	395	400
Cys Gly Gln Leu Gly Asn Trp Arg Ala Ser Pro Pro Ala Ser Ala Ala			
	405	410	415
Ala Pro Pro Glu Leu Gln Pro His Ser Glu Ser Ser Asp Leu Leu Tyr			
	420	425	430
Thr Pro Ser Tyr Ser Leu Pro Phe Ser Tyr His Tyr Gly His Phe Pro			
	435	440	445
Leu Asp Ser His Val Phe Ser Ser Lys Lys Pro Met Leu Pro Ala Lys			
	450	455	460
Phe Gly Gln Pro Gln Gly Ser Pro Cys Glu Val Ala Arg Phe Phe Leu			
465	470	475	480
Ser Thr Leu Pro Ala Ser Gly Glu Cys Gln Trp His Tyr Ala Asn Pro			
	485	490	495
Leu Val Pro Ser Ser Ser Pro Ala Lys Asn Pro Pro Glu Pro Pro			
	500	505	510
Ala Asn Thr Ala Arg His Ser Leu Val Pro Ser Tyr Glu Ala Pro Ala			
	515	520	525
Ala Ala Val Arg Arg Phe Gly Glu Asp Thr Ala Pro Pro Ser Phe Pro			
	530	535	540
Ser Cys Gly His Tyr Arg Glu Glu Pro Ala Leu Gly Pro Ala Lys Ala			
545	550	555	560
Ala Arg Gln Ala Ala Arg Asp Gly Ala Arg Leu Ala Leu Ala Arg Ala			
	565	570	575
Ala Pro Glu Cys Cys Ala Pro Pro Thr Pro Glu Ala Pro Gly Ala Pro			
	580	585	590
Ala Gln Leu Pro Phe Val Leu Leu Asn Tyr His Arg Val Leu Ala Arg			
	595	600	605

Arg Gly Pro Leu Gly Gly Ala Ala Pro Ala Ala Ser Gly Leu Ala Cys  
610 615 620

Ala Pro Gly Gly Pro Glu Ala Ala Thr Gly Ala Leu Arg Leu Arg His  
625 630 635 640

Pro Ser Pro Ala Ala Thr Ser Pro Pro Gly Ala Pro Leu Pro His Tyr  
645 650 655

Leu Gly Ala Ser Val Ile Ile Thr Asn Gly Arg  
660 665

<210> 111  
<211> 1804  
<212> DNA  
<213> human organism

<400> 111  
atgaacggac gctgcacatcg cccgtccctg ccctactcac ccgtcagctc cccgcagtcc 60  
tcgcctcgcc tgccccggcg gccgacagtg gagtctcacc acgtctccat cacgggtatg 120  
caggactgtg tgcagctgaa tcagtataacc ctgaaggatg aaattggaaa gggctcctat 180  
ggtgtcgtca agttggccta caatgaaaat gacaataacct actatgcaat gaaggtgctg 240  
tccaaaaaga agctgatccg gcaggccggc tttccacgtc gccctccacc ccgaggcacc 300  
cggccagctc ctggaggctg catccagccc agggggccca ttgagcagggt gtaccaggaa 360  
attgccatcc tcaagaagct ggaccacccc aatgtggtga agctggtgaa ggtcctggat 420  
gaccccaatg aggaccatct gtacatggtg ttcgaactgg tcaaccaagg gcccgtgatg 480  
gaagtggcca ccctcaaacc actctctgaa gaccaggccc gtttctactt ccaggatctg 540  
atcaaaggca tcgagttactt acactaccag aagatcatcc accgtgacat caaaccttcc 600  
aacctcctgg tcggagaaga tgggcacatc aagatcgctg actttggtgt gagcaatgaa 660  
ttcaaggcca gtgacgcgct cctctccaaac accgtggca cgccccgcctt catggcaccc 720  
gagtcgctct ctgagaccccg caagatcttc tctggaaagg cttggatgt ttggccatg 780  
ggtgtgacac tatactgctt tgtctttggc cagtccccat tcatggacga gcggatcatg 840  
tgtttacaca gtaagatcaa gagtcaggcc ctggaaatttc cagaccagcc cgacatagct 900  
gaggacttga aggacctgat caccgtatg ctggacaaga accccgagtc gaggatcg 960  
gtgccggaaa tcaagctgca cccctgggtc acgaggcatg gggcggagcc gttgccgtcg 1020

gaggatgaga	actgcacgct	ggtcgaagtg	actgaagagg	aggtcgagaa	ctcagtcaaa	1080
cacattccca	gcttggcaac	cgtgatcctg	gtgaagacca	tgatacgtaa	acgctcctt	1140
gggaacctcat	tcgagggcag	ccggcgggag	gaacgctcac	tgtcagcgcc	tggaaacttg	1200
ctcaccaaaa	aaccaaccag	ggaatgtgag	tccctgtctg	agctcaagac	ctagaaaata	1260
agtccccttc	ctgcctgttg	caaagtaacg	taagagttcc	ctcacccgag	tggatgcaga	1320
cgttcttgct	gtcagccacc	ttccttcata	cacatagcca	gcccagggtg	accagaacgt	1380
cccaggacag	atgaggctt	gtgtccttat	gagagtggga	gaacctggtg	ggcacccctg	1440
gtgcaggtgc	tgtggtggtt	ggggacccca	ctgccttcc	cactgagcac	atcatggcta	1500
cctgacttgg	tgggagttcc	attcagtcac	ttctgtttct	taaacatagc	tttactgagg	1560
tacaattcac	ataccatgta	attcacccac	gggaagtgta	tgattcagtg	gtttctaata	1620
cacacttctg	cagccattac	caccgtcaac	tttacgacat	tttcatcagc	ccaagaagac	1680
accctacact	ccttagctgt	ccccatccaa	ctccccacc	ccagtaacca	ctcagaatag	1740
gtatggattt	gcctattctg	gacgtttcgt	ataaatggcg	tcatacacta	aaaaaaaaaa	1800
aaaaa						1804

<210> 112  
 <211> 417  
 <212> PRT  
 <213> human organism

<400> 112

Met	Asn	Gly	Arg	Cys	Ile	Cys	Pro	Ser	Leu	Pro	Tyr	Ser	Pro	Val	Ser
1									10						15

Ser	Pro	Gln	Ser	Ser	Pro	Arg	Leu	Pro	Arg	Arg	Pro	Thr	Val	Glu	Ser
20								25						30	

His	His	Val	Ser	Ile	Thr	Gly	Met	Gln	Asp	Cys	Val	Gln	Leu	Asn	Gln
35								40				45			

Tyr	Thr	Leu	Lys	Asp	Glu	Ile	Gly	Lys	Gly	Ser	Tyr	Gly	Val	Val	Lys
50						55					60				

Leu	Ala	Tyr	Asn	Glu	Asn	Asp	Asn	Thr	Tyr	Tyr	Ala	Met	Lys	Val	Leu
65									70			75		80	

Ser Lys Lys Lys Leu Ile Arg Gln Ala Gly Phe Pro Arg Arg Pro Pro  
85 90 95

Pro Arg Gly Thr Arg Pro Ala Pro Gly Gly Cys Ile Gln Pro Arg Gly  
100 105 110

Pro Ile Glu Gln Val Tyr Gln Glu Ile Ala Ile Leu Lys Lys Leu Asp  
115 120 125

His Pro Asn Val Val Lys Leu Val Glu Val Leu Asp Asp Pro Asn Glu  
130 135 140

Asp His Leu Tyr Met Val Phe Glu Leu Val Asn Gln Gly Pro Val Met  
145 150 155 160

Glu Val Pro Thr Leu Lys Pro Leu Ser Glu Asp Gln Ala Arg Phe Tyr  
165 170 175

Phe Gln Asp Leu Ile Lys Gly Ile Glu Tyr Leu His Tyr Gln Lys Ile  
180 185 190

Ile His Arg Asp Ile Lys Pro Ser Asn Leu Leu Val Gly Glu Asp Gly  
195 200 205

His Ile Lys Ile Ala Asp Phe Gly Val Ser Asn Glu Phe Lys Gly Ser  
210 215 220

Asp Ala Leu Leu Ser Asn Thr Val Gly Thr Pro Ala Phe Met Ala Pro  
225 230 235 240

Glu Ser Leu Ser Glu Thr Arg Lys Ile Phe Ser Gly Lys Ala Leu Asp  
245 250 255

Val Trp Ala Met Gly Val Thr Leu Tyr Cys Phe Val Phe Gly Gln Cys  
260 265 270

Pro Phe Met Asp Glu Arg Ile Met Cys Leu His Ser Lys Ile Lys Ser  
275 280 285

Gln Ala Leu Glu Phe Pro Asp Gln Pro Asp Ile Ala Glu Asp Leu Lys  
290 295 300

Asp Leu Ile Thr Arg Met Leu Asp Lys Asn Pro Glu Ser Arg Ile Val

305	310	315	320
Val Pro Glu Ile Lys Leu His Pro Trp Val Thr Arg His Gly Ala Glu			
325	330	335	
Pro Leu Pro Ser Glu Asp Glu Asn Cys Thr Leu Val Glu Val Thr Glu			
340	345	350	
Glu Glu Val Glu Asn Ser Val Lys His Ile Pro Ser Leu Ala Thr Val			
355	360	365	
Ile Leu Val Lys Thr Met Ile Arg Lys Arg Ser Phe Gly Asn Pro Phe			
370	375	380	
Glu Gly Ser Arg Arg Glu Glu Arg Ser Leu Ser Ala Pro Gly Asn Leu			
385	390	395	400
Leu Thr Lys Lys Pro Thr Arg Glu Cys Glu Ser Leu Ser Glu Leu Lys			
405	410	415	

Thr

<210> 113			
<211> 429			
<212> DNA			
<213> human organism			
<400> 113			
atgaaacctc tgatatggac atggtcagat gttgaaggcc agaggccggc tctgctcatc	60		
tgcacagctg cagcaggacc cacgcaggga gttaagggtt atggcaagcc ctttgagcca	120		
agaagtgtga aaaacataca ctctactcct gcttacccag atgccacaat gcacagacaa	180		
ctcctggctc cggtggaagg aaggatggca gagacattga atcagaaaact ccatgttgcc	240		
aatgtgctgg aagatgaccc cggctaccta cctcacgtct acagcgagga aggggagtgt	300		
ggaggggccc catccctcag ctctctggcc agcttggAAC aggagttgca acctgatttG	360		
ctggactctt tgggttcaaa agcgactccg tttgagggAAA tatattcaga gtcaggtgtt	420		
ccttcctaa	429		
<210> 114			
<211> 142			
<212> PRT			

<213> human organism

<400> 114

Met Lys Pro Leu Ile Trp Thr Trp Ser Asp Val Glu Gly Gln Arg Pro  
1 5 10 15

Ala Leu Leu Ile Cys Thr Ala Ala Ala Gly Pro Thr Gln Gly Val Lys  
20 25 30

Gly Tyr Gly Lys Pro Phe Glu Pro Arg Ser Val Lys Asn Ile His Ser  
35 40 45

Thr Pro Ala Tyr Pro Asp Ala Thr Met His Arg Gln Leu Leu Ala Pro  
50 55 60

Val Glu Gly Arg Met Ala Glu Thr Leu Asn Gln Lys Leu His Val Ala  
65 70 75 80

Asn Val Leu Glu Asp Asp Pro Gly Tyr Leu Pro His Val Tyr Ser Glu  
85 90 95

Glu Gly Glu Cys Gly Gly Ala Pro Ser Leu Ser Ser Leu Ala Ser Leu  
100 105 110

Glu Gln Glu Leu Gln Pro Asp Leu Leu Asp Ser Leu Gly Ser Lys Ala  
115 120 125

Thr Pro Phe Glu Glu Ile Tyr Ser Glu Ser Gly Val Pro Ser  
130 135 140

<210> 115

<211> 1270

<212> DNA

<213> human organism

<400> 115

cgaatgcagg cgacttgcga gctgggagcg atttaaaacg ctttggattc ccccgccctg 60

ggtgtgggaga gcgagctggg tgccccctag attccccgcc cccgcaccc atgagccgac 120

cctcggctcc atggagcccg gcaattatgc cacctggat ggagccaagg atatcgaagg 180

cttgctggga gcgggagggg ggcggaatct ggtcgcccac tcccctctga ccagccaccc 240

agcggcgccct acgctgatgc ctgctgtcaa ctatgcccc ttggatctgc caggctcgcc 300

ggagccgcca aagcaatgcc acccatgccc tggggtgccc cagggacgt cccagctcc 360

cgtgccttat	ggttactttg	gaggcgggta	ctactcctgc	cgagtgtccc	ggagctcgct	420
gaaaccctgt	gcccaggcag	ccaccctggc	cgcgtacccc	gcggagactc	ccacggccgg	480
ggaagagtagc	cccagtcgcc	ccactgagtt	tgccttctat	ccggatatac	cggaaaccta	540
ccacgctatg	gccagttacc	tggacgtgtc	tgtggtgca	actctgggtg	ctcctggaga	600
accgcgacat	gactccctgt	tgcctgtgga	cagttaccag	tcttgggctc	tcgctgggtgg	660
ctggaacagc	cagatgtgtt	gccagggaga	acagaaccca	ccaggtccct	tttggaaaggc	720
agcatttgca	gactccagcg	ggcagcaccc	tcctgacgcc	tgcgccttgc	gtcgccggccg	780
caagaaaacgc	attccgtaca	gcaagggggca	gttgcgggag	ctggagcggg	agtatgcggc	840
taacaagttc	atcaccaagg	acaagaggcg	caagatctcg	gcagccacca	gcctctcgga	900
cgccccagatt	accatctggt	ttcagaaccg	ccgggtcaaa	gagaagaagg	ttctcgccaa	960
gggtgtcct	ggggagacca	gaaacctgcc	aagcccaggc	tggggccaag	gactctgctg	1020
agaggccccct	agagacaaca	cccttcccag	gccactggct	gctggactgt	tcctcaggag	1080
cggcctgggt	accaggatatg	tgcagggaga	cggAACCCCA	tgtgacaggc	ccactccacc	1140
agggttccca	aagaacctgg	cccagtcata	atcattcatc	ctcacagtgg	caataatcac	1200
gataaccagt						1260
						1270

<210> 116  
 <211> 284  
 <212> PRT  
 <213> human organism

<400> 116

Met	Glu	Pro	Gly	Asn	Tyr	Ala	Thr	Leu	Asp	Gly	Ala	Lys	Asp	Ile	Glu
1								5				10			15

Gly	Leu	Leu	Gly	Ala	Gly	Gly	Gly	Arg	Asn	Leu	Val	Ala	His	Ser	Pro
								20				25			30

Leu	Thr	Ser	His	Pro	Ala	Ala	Pro	Thr	Leu	Met	Pro	Ala	Val	Asn	Tyr
								35				40			45

Ala	Pro	Leu	Asp	Leu	Pro	Gly	Ser	Ala	Glu	Pro	Pro	Lys	Gln	Cys	His
								50				55			60

Pro Cys Pro Gly Val Pro Gln Gly Thr Ser Pro Ala Pro Val Pro Tyr  
65 70 75 80

Gly Tyr Phe Gly Gly Tyr Tyr Ser Cys Arg Val Ser Arg Ser Ser  
85 90 95

Leu Lys Pro Cys Ala Gln Ala Ala Thr Leu Ala Ala Tyr Pro Ala Glu  
100 105 110

Thr Pro Thr Ala Gly Glu Glu Tyr Pro Ser Arg Pro Thr Glu Phe Ala  
115 120 125

Phe Tyr Pro Gly Tyr Pro Gly Thr Tyr His Ala Met Ala Ser Tyr Leu  
130 135 140

Asp Val Ser Val Val Gln Thr Leu Gly Ala Pro Gly Glu Pro Arg His  
145 150 155 160

Asp Ser Leu Leu Pro Val Asp Ser Tyr Gln Ser Trp Ala Leu Ala Gly  
165 170 175

Gly Trp Asn Ser Gln Met Cys Cys Gln Gly Glu Gln Asn Pro Pro Gly  
180 185 190

Pro Phe Trp Lys Ala Ala Phe Ala Asp Ser Ser Gly Gln His Pro Pro  
195 200 205

Asp Ala Cys Ala Phe Arg Arg Gly Arg Lys Lys Arg Ile Pro Tyr Ser  
210 215 220

Lys Gly Gln Leu Arg Glu Leu Glu Arg Glu Tyr Ala Ala Asn Lys Phe  
225 230 235 240

Ile Thr Lys Asp Lys Arg Arg Lys Ile Ser Ala Ala Thr Ser Leu Ser  
245 250 255

Glu Arg Gln Ile Thr Ile Trp Phe Gln Asn Arg Arg Val Lys Glu Lys  
260 265 270

Lys Val Leu Ala Lys Val Lys Asn Ser Ala Thr Pro  
275 280

<211> 2856  
 <212> DNA  
 <213> human organism

<400> 117	
gtaaccgcta ctcccgaca ccagaccacc gccttccgta cacaggggcc cgcatcccac	60
cctcccgac ctaagagcct gggtcccctg tttccggagg tccgcttccc ggccccaga	120
ttctggcatc ccagccctca gtgtccaaga cccaggcagc cgggtcccc gcctcccgaa	180
tccaggcgtc cgggatctgc gccaccagaa cctagcctcc tgcatcaccc cggccatctgg	240
gggcactcaa cctcctggag ccaagggccc cacgtcccac ccagagaaac tctcgattc	300
ccagctccta gggccaagga acccgggcgc tccgaactcc cagcttcgg acatctggca	360
cacggggcag agcagagaag ctcagcgccc agcctggga atttaaacac tccagcttcc	420
aagagccaag gaacttcagt gctgtgaact cacaactcta aggagccctc caaagttcca	480
gtctccaggt gctgttactc aactcagtcc taggaacgtc gggccttggg aaggagccca	540
agcgctccca gccagcttcc aggcgctaag aaaccccggt gcttcccata atggtgccg	600
atcctcctcg agactccaag gggctcgtag cggcggagcc caccgccaac gggggcctgg	660
cgtggccctc catcgaggac caaggcgcgg cagcaggcgg ctactgcggg tcccggacc	720
aggtgcgcgg ctgccttcga gccaacctgc ttgtgctgct gacagtggtg gccgtggtag	780
ccggcgtggc gctggactg ggggtgtcgg gggccggggg tgcgctggcg ttggggccgg	840
agcgctttag ggccttcgtc ttccggggcg agctgctgct gcgctgctg cggatgatca	900
tcttgcgcgt ggtgggtgtc agcttgatcg gcccggccgc cagcctggac cccggcgcgc	960
tcggccgtct gggcgccctgg ggcgtgctct tttcctggg caccacgctg ctggcgtcgg	1020
cgctcggagt gggcttggcg ctggctctgc agccggccgc cgcctccgccc gccatcaacg	1080
cctccgtggg agccgcgggc agtgcggaaa atgccccag caaggaggtg ctgcatttgt	1140
tcctggatct tgcgagaaat atcttcctt ccaacctggt gtcagcagcc tttcgctcat	1200
actctaccac ctatgaagag aggaatatca ccggaaaccag ggtgaagggtg cccgtggggc	1260
aggaggtgga gggatgaac atcctgggct tggtagtgtt tgccatcgac tttgggtgtgg	1320
cgctcggaaa gctggggcct gaagggggagc tgcttatccg cttttcaac tccttcaatg	1380
aggccaccat ggttctggtc tcctggatca tgtggtacgc ccctgtgggc atcatgttcc	1440
tggtaggtgg caagatcgatc gagatggagg atgtgggttt actctttgcc cgccttggca	1500
agtacattct gtgcgtgcctg ctgggtcact ccatccatgg gtcctggta ctgcccctca	1560

tctacttcct	cttcacccgc	aaaaacccct	accgcttcct	gtggggcatc	gtgacgccgc	1620
tggccactgc	ctttgggacc	tcttccagtt	ccgccacgct	gccgctgatg	atgaagtgcg	1680
tggaggagaa	taatggcgtg	gccaaggcaca	tcagccgttt	catcctgccc	atcgccgcca	1740
ccgtcaacat	ggacggtgcc	gcgctttcc	agtgcgtggc	cgcagtgttc	attgcacagc	1800
tcagccagca	gtccttggac	ttcgtaaaga	tcatcaccat	cctggtcacg	gccacagcgt	1860
ccagcgtggg	ggcagcgggc	atccctgctg	gaggtgtcct	cactctggcc	atcatcctcg	1920
aagcagtcaa	cctccggc	gaccatatct	ccttgatcct	ggctgtggac	tggctagtcg	1980
accggtcctg	taccgtcctc	aatgtagaag	gtgacgctct	gggggcagga	ctcctccaaa	2040
attatgtgga	ccgtacggag	tcgagaagca	cagagcctga	gttgatacaa	gtgaagagtg	2100
agctgcccct	ggatccgctg	ccagtccccca	ctgaggaagg	aaacccccc	ctcaaacact	2160
atcgggggcc	cgcaggggat	gccacggtcg	cctctgagaa	ggaatcagtc	atgtaaaccc	2220
cgggagggac	cttccctgcc	ctgctggggg	tgctcttgg	acactggatt	atgaggaatg	2280
gataaatgga	tgagctaggg	ctctgggggt	ctgcctgcac	actctggga	gccaggggcc	2340
ccagcacccct	ccaggacagg	agatctggga	tgcctggctg	ctggagtaca	tgtgttcaca	2400
agggttactc	ctcaaaaaccc	ccagttctca	ctcatgtccc	caactcaagg	ctagaaaaca	2460
gcaagatgga	gaaataatgt	tctgctgcgt	ccccaccgtg	acctgcctgg	cctccctgt	2520
ctcagggagc	aggtcacagg	tcaccatggg	gaattctagc	ccccactggg	gggatgttac	2580
aacaccatgc	tggttatTTT	ggcggctgta	gttgtgggg	gatgtgtgtg	tgcacgtgtg	2640
tgtgtgtgt	tgtgtgtgt	tgtgtgtgt	ttctgtgacc	tcctgtcccc	atggtagtc	2700
ccaccctgtc	cccagatccc	ctattccctc	cacaataaca	gaaacactcc	cagggactct	2760
ggggagaggc	tgaggacaaa	tacctgctgt	cactccagag	gacatTTTT	ttagcaataa	2820
aattgagtgt	caactattta	aaaaaaaaaa	aaaaaaaaaa			2856

<210> 118  
 <211> 541  
 <212> PRT  
 <213> human organism

<400> 118

Met	Val	Ala	Asp	Pro	Pro	Arg	Asp	Ser	Lys	Gly	Leu	Ala	Ala	Glu
1														15

Pro Thr Ala Asn Gly Gly Leu Ala Leu Ala Ser Ile Glu Asp Gln Gly

20

25

30

Ala Ala Ala Gly Gly Tyr Cys Gly Ser Arg Asp Gln Val Arg Arg Cys  
35 40 45

Leu Arg Ala Asn Leu Leu Val Leu Leu Thr Val Val Ala Val Val Ala  
50 55 60

Gly Val Ala Leu Gly Leu Gly Val Ser Gly Ala Gly Gly Ala Leu Ala  
65 70 75 80

Leu Gly Pro Glu Arg Leu Ser Ala Phe Val Phe Pro Gly Glu Leu Leu  
85 90 95

Leu Arg Leu Leu Arg Met Ile Ile Leu Pro Leu Val Val Cys Ser Leu  
100 105 110

Ile Gly Gly Ala Ala Ser Leu Asp Pro Gly Ala Leu Gly Arg Leu Gly  
115 120 125

Ala Trp Ala Leu Leu Phe Phe Leu Val Thr Thr Leu Leu Ala Ser Ala  
130 135 140

Leu Gly Val Gly Leu Ala Leu Ala Leu Gln Pro Gly Ala Ala Ser Ala  
145 150 155 160

Ala Ile Asn Ala Ser Val Gly Ala Ala Gly Ser Ala Glu Asn Ala Pro  
165 170 175

Ser Lys Glu Val Leu Asp Ser Phe Leu Asp Leu Ala Arg Asn Ile Phe  
180 185 190

Pro Ser Asn Leu Val Ser Ala Ala Phe Arg Ser Tyr Ser Thr Thr Tyr  
195 200 205

Glu Glu Arg Asn Ile Thr Gly Thr Arg Val Lys Val Pro Val Gly Gln  
210 215 220

Glu Val Glu Gly Met Asn Ile Leu Gly Leu Val Val Phe Ala Ile Val  
225 230 235 240

Phe Gly Val Ala Leu Arg Lys Leu Gly Pro Glu Gly Glu Leu Leu Ile  
245 250 255

Arg Phe Phe Asn Ser Phe Asn Glu Ala Thr Met Val Leu Val Ser Trp  
260 265 270

Ile Met Trp Tyr Ala Pro Val Gly Ile Met Phe Leu Val Ala Gly Lys  
275 280 285

Ile Val Glu Met Glu Asp Val Gly Leu Leu Phe Ala Arg Leu Gly Lys  
290 295 300

Tyr Ile Leu Cys Cys Leu Leu Gly His Ala Ile His Gly Leu Leu Val  
305 310 315 320

Leu Pro Leu Ile Tyr Phe Leu Phe Thr Arg Lys Asn Pro Tyr Arg Phe  
325 330 335

Leu Trp Gly Ile Val Thr Pro Leu Ala Thr Ala Phe Gly Thr Ser Ser  
340 345 350

Ser Ser Ala Thr Leu Pro Leu Met Met Lys Cys Val Glu Glu Asn Asn  
355 360 365

Gly Val Ala Lys His Ile Ser Arg Phe Ile Leu Pro Ile Gly Ala Thr  
370 375 380

Val Asn Met Asp Gly Ala Ala Leu Phe Gln Cys Val Ala Ala Val Phe  
385 390 395 400

Ile Ala Gln Leu Ser Gln Gln Ser Leu Asp Phe Val Lys Ile Ile Thr  
405 410 415

Ile Leu Val Thr Ala Thr Ala Ser Ser Val Gly Ala Ala Gly Ile Pro  
420 425 430

Ala Gly Gly Val Leu Thr Leu Ala Ile Ile Leu Glu Ala Val Asn Leu  
435 440 445

Pro Val Asp His Ile Ser Leu Ile Leu Ala Val Asp Trp Leu Val Asp  
450 455 460

Arg Ser Cys Thr Val Leu Asn Val Glu Gly Asp Ala Leu Gly Ala Gly  
465 470 475 480

Leu Leu Gln Asn Tyr Val Asp Arg Thr Glu Ser Arg Ser Thr Glu Pro  
485 490 495

Glu Leu Ile Gln Val Lys Ser Glu Leu Pro Leu Asp Pro Leu Pro Val  
500 505 510

Pro Thr Glu Glu Gly Asn Pro Leu Leu Lys His Tyr Arg Gly Pro Ala  
515 520 525

Gly Asp Ala Thr Val Ala Ser Glu Lys Glu Ser Val Met  
530 535 540

<210> 119  
<211> 1993  
<212> DNA  
<213> human organism

<400> 119  
ctagttaagg cggcacaggg ccgaggcgta gtgtgggtga ctccctccgtt cttgggtcc 60  
cgtcgcttgt gatactgcag ttcaagccatg gcagaaccgc agcccccgtc cggcggcctc 120  
acggacgagg ccgcctcag ttgctgctcc gacgcggacc ccagtaccaa ggattttcta 180  
ttgcagcaga ccatgctacg agtgaaggat cctaagaagt cactggattt ttatactaga 240  
gttcttgaa tgacgcta at caaaaatgt gat tttccca ttatgaagtt ttcactctac 300  
ttcttgctt atgaggataa aaatgacatc cctaaagaaa aagatgaaaa aatagcctgg 360  
gctcgctcca gaaaagctac acttgagctg acacacaatt gggcactga agatgatgcg 420  
acccagagtt accacaatgg caattcagac cctcgaggat tcggtcata tggattgct 480  
gttcctgatg tatacagtgc ttgtaaaagg tttgaagaac tgggagtcaa atttgcgt 540  
aaacctgatg atggtaaat gaaaggcctg gcatttattc aagatcctga tggctactgg 600  
attgaaattt tgaatcctaa caaaatggca accttaatgt agtgcgtga gaattctcct 660  
ttgagatttc agaagaaagg aaacaatgtg attcaagata ttacatacc agaagcatct 720  
aggactgatg gatcaactgtc ccgattcaaa ttattctca gtccatttcc cttccatt 780  
tcagctgttc ctttcacct aactgttcag tcattctggt tttcaagcag tgcttatct 840  
catgtccttg aatatagttg tgtaacttta ttttttaggt aataattaga acagttccct 900  
tcagaggctg cattgcctt cttctgccac ctaaatatta cttcccttca aatctgcctt 960  
tgaatcatca tttttaaaaa aaaattaaca tgttttgtt gtagttatct tctgggttt 1020

caattcctca gaaacaactt ttttcacaac ggaaaggaaa gaacactagt gttctttcag	1080
taaagtacaa agtgttatt ttacaaaaga gtaggtactc ttgagagcaa ttcaaatcat	1140
gctgacaagg atactgatag aaaaagtat ttcttcttat tataaagtac atttaaagtt	1200
caaggactaa ctttatattt ttgggaaagg ggaggaggaa ggaaatgata tggtacccag	1260
acactggct aggctgcaac ttatctcat ttaatactcc cagctgtcat gtgagaaaga	1320
aagcaggcta ggcattgtgaa atcaatttca tggatttata atggattta gagggcatca	1380
atcagctcaa ctcaagattt cataatcatt ttagtattt agatttgcc tcaaagttgt	1440
agtacctcac aataccctcca ctggttcct gttgtaaaaa cttcagtga gtttgcatt	1500
tgtgcttttg gctcttggc tggagtaccg tggtagggaa gtaaacacta gaagtctta	1560
gtacaaaact gctctaggaa cacctggta tccctacaca agttagttt atatttctca	1620
taaagagtct tccctatccc aaggcttca tgatgccagt agccatatat gataaattat	1680
gttcagtgtat aacttagtta tcagaaatca gtcagtggt cttccccggcc atgattcaca	1740
ttttagttagt tttttttttt caaagtgtt tggaaaatct ctaatggctc agaaaataaa	1800
aacatccagt ttgtggatga ctatatttag atttctctag actcttagtgg aagacctttg	1860
gaaaggccat gccaaccgtg cttgtactgc tagaaggact ttatgtttcc tttttgggtg	1920
aatggattt atgtgagtgc tttaaacaat tagcaataact tatagactga aataaaatga	1980
aacttcaaat aag	1993

<210> 120  
<211> 184  
<212> PRT  
<213> human organism

<400> 120

```

Met Ala Glu Pro Gln Pro Pro Ser Gly Gly Leu Thr Asp Glu Ala Ala
1           5           10          15

```

Leu Ser Cys Cys Ser Asp Ala Asp Pro Ser Thr Lys Asp Phe Leu Leu  
                  20                 25                 30

Gln Gln Thr Met Leu Arg Val Lys Asp Pro Lys Lys Ser Leu Asp Phe  
                   35                   40                   45

Tyr Thr Arg Val Leu Gly Met Thr Leu Ile Gln Lys Cys Asp Phe Pro  
 50 55 60

Ile Met Lys Phe Ser Leu Tyr Phe Leu Ala Tyr Glu Asp Lys Asn Asp  
65                    70                    75                    80

Ile Pro Lys Glu Lys Asp Glu Lys Ile Ala Trp Ala Leu Ser Arg Lys  
85                    90                    95

Ala Thr Leu Glu Leu Thr His Asn Trp Gly Thr Glu Asp Asp Ala Thr  
100                    105                    110

Gln Ser Tyr His Asn Gly Asn Ser Asp Pro Arg Gly Phe Gly His Ile  
115                    120                    125

Gly Ile Ala Val Pro Asp Val Tyr Ser Ala Cys Lys Arg Phe Glu Glu  
130                    135                    140

Leu Gly Val Lys Phe Val Lys Lys Pro Asp Asp Gly Lys Met Lys Gly  
145                    150                    155                    160

Leu Ala Phe Ile Gln Asp Pro Asp Gly Tyr Trp Ile Glu Ile Leu Asn  
165                    170                    175

Pro Asn Lys Met Ala Thr Leu Met  
180

<210> 121  
<211> 808  
<212> DNA  
<213> human organism

<400> 121  
ccgacgccag gtcctgccgt cccgcccacc gtccgggagc gaaccgcgtcg tcccgcaactg        60  
gagtccgcga tggcttcagt gacagatggt aaacatggag tcaaagatgc ctctgaccag        120  
aattttgact acatgtttaa actgcttatac attggcaaca gcagtgttgg caagacctcc        180  
ttcctcttgc gctatgctga tgacacgttc accccagcct tcgtagcac cgtgggcac        240  
gacttcaagg tgaagacagt ctaccgtcac gagaagcggg tgaaactgca gatctggac        300  
acagctgggc aggagcggta cgggaccatc acaacagcct attaccgtgg ggccatgggc        360  
ttcattctga tgtatgacat caccaatgaa gagtccttca atgctgtcca agactggct        420  
actcagatca agacctactc ctgggacaat gcacaagtta ttctggtgg gaacaagtgt        480  
gacatggagg aagagagggt tgttcccact gagaagggcc agtccttgc agagcagct        540

gggtttgatt tctttgaagc cagtgcacaaag gagaacatca gtgttaaggca ggccttttag 600  
cgccctggtgg atgccatgg tgacaagatg tctgattcgc tggacacaga cccgtcgatg 660  
ctgggctcct ccaagaacac gcgtctctcg gacacccac cgctgctgca gcagaactgc 720  
tcatgcttagc aaggcccacc ttccctgacct cccctcattg tggccccaca cccaagtctg 780  
cttctccctg ttacacactg tccgctct 808

<210> 122  
<211> 219  
<212> PRT  
<213> human organism

<400> 122

Met Ala Ser Val Thr Asp Gly Lys His Gly Val Lys Asp Ala Ser Asp  
1 5 10 15

Gln Asn Phe Asp Tyr Met Phe Lys Leu Leu Ile Ile Gly Asn Ser Ser  
20 25 30

Val Gly Lys Thr Ser Phe Leu Leu Arg Tyr Ala Asp Asp Thr Phe Thr  
35 40 45

Pro Ala Phe Val Ser Thr Val Gly Ile Asp Phe Lys Val Lys Thr Val  
50 55 60

Tyr Arg His Glu Lys Arg Val Lys Leu Gln Ile Trp Asp Thr Ala Gly  
65 70 75 80

Gln Glu Arg Tyr Arg Thr Ile Thr Thr Ala Tyr Tyr Arg Gly Ala Met  
85 90 95

Gly Phe Ile Leu Met Tyr Asp Ile Thr Asn Glu Glu Ser Phe Asn Ala  
100 105 110

Val Gln Asp Trp Ala Thr Gln Ile Lys Thr Tyr Ser Trp Asp Asn Ala  
115 120 125

Gln Val Ile Leu Val Gly Asn Lys Cys Asp Met Glu Glu Glu Arg Val  
130 135 140

Val Pro Thr Glu Lys Gly Gln Leu Leu Ala Glu Gln Leu Gly Phe Asp  
145 150 155 160

Phe Phe Glu Ala Ser Ala Lys Glu Asn Ile Ser Val Arg Gln Ala Phe  
165 170 175

Glu Arg Leu Val Asp Ala Ile Cys Asp Lys Met Ser Asp Ser Leu Asp  
180 185 190

Thr Asp Pro Ser Met Leu Gly Ser Ser Lys Asn Thr Arg Leu Ser Asp  
195 200 205

Thr Pro Pro Leu Leu Gln Asn Cys Ser Cys  
210 215

<210> 123  
<211> 5060  
<212> DNA  
<213> human organism

<400> 123  
acgcagagcg ctgctggct gccgggtctc ccgcatttcctc ctcctgtctcc aaggggctcc 60  
tgcattgaggg cgcggttagag acccggaccc gcgcgcgtgct cctgcccgttt cgctgcgc 120  
cgccccggcc cggctcagcc aggccccgcg gtgagccatg attcgccctcg gggctcccc 180  
gtcgctggtg ctgctgacgc tgctcgctcg ccgtgtcctt cggtgtcagg gccaggatgt 240  
ccaggaggct ggcagctgtg tgcaaggatgg gcagaggtat aatgataagg atgtgtggaa 300  
gccggagccc tgccggatct gtgtctgtga cactggact gtcctctgcg acgacataat 360  
ctgtgaagac gtgaaagact gcctcagccc tgagatcccc ttcggagagt gctgccccat 420  
ctgccccact gacctcgcca ctgccagtgg gcaaccagga ccaaaggac agaaaggaga 480  
acctggagac atcaaggata ttgttaggacc caaaggaccc cctgggcctc agggacactgc 540  
aggggaacaa ggacccagag gggatcgtgg tgacaaaaggt gaaaaaggtg cccctggacc 600  
tcgtggcaga gatggagaac ctgggacccc tggaaatccc ggccccctg gtcctccgg 660  
ccccccctggc ttgggtggaaa ctttgctgcc cagatggctg gaggatttg 720  
tggaaaaggct ggtggcgccc agttggaggt aatgcaagga ccaatgggcc ccatgggacc 780  
tcgaggaccc ctggggccctg caggtgtctcc tgggcctcaa ggatttcaag gcaatcctgg 840  
tgaacctggc gaacctggc tgctctggcc catgggtccc cgtggtcctc ctgggtcccc 900  
tgaaaaagcc ggtgatgatg gtgaagctgg aaaacctgga aaagctggc aaagggggtcc 960  
gcctggtcct cagggtgctc gtggttccca aggaacccca ggccttcctg gtgtcaaagg 1020

tcacagaggt tatccaggcc tggacggtgc taagggagag gcgggtgctc ctggtgtgaa 1080  
gggtgagagt gttccccgg gtgagaacgg atctccggc ccaatggtc ctcgtggcct 1140  
gcctggtaa agaggacgga ctggccctgc tggcgctgag ggtgcccggag gcaacgatgg 1200  
tcagccaggc cccgcaggc tcctgggtcc tgtcggtcct gctggtggtc ctggcttccc 1260  
tggtgctcct ggagccaagg gtgaagccgg ccccactggt gcccgtggc ctgaagggtgc 1320  
tcaaggtcct cgccgtgaac ctggtactcc tgggtcccct gggcctgctg gtgcctccgg 1380  
taaccctgga acagatggaa ttccctggagc caaaggatct gctggtgctc ctggcattgc 1440  
tggtgctcct ggcttcctg gcccacgggg tcctcctggc cctcaagggtg caactggtcc 1500  
tctggggcccg aaaggtcaga cgggtgaacc tggtattgct ggctcaaag gtgaacaagg 1560  
ccccaaaggga gaacctggcc ctgctggccc ccagggagcc cctggaccccg ctggtgaaaga 1620  
aggcaagaga ggtgcccgtg gagagcctgg tggcggtggg cccatcggtc cccctggaga 1680  
aagaggtgct cccggaaacc gcggtttccc aggtcaagat ggtctggcag gtcccaagg 1740  
agccccctgga gagcgagggc ccagtggtct tgctggcccc aagggagcca acggtgaccc 1800  
tggccgtcct ggagaacctg gccttcctgg agccgggggt ctcactggcc gccctggta 1860  
tgctggtcct caaggcaaag ttggcccttc tggagccctt ggtgaagatg gtcgtcctgg 1920  
acctccaggt cctcaggggg ctctgtggca gcctgggtgc atgggtttcc ctggccccaa 1980  
aggtgccaac ggtgagcctg gcaaagctgg tgagaaggga ctgcctggtg ctccctggtct 2040  
gaggggtctt cctggcaaag atggtgagac aggtgctgca ggacccctg gccctgctgg 2100  
acctgctggt gaacgaggcg agcagggtgc tcctggcca tctgggttcc agggacttcc 2160  
tggccctcct ggtcccccaag gtgaagggtgg aaaaccaggt gaccagggtg ttcccggtga 2220  
agctggagcc cctggcctcg tgggtcccag ggtgaacgaa ggtttccag gtgaacgtgg 2280  
ctctcccggt gcccaggggcc tccagggtcc ccgtggcctc cccggcactc ctggcactga 2340  
tggtcccaaag ggtgcacatcg gcccagcagg ccccccctggc gcacaggggcc ctccaggtct 2400  
tcagggaatg cctggcgaga ggggagcagc tggtatcgct gggcccaaag ggcacagggg 2460  
tgacgttggt gagaaggcc ctgaggggagc ccctggaaag gatggtggtac gaggcctgac 2520  
aggtcccatt ggccccctg gcccagctgg tgctaacggc gagaaggggag aagttggacc 2580  
tcctggtcct gcaggaagtg ctggtgctcg tggcgctccg ggtgaacgtg gagagactgg 2640  
cccccccgga ccagcgggat ttgctgggcc tcctgggtct gatggccagc ctggggccaa 2700  
gggtgagcaa ggagaggccg gccagaaagg cgatgctggt gcccctggc ctcagggccc 2760

ctctggagca cctgggcctc aggtcctac tggagtgact ggtcctaaag gagcccagg 2820  
tgcccaaggc cccccgggag ccactggatt ccctggagct gctggcccg ttggaccccc 2880  
aggctccaat ggcaaccctg gacccctgg tccccctggt cttctggaa aagatggtcc 2940  
caaagggtgct cgaggagaca gcggccccc tggccgagct ggtgaacccg gcctccaagg 3000  
tcctgctgga cccccctggcg agaagggaga gcctggagat gacggtccct ctggtgccga 3060  
aggcacca ggtccccagg gtctggctgg tcagagaggc atcgtcggtc tgccctggca 3120  
acgtggtgag agaggattcc ctggcttgcc tggcccatcg ggtgagcccg gcaagcaggg 3180  
tgctcctgga gcatctggag acagagggtcc tcctggccccc gtgggtcctc ctggcctgac 3240  
gggtcctgca ggtgaacccg gacgagaggg aagccccgt gctgatggcc cccctggcag 3300  
agatggcgct gctggagtca agggtgatcg tggtgagact ggtgctgtgg gagctcctgg 3360  
agccctggg cccccctggct cccctggccc cgctggtcca actggcaagc aaggagacag 3420  
aggagaagct ggtgcacaag gccccatggg accctcagga ccagctggag cccggggaaat 3480  
ccagggtcct caaggccccca gaggtgacaa aggagaggct ggagagcctg gcgagagagg 3540  
cctgaaggga caccgtggct tcactggct gcagggtctg cccggccctc ctggccttc 3600  
tggagaccaa ggtgcttctg gtcctgctgg tccttctggc cctagaggtc tcctggccc 3660  
cgtcggtccc tctggcaaag atggtgctaa tggaatccct ggccccattg ggcctcctgg 3720  
tccccgtgga cgatcaggcg aaaccggtcc tgctggctt cctggaaatc ctggccccc 3780  
tggcctcca ggtccccctg gccctggcat cgacatgtcc gccttgctg gcttaggccc 3840  
gagagagaag ggccccgacc ccctgcagta catgcgggcc gaccaggcag ccggtgtggcct 3900  
gagacagcat gacgcccagg tggatgccac actcaagtcc ctcaacaacc agattgagag 3960  
catccgcagc cccgagggtct cccgcaagaa ccctgctcgc acctgcagag acctgaaact 4020  
ctgccacccct gagtggaaaga gtggagacta ctggattgac cccaaccaag gctgcacctt 4080  
ggacgcccattg aagggtttct gcaacatggg gactggcgag acttgcgtct accccaaatcc 4140  
agcaaacgtt cccaaagaaga actgggtggag cagcaagagc aaggagaaga aacacatctg 4200  
gtttggagaa accatcaatg gtggcttcca tttcagctat ggagatgaca atctggctcc 4260  
caacactgccc aacgtccaga tgaccttcct acgcctgctg tccacggaaag gctcccagaa 4320  
catcacctac cactgcaaga acagcattgc ctatctggac gaagcagctg gcaacctcaa 4380  
gaaggccctg ctcatccagg gctccaaatga cgtggagatc cgggcagagg gcaatagcag 4440

gttacgtac actgccctga	aggatggctg	cacgaaacat	accggtaagt	ggggcaagac	4500
tgttatcgag taccggtcac	agaagacctc	acgcctcccc	atcattgaca	ttgcacccat	4560
ggacatagga gggcccgagc	aggaattcgg	tgtggacata	gggcccgtct	gcttcttgta	4620
aaaacctgaa cccagaaaaca	acacaatccg	ttgcaaacc	aaaggaccca	agtactttcc	4680
aatctcagtc actctaggac	tctgcactga	atggctgacc	tgacctgatg	tccattcatc	4740
ccaccctctc acagttcgg	cttttctccc	ctctcttct	aagagacctg	aactggcag	4800
actgcaaaat aaaatctcg	ggttctat	tttattgtc	ttcctgttaag	accttcgggt	4860
caaggcagag gcaggaaact	aactggtgtg	agtcaaatgc	cccctgagtg	actgccccca	4920
gcccaggcca gaagacctcc	cttcaggtgc	cgggcgcagg	aactgtgtgt	gtcctacaca	4980
atggtgctat tctgtgtcaa	acacctctgt	atttttaaa	acatcaattt	atattaaaaa	5040
tgaaaagatt attggaaagt					5060

<210> 124

<211> 1487

<212> PRT

<213> human organism

<400> 124

Met Ile Arg Leu Gly Ala Pro Gln Ser Leu Val	Leu	Leu	Leu
1	5	10	15

Val Ala Ala Val Leu Arg Cys Gln Gly Gln Asp Val	Gln	Glu	Ala	Gly
20	25	30		

Ser Cys Val Gln Asp Gly Gln Arg Tyr Asn Asp Lys Asp Val Trp Lys				
35	40	45		

Pro Glu Pro Cys Arg Ile Cys Val Cys Asp Thr Gly Thr Val Leu Cys				
50	55	60		

Asp Asp Ile Ile Cys Glu Asp Val Lys Asp Cys Leu Ser Pro Glu Ile				
65	70	75	80	

Pro Phe Gly Glu Cys Cys Pro Ile Cys Pro Thr Asp Leu Ala Thr Ala				
85	90	95		

Ser Gly Gln Pro Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Asp Ile				
100	105	110		

Lys Asp Ile Val Gly Pro Lys Gly Pro Pro Gly Pro Gln Gly Pro Ala  
115 120 125

Gly Glu Gln Gly Pro Arg Gly Asp Arg Gly Asp Lys Gly Glu Lys Gly  
130 135 140

Ala Pro Gly Pro Arg Gly Arg Asp Gly Glu Pro Gly Thr Pro Gly Asn  
145 150 155 160

Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly  
165 170 175

Gly Asn Phe Ala Ala Gln Met Ala Gly Gly Phe Asp Glu Lys Ala Gly  
180 185 190

Gly Ala Gln Leu Gly Val Met Gln Gly Pro Met Gly Pro Met Gly Pro  
195 200 205

Arg Gly Pro Pro Gly Pro Ala Gly Ala Pro Gly Pro Gln Gly Phe Gln  
210 215 220

Gly Asn Pro Gly Glu Pro Gly Glu Pro Gly Val Ser Gly Pro Met Gly  
225 230 235 240

Pro Arg Gly Pro Pro Gly Pro Pro Gly Lys Pro Gly Asp Asp Gly Glu  
245 250 255

Ala Gly Lys Pro Gly Lys Ala Gly Glu Arg Gly Pro Pro Gly Pro Gln  
260 265 270

Gly Ala Arg Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly Val Lys Gly  
275 280 285

His Arg Gly Tyr Pro Gly Leu Asp Gly Ala Lys Gly Glu Ala Gly Ala  
290 295 300

Pro Gly Val Lys Gly Glu Ser Gly Ser Pro Gly Glu Asn Gly Ser Pro  
305 310 315 320

Gly Pro Met Gly Pro Arg Gly Leu Pro Gly Glu Arg Gly Arg Thr Gly  
325 330 335

Pro Ala Gly Ala Ala Gly Ala Arg Gly Asn Asp Gly Gln Pro Gly Pro  
340 345 350

Ala Gly Pro Pro Gly Pro Val Gly Pro Ala Gly Gly Pro Gly Phe Pro  
355 360 365

Gly Ala Pro Gly Ala Lys Gly Glu Ala Gly Pro Thr Gly Ala Arg Gly  
370 375 380

Pro Glu Gly Ala Gln Gly Pro Arg Gly Glu Pro Gly Thr Pro Gly Ser  
385 390 395 400

Pro Gly Pro Ala Gly Ala Ser Gly Asn Pro Gly Thr Asp Gly Ile Pro  
405 410 415

Gly Ala Lys Gly Ser Ala Gly Ala Pro Gly Ile Ala Gly Ala Pro Gly  
420 425 430

Phe Pro Gly Pro Arg Gly Pro Pro Gly Pro Gln Gly Ala Thr Gly Pro  
435 440 445

Leu Gly Pro Lys Gly Gln Thr Gly Glu Pro Gly Ile Ala Gly Phe Lys  
450 455 460

Gly Glu Gln Gly Pro Lys Gly Glu Pro Gly Pro Ala Gly Pro Gln Gly  
465 470 475 480

Ala Pro Gly Pro Ala Gly Glu Glu Gly Lys Arg Gly Ala Arg Gly Glu  
485 490 495

Pro Gly Gly Val Gly Pro Ile Gly Pro Pro Gly Glu Arg Gly Ala Pro  
500 505 510

Gly Asn Arg Gly Phe Pro Gly Gln Asp Gly Leu Ala Gly Pro Lys Gly  
515 520 525

Ala Pro Gly Glu Arg Gly Pro Ser Gly Leu Ala Gly Pro Lys Gly Ala  
530 535 540

Asn Gly Asp Pro Gly Arg Pro Gly Glu Pro Gly Leu Pro Gly Ala Arg  
545 550 555 560

Gly Leu Thr Gly Arg Pro Gly Asp Ala Gly Pro Gln Gly Lys Val Gly

565

570

575

Pro Ser Gly Ala Pro Gly Glu Asp Gly Arg Pro Gly Pro Pro Gly Pro  
580 585 590

Gln Gly Ala Arg Gly Gln Pro Gly Val Met Gly Phe Pro Gly Pro Lys  
595 600 605

Gly Ala Asn Gly Glu Pro Gly Lys Ala Gly Glu Lys Gly Leu Pro Gly  
610 615 620

Ala Pro Gly Leu Arg Gly Leu Pro Gly Lys Asp Gly Glu Thr Gly Ala  
625 630 635 640

Ala Gly Pro Pro Gly Pro Ala Gly Pro Ala Gly Glu Arg Gly Glu Gln  
645 650 655

Gly Ala Pro Gly Pro Ser Gly Phe Gln Gly Leu Pro Gly Pro Pro Gly  
660 665 670

Pro Pro Gly Glu Gly Gly Lys Pro Gly Asp Gln Gly Val Pro Gly Glu  
675 680 685

Ala Gly Ala Pro Gly Leu Val Gly Pro Arg Gly Glu Arg Gly Phe Pro  
690 695 700

Gly Glu Arg Gly Ser Pro Gly Ala Gln Gly Leu Gln Gly Pro Arg Gly  
705 710 715 720

Leu Pro Gly Thr Pro Gly Thr Asp Gly Pro Lys Gly Ala Ser Gly Pro  
725 730 735

Ala Gly Pro Pro Gly Ala Gln Gly Pro Pro Gly Leu Gln Gly Met Pro  
740 745 750

Gly Glu Arg Gly Ala Ala Gly Ile Ala Gly Pro Lys Gly Asp Arg Gly  
755 760 765

Asp Val Gly Glu Lys Gly Pro Glu Gly Ala Pro Gly Lys Asp Gly Gly  
770 775 780

Arg Gly Leu Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly Ala Asn  
785 790 795 800

Gly Glu Lys Gly Glu Val Gly Pro Pro Gly Pro Ala Gly Ser Ala Gly  
805 810 815

Ala Arg Gly Ala Pro Gly Glu Arg Gly Glu Thr Gly Pro Pro Gly Pro  
820 825 830

Ala Gly Phe Ala Gly Pro Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys  
835 840 845

Gly Glu Gln Gly Glu Ala Gly Gln Lys Gly Asp Ala Gly Ala Pro Gly  
850 855 860

Pro Gln Gly Pro Ser Gly Ala Pro Gly Pro Gln Gly Pro Thr Gly Val  
865 870 875 880

Thr Gly Pro Lys Gly Ala Arg Gly Ala Gln Gly Pro Pro Gly Ala Thr  
885 890 895

Gly Phe Pro Gly Ala Ala Gly Arg Val Gly Pro Pro Gly Ser Asn Gly  
900 905 910

Asn Pro Gly Pro Pro Gly Pro Pro Gly Pro Ser Gly Lys Asp Gly Pro  
915 920 925

Lys Gly Ala Arg Gly Asp Ser Gly Pro Pro Gly Arg Ala Gly Glu Pro  
930 935 940

Gly Leu Gln Gly Pro Ala Gly Pro Pro Gly Glu Lys Gly Glu Pro Gly  
945 950 955 960

Asp Asp Gly Pro Ser Gly Ala Glu Gly Pro Pro Gly Pro Gln Gly Leu  
965 970 975

Ala Gly Gln Arg Gly Ile Val Gly Leu Pro Gly Gln Arg Gly Glu Arg  
980 985 990

Gly Phe Pro Gly Leu Pro Gly Pro Ser Gly Glu Pro Gly Lys Gln Gly  
995 1000 1005

Ala Pro Gly Ala Ser Gly Asp Arg Gly Pro Pro Gly Pro Val Gly  
1010 1015 1020

Pro Pro Gly Leu Thr Gly Pro Ala Gly Glu Pro Gly Arg Glu Gly  
1025 1030 1035

Ser Pro Gly Ala Asp Gly Pro Pro Gly Arg Asp Gly Ala Ala Gly  
1040 1045 1050

Val Lys Gly Asp Arg Gly Glu Thr Gly Ala Val Gly Ala Pro Gly  
1055 1060 1065

Ala Pro Gly Pro Pro Gly Ser Pro Gly Pro Ala Gly Pro Thr Gly  
1070 1075 1080

Lys Gln Gly Asp Arg Gly Glu Ala Gly Ala Gln Gly Pro Met Gly  
1085 1090 1095

Pro Ser Gly Pro Ala Gly Ala Arg Gly Ile Gln Gly Pro Gln Gly  
1100 1105 1110

Pro Arg Gly Asp Lys Gly Glu Ala Gly Glu Pro Gly Glu Arg Gly  
1115 1120 1125

Leu Lys Gly His Arg Gly Phe Thr Gly Leu Gln Gly Leu Pro Gly  
1130 1135 1140

Pro Pro Gly Pro Ser Gly Asp Gln Gly Ala Ser Gly Pro Ala Gly  
1145 1150 1155

Pro Ser Gly Pro Arg Gly Pro Pro Gly Pro Val Gly Pro Ser Gly  
1160 1165 1170

Lys Asp Gly Ala Asn Gly Ile Pro Gly Pro Ile Gly Pro Pro Gly  
1175 1180 1185

Pro Arg Gly Arg Ser Gly Glu Thr Gly Pro Ala Gly Pro Pro Gly  
1190 1195 1200

Asn Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Gly Ile  
1205 1210 1215

Asp Met Ser Ala Phe Ala Gly Leu Gly Pro Arg Glu Lys Gly Pro  
1220 1225 1230

Asp Pro Leu Gln Tyr Met Arg Ala Asp Gln Ala Ala Gly Gly Leu  
1235 1240 1245

Arg Gln His Asp Ala Glu Val Asp Ala Thr Leu Lys Ser Leu Asn  
1250 1255 1260

Asn Gln Ile Glu Ser Ile Arg Ser Pro Glu Gly Ser Arg Lys Asn  
1265 1270 1275

Pro Ala Arg Thr Cys Arg Asp Leu Lys Leu Cys His Pro Glu Trp  
1280 1285 1290

Lys Ser Gly Asp Tyr Trp Ile Asp Pro Asn Gln Gly Cys Thr Leu  
1295 1300 1305

Asp Ala Met Lys Val Phe Cys Asn Met Glu Thr Gly Glu Thr Cys  
1310 1315 1320

Val Tyr Pro Asn Pro Ala Asn Val Pro Lys Lys Asn Trp Trp Ser  
1325 1330 1335

Ser Lys Ser Lys Glu Lys Lys His Ile Trp Phe Gly Glu Thr Ile  
1340 1345 1350

Asn Gly Gly Phe His Phe Ser Tyr Gly Asp Asp Asn Leu Ala Pro  
1355 1360 1365

Asn Thr Ala Asn Val Gln Met Thr Phe Leu Arg Leu Leu Ser Thr  
1370 1375 1380

Glu Gly Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Ile Ala  
1385 1390 1395

Tyr Leu Asp Glu Ala Ala Gly Asn Leu Lys Lys Ala Leu Leu Ile  
1400 1405 1410

Gln Gly Ser Asn Asp Val Glu Ile Arg Ala Glu Gly Asn Ser Arg  
1415 1420 1425

Phe Thr Tyr Thr Ala Leu Lys Asp Gly Cys Thr Lys His Thr Gly  
1430 1435 1440

Lys Trp Gly Lys Thr Val Ile Glu Tyr Arg Ser Gln Lys Thr Ser

1445

1450

1455

Arg Leu Pro Ile Ile Asp Ile Ala Pro Met Asp Ile Gly Gly Pro  
 1460 1465 1470

Glu Gln Glu Phe Gly Val Asp Ile Gly Pro Val Cys Phe Leu  
 1475 1480 1485

<210> 125  
 <211> 1505  
 <212> DNA  
 <213> human organism

<400> 125	
gctggtcgga ggctcgcagt gctgtcggcg agaagcagtc gggtttggag cgcttgggtc	60
gcgttggtgc gcgggtggAAC gcgcCcAGGG ACCCCAGTTC CCGCgAGCAG ctccgcGCCG	120
cgcctgagAG actaAGCTGA aactgCTGCT cAGCTCCAA gATGGTGCCA CCCAAATTGC	180
atgtGTTTT CTGCTCTGC ggCTGCCTGG CTGTGGTTA TCCTTTGAC tggcaataca	240
taaATCCTGT TGCCCATATG AAATCATCAG CATGGGTCAA CAAAATAACAA gtACTGATGG	300
ctgCTGCAAG CTTCGGCCAA ACTAAAATCC CCCGGGGAAA TGGGCCTTAT TCCGTTGGTT	360
gtacAGACTT AATGTTGAT CACACTAATA AGGGCACCTT CTGCGTTA TATTATCCAT	420
CCCAAGATAA TGATCGCCTT GACACCCTTT GGATCCAAA TAAAGAATAT TTTTGGGTc	480
ttAGCAAATT TCTTGGAAACA CACTGGCTTA TGGGCAACAT TTTGAGGTta CTCTTGGTT	540
caATGACAAC TCCtGCAAAC TGAATTCCC CTCTGAGGCC TGGTGAaaaaa TATCCACTTG	600
ttGTTTTTC TCATGGTCTT GGGGcATTCA GGACACTTTA TTCTGCTATT GGCATTGACC	660
tggcatCTCA TGGTTTATA GTGCTGCTG TAGAACACAG AGATAGATCT GCATCTGCAA	720
CTTACTATT CAAGGACCAA TCTGCTGCAG AAATAGGGGA CAAGTCTTGG CTCTACCTTA	780
GAACCCtGAA ACAAGAGGAG GAGACACATA TACGAAATGA GCAGGTACGG CAAAGAGCAA	840
AAGAATGTTc CCAAGCTCTC AGTCTGATTc TTGACATTGA TCATGGAAAG CCAGTGAAGA	900
ATGCATTAGA TTAAAGTTT GATATGGAAC AACTGAAGGA CTCTATTGAT AGGGAAAAAA	960
TAGCAGTAAT TGGACATTCT TTTGGTGGAG CAACCGTTAT TCAGACTCTT AGTGAAGATC	1020
AGAGATTCAg ATGTGGTATT GCCCTGGATG CATGGATGTT TCCACTGGGT GATGAAGTAT	1080
ATTCCAGAAAT TCCTCAGCCC CTCTTTTA TCAACTCTGA ATATTCcaa TATCCTGCTA	1140
ATATCATAAA AATGAAAAAA TGCTACTCAC CTGATAAAGA AAGAAAGATG ATTACAATCA	1200

ggggttcagt ccaccagaat tttgctgact tcactttgc aactggcaaa ataattggac 1260  
acatgctcaa attaaaggga gacatagatt caaatgtgc tattgatctt agcaacaag 1320  
cttcattagc attcttacaa aagcatttag gacttcataa agatttgat cagtggact 1380  
gcttgattga aggagatgtat gagaatctta ttccagggac caacattaac acaaccaatc 1440  
aacacatcat gttacagaac tcttcagggaa tagagaaata caattaggat taaaataggt 1500  
ttttt 1505

<210> 126  
<211> 441  
<212> PRT  
<213> human organism

<400> 126

Met Val Pro Pro Lys Leu His Val Leu Phe Cys Leu Cys Gly Cys Leu  
1 5 10 15

Ala Val Val Tyr Pro Phe Asp Trp Gln Tyr Ile Asn Pro Val Ala His  
20 25 30

Met Lys Ser Ser Ala Trp Val Asn Lys Ile Gln Val Leu Met Ala Ala  
35 40 45

Ala Ser Phe Gly Gln Thr Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser  
50 55 60

Val Gly Cys Thr Asp Leu Met Phe Asp His Thr Asn Lys Gly Thr Phe  
65 70 75 80

Leu Arg Leu Tyr Tyr Pro Ser Gln Asp Asn Asp Arg Leu Asp Thr Leu  
85 90 95

Trp Ile Pro Asn Lys Glu Tyr Phe Trp Gly Leu Ser Lys Phe Leu Gly  
100 105 110

Thr His Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met  
115 120 125

Thr Thr Pro Ala Asn Trp Asn Ser Pro Leu Arg Pro Gly Glu Lys Tyr  
130 135 140

Pro Leu Val Val Phe Ser His Gly Leu Gly Ala Phe Arg Thr Leu Tyr

145	150	155	160
Ser Ala Ile Gly Ile Asp Leu Ala Ser His Gly Phe Ile Val Ala Ala			
165	170		175
Val Glu His Arg Asp Arg Ser Ala Ser Ala Thr Tyr Tyr Phe Lys Asp			
180	185	190	
Gln Ser Ala Ala Glu Ile Gly Asp Lys Ser Trp Leu Tyr Leu Arg Thr			
195	200	205	
Leu Lys Gln Glu Glu Glu Thr His Ile Arg Asn Glu Gln Val Arg Gln			
210	215	220	
Arg Ala Lys Glu Cys Ser Gln Ala Leu Ser Leu Ile Leu Asp Ile Asp			
225	230	235	240
His Gly Lys Pro Val Lys Asn Ala Leu Asp Leu Lys Phe Asp Met Glu			
245	250		255
Gln Leu Lys Asp Ser Ile Asp Arg Glu Lys Ile Ala Val Ile Gly His			
260	265	270	
Ser Phe Gly Gly Ala Thr Val Ile Gln Thr Leu Ser Glu Asp Gln Arg			
275	280	285	
Phe Arg Cys Gly Ile Ala Leu Asp Ala Trp Met Phe Pro Leu Gly Asp			
290	295	300	
Glu Val Tyr Ser Arg Ile Pro Gln Pro Leu Phe Phe Ile Asn Ser Glu			
305	310	315	320
Tyr Phe Gln Tyr Pro Ala Asn Ile Ile Lys Met Lys Lys Cys Tyr Ser			
325	330	335	
Pro Asp Lys Glu Arg Lys Met Ile Thr Ile Arg Gly Ser Val His Gln			
340	345	350	
Asn Phe Ala Asp Phe Thr Phe Ala Thr Gly Lys Ile Ile Gly His Met			
355	360	365	
Leu Lys Leu Lys Gly Asp Ile Asp Ser Asn Val Ala Ile Asp Leu Ser			
370	375	380	

Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu His Lys  
385 390 395 400

Asp Phe Asp Gln Trp Asp Cys Leu Ile Glu Gly Asp Asp Glu Asn Leu  
405 410 415

Ile Pro Gly Thr Asn Ile Asn Thr Thr Asn Gln His Ile Met Leu Gln  
420 425 430

Asn Ser Ser Gly Ile Glu Lys Tyr Asn  
435 440

<210> 127  
<211> 1758  
<212> DNA  
<213> human organism

<400>	127	
cacgagccgc acgaggattt ccagctcagc gatgccccca ggtccctggg agagctgctt	60	
ctgggtgggg ggcctcattt tgtggctcag cgttggaaagt tcaggggatg cacctcctac	120	
cccacagcca aagtgcgctg acttccagag cgccaacctt tttgaaggca ccgatctcaa	180	
agtccagttt ctcctctttg tcccttcgaa tcctagctgt gggcagctag tagaaggaag	240	
cagtgacctc caaaactctg ggttcaatgc cactctggga accaaactaa ttatccatgg	300	
attcagggtt ttaggaacaa agccttcctg gattgacaca tttatttagaa cccttctgcq	360	
tgcaacgaat gctaattgtga ttgccgtgga ctggatttat gggtctacag gagtctactt	420	
ctcagctgtg aaaaatgtga ttaagttgag cctcgagatc tccctttcc tcaataaaact	480	
cctggtgctg ggtgtgtcgg aatcctcaat ccacatcatt ggtgttagcc tggggggccca	540	
cgttgggggc atgggtggac agctcttcgg aggccagctg ggacagatca caggcctgga	600	
ccccgctgga cctgagttaca ccagggccag tgtggaaagag cgcttggatg ctggagatgc	660	
cctcttcgtg gaagccatcc acacagacac cgacaatttgc ggtattcggta ttcccgttgg	720	
acatgtggac tacttcgtca acggaggcca agaccaacct ggctgccccca ctttctttta	780	
cgcaggttat agttatctga tctgtgtatca catgagggt gtgcacccct acatcagcgc	840	
cctggagaat tcctgtccac tgatggccctt tccctgtgcc agctacaagg ctttccttgc	900	
tggacgctgt ctggattgct ttaacccttt tctgcttcc tgcccaagga taggactgg	960	
ggaacaagggt ggtgtcaaga tagagccgct ccccaaggaa gtgaaagtct acctcctgac	1020	

tacttccagt gctccgtact	gcatgcata	cagcctcg	tgat	ttca	tgaaggaa	act	1080						
gagaaaacaag	gacaccaaca	tcgaggttac	cttccttagc	agtaacatca	cctcttc	atc	1140						
taagatcacc	atacctaagc	agcaacgcta	tggaaagga	atcatagccc	atgccacccc		1200						
acaatgccag	ataaaccaag	tgaaattcaa	gtttcagtct	tccaaccgag	tttggaaaaa		1260						
agaccggact	accattattg	ggaagttctg	ca	tgc	cc	tt	1320						
aaagatggtc	tgcttacctg	aaccagt	gaa	cttacaagca	agtgt	actg	tttcc	1380					
cctgaagata	gcctgtgtgt	agttt	aa	acct	ggcagg	aca	cat	ctcc	cattttttt	1440			
ttttttttt	gagagagagg	tgtgatgagg	gatgt	gtgt	tg	cag	ctt	at	tg	tagaccat	1500		
tactactaag	gagaaaagca	aagctttc	ttat	ttc	cct	cataatc	ac	tac	cctgg	gag	1560		
gggagggaga	actcat	ttta	caga	acttgg	ttt	c	tttgc	cgat	ctt	tat	gata	1620	
ttttagctt	cccatgcata	ctta	actg	ca	ctt	gtt	at	tc	c	ttggc	attcg	actt	1680
aggattcaat	agaaacatgt	acagg	gtaaa	caat	tttta	aaaataaa	ac	ttc	atgg	agt		1740	
aaaaaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	1758

<210> 128

<211> 456

<212> PRT

<213> human organism

<400> 128

Met	Pro	Pro	Gly	Pro	Trp	Glu	Ser	Cys	Phe	Trp	Val	Gly	Gly	Leu	Ile
1															
														10	15

Leu	Trp	Leu	Ser	Val	Gly	Ser	Ser	Gly	Asp	Ala	Pro	Pro	Thr	Pro	Gln	
														20	25	30

Pro	Lys	Cys	Ala	Asp	Phe	Gln	Ser	Ala	Asn	Leu	Phe	Glu	Gly	Thr	Asp	
														35	40	45

Leu	Lys	Val	Gln	Phe	Leu	Leu	Phe	Val	Pro	Ser	Asn	Pro	Ser	Cys	Gly	
														50	55	60

Gln	Leu	Val	Glu	Gly	Ser	Ser	Asp	Leu	Gln	Asn	Ser	Gly	Phe	Asn	Ala		
														65	70	75	80

Thr	Leu	Gly	Thr	Lys	Leu	Ile	Ile	His	Gly	Phe	Arg	Val	Leu	Gly	Thr	
														85	90	95

Lys Pro Ser Trp Ile Asp Thr Phe Ile Arg Thr Leu Leu Arg Ala Thr  
100 105 110

Asn Ala Asn Val Ile Ala Val Asp Trp Ile Tyr Gly Ser Thr Gly Val  
115 120 125

Tyr Phe Ser Ala Val Lys Asn Val Ile Lys Leu Ser Leu Glu Ile Ser  
130 135 140

Leu Phe Leu Asn Lys Leu Leu Val Leu Gly Val Ser Glu Ser Ser Ile  
145 150 155 160

His Ile Ile Gly Val Ser Leu Gly Ala His Val Gly Gly Met Val Gly  
165 170 175

Gln Leu Phe Gly Gly Gln Leu Gly Gln Ile Thr Gly Leu Asp Pro Ala  
180 185 190

Gly Pro Glu Tyr Thr Arg Ala Ser Val Glu Glu Arg Leu Asp Ala Gly  
195 200 205

Asp Ala Leu Phe Val Glu Ala Ile His Thr Asp Thr Asp Asn Leu Gly  
210 215 220

Ile Arg Ile Pro Val Gly His Val Asp Tyr Phe Val Asn Gly Gly Gln  
225 230 235 240

Asp Gln Pro Gly Cys Pro Thr Phe Phe Tyr Ala Gly Tyr Ser Tyr Leu  
245 250 255

Ile Cys Asp His Met Arg Ala Val His Leu Tyr Ile Ser Ala Leu Glu  
260 265 270

Asn Ser Cys Pro Leu Met Ala Phe Pro Cys Ala Ser Tyr Lys Ala Phe  
275 280 285

Leu Ala Gly Arg Cys Leu Asp Cys Phe Asn Pro Phe Leu Leu Ser Cys  
290 295 300

Pro Arg Ile Gly Leu Val Glu Gln Gly Gly Val Lys Ile Glu Pro Leu  
305 310 315 320

Pro Lys Glu Val Lys Val Tyr Leu Leu Thr Thr Ser Ser Ala Pro Tyr  
325 330 335

Cys Met His His Ser Leu Val Glu Phe His Leu Lys Glu Leu Arg Asn  
340 345 350

Lys Asp Thr Asn Ile Glu Val Thr Phe Leu Ser Ser Asn Ile Thr Ser  
355 360 365

Ser Ser Lys Ile Thr Ile Pro Lys Gln Gln Arg Tyr Gly Lys Gly Ile  
370 375 380

Ile Ala His Ala Thr Pro Gln Cys Gln Ile Asn Gln Val Lys Phe Lys  
385 390 395 400

Phe Gln Ser Ser Asn Arg Val Trp Lys Lys Asp Arg Thr Thr Ile Ile  
405 410 415

Gly Lys Phe Cys Thr Ala Leu Leu Pro Val Asn Asp Arg Glu Lys Met  
420 425 430

Val Cys Leu Pro Glu Pro Val Asn Leu Gln Ala Ser Val Thr Val Ser  
435 440 445

Cys Asp Leu Lys Ile Ala Cys Val  
450 455

<210> 129

<211> 2238

<212> DNA

<213> human organism

<400> 129  
cgttgccggg tcgcaggtcc cgccagtgcg agcgcaacgg aggtcgaagg cgttcagact 60  
cttagctgaa cgcggagctg cggcggtat gctgtggagc ggctgccggc gtttcggggc 120  
gcccctcggc tgcctgccc gcggtctccg ggtcctcgtc cagaccggcc accggagctt 180  
gacctcctgc atcgaccctt ccatgggact taatgaagag cagaaagaat ttcaaaaagt 240  
ggccttgac tttgctgccc gagagatggc tccaaatatg gcagagtggg accagaagga 300  
gctgttcca gtggatgtga tgccgaaggc agcccagcta ggcttcggag gggctcacat 360  
acaaacagat gtgggcgggt ctgggctgtc acgtcttgat acctctgtca ttttgaagc 420

cttggctaca ggctgcacca gcaccacagc ctatataagc atccacaaca tgtgtgcctg 480  
gatgattgat agcttcggaa atgaggaaca gaggcacaaa ttttgcac cgctctgtac 540  
catggagaag tttgcttcct actgcctcac tgaaccagga agtgggagtg atgctgcctc 600  
tcttcgtacc tccgctaaga aacagggaga tcattacatc ctcaatggct ccaaggcctt 660  
catcagtggt gctggtgagt cagacatcta tgtggtcatg tgccgaacag gaggaccagg 720  
ccccaaaggc atctcatgca tagttgtga gaaggggacc cctggcctca gctttggcaa 780  
gaaggagaaa aagggtgggt ggaactccca gccaacacga gctgtgatct tcgaagactg 840  
tgctgtccct gtggccaaca gaattggag cgaggggcag ggcttcctca ttgccgtgag 900  
aggactgaac ggagggagga tcaatattgc ttcctgctcc ctgggggctg cccacgcctc 960  
tgtcatcctc acccgagacc acctcaatgt ccggaagcag tttggagagc ctctggccag 1020  
taaccagtac ttgcaattca cactggctga tatggcaaca aggctggtgg ccgcgcggct 1080  
gatggtccgc aatgcagcag tggctctgca ggaggagagg aaggatgcag tggccttgc 1140  
ctccatggcc aagctcttg ctacagatga atgcttcgcc atctgcaacc aggccctgca 1200  
gatgcacggg ggctacggct acctgaagga ttacgctgtt cagcagtagc tgcgggactc 1260  
cagggtccac cagattctag aaggtgcaaa tgaagtgtatg aggatactga tctctagaag 1320  
cctgcttcag gagtagaacc cacacttgtt ctggcctgggt gttcagtgcg actgcagtca 1380  
gtgttgagtg gtgccatgtg ggccgctcta ttccaaagga atcatggatt agacccaagg 1440  
gctgagctcc tctaggccag gacctgcacc ctgtgtgttgc gcaccagcat cgggtcttgg 1500  
actggggcag aatccccagt ggaaccggaa gagctggact gatgagaaac atcagaagaa 1560  
cacatactac cttgtttcc taatgccaga agggtgacca gtgaagattc accgtcaaacc 1620  
catgaaagtc ctttcttggta tccactttat cttgatttagt ctgcattttta ctagttcact 1680  
ggatccctcc tctaggggcc tggggacttt cactgatgct cttcctgatt ctagagcaaa 1740  
ggtgtggaa gggaaatgg aggaatgccc tcctgtctgt gtcgttctct gtgccacagc 1800  
tacagatgca gaaggtttct ctggatagca cacctctgaa tgtaaatcat gataaaatgg 1860  
atatttggaa acttactcct aagctgtat gtagggtgta tttctacttc tggactgcct 1920  
caatatcaag ggctgagact tttgaatgtt gaatatttgt tgggtttcat gttaagacgc 1980  
ctgtggtcca ggagtgcata tcagtgtttc tgccctgtat aaacactttt aatattttt 2040  
tgtgtttttt tttccctttc tgaagctgtt ctcctttta aatattttta atcacattga 2100  
taaaaatctat cttcatcca cctctggttc tactatagtt gatTTTATT ttaaatgttt 2160

aattgtat~~t~~ gattaaacac ttaactggat tttggaataa taaaactctc gtccaa~~ttt~~g 2220  
gctttaaaaa aaaaaaaaaa 2238

<210> 130  
<211> 415  
<212> PRT  
<213> human organism

<400> 130

Met Leu Trp Ser Gly Cys Arg Arg Phe Gly Ala Arg Leu Gly Cys Leu  
1 5 10 15

Pro Gly Gly Leu Arg Val Leu Val Gln Thr Gly His Arg Ser Leu Thr  
20 25 30

Ser Cys Ile Asp Pro Ser Met Gly Leu Asn Glu Glu Gln Lys Glu Phe  
35 40 45

Gln Lys Val Ala Phe Asp Phe Ala Ala Arg Glu Met Ala Pro Asn Met  
50 55 60

Ala Glu Trp Asp Gln Lys Glu Leu Phe Pro Val Asp Val Met Arg Lys  
65 70 75 80

Ala Ala Gln Leu Gly Phe Gly Val Tyr Ile Gln Thr Asp Val Gly  
85 90 95

Gly Ser Gly Leu Ser Arg Leu Asp Thr Ser Val Ile Phe Glu Ala Leu  
100 105 110

Ala Thr Gly Cys Thr Ser Thr Ala Tyr Ile Ser Ile His Asn Met  
115 120 125

Cys Ala Trp Met Ile Asp Ser Phe Gly Asn Glu Glu Gln Arg His Lys  
130 135 140

Phe Cys Pro Pro Leu Cys Thr Met Glu Lys Phe Ala Ser Tyr Cys Leu  
145 150 155 160

Thr Glu Pro Gly Ser Gly Ser Asp Ala Ala Ser Leu Leu Thr Ser Ala  
165 170 175

Lys Lys Gln Gly Asp His Tyr Ile Leu Asn Gly Ser Lys Ala Phe Ile  
180 185 190

Ser Gly Ala Gly Glu Ser Asp Ile Tyr Val Val Met Cys Arg Thr Gly  
195 200 205

Gly Pro Gly Pro Lys Gly Ile Ser Cys Ile Val Val Glu Lys Gly Thr  
210 215 220

Pro Gly Leu Ser Phe Gly Lys Lys Glu Lys Lys Val Gly Trp Asn Ser  
225 230 235 240

Gln Pro Thr Arg Ala Val Ile Phe Glu Asp Cys Ala Val Pro Val Ala  
245 250 255

Asn Arg Ile Gly Ser Glu Gly Gln Gly Phe Leu Ile Ala Val Arg Gly  
260 265 270

Leu Asn Gly Gly Arg Ile Asn Ile Ala Ser Cys Ser Leu Gly Ala Ala  
275 280 285

His Ala Ser Val Ile Leu Thr Arg Asp His Leu Asn Val Arg Lys Gln  
290 295 300

Phe Gly Glu Pro Leu Ala Ser Asn Gln Tyr Leu Gln Phe Thr Leu Ala  
305 310 315 320

Asp Met Ala Thr Arg Leu Val Ala Ala Arg Leu Met Val Arg Asn Ala  
325 330 335

Ala Val Ala Leu Gln Glu Glu Arg Lys Asp Ala Val Ala Leu Cys Ser  
340 345 350

Met Ala Lys Leu Phe Ala Thr Asp Glu Cys Phe Ala Ile Cys Asn Gln  
355 360 365

Ala Leu Gln Met His Gly Gly Tyr Gly Tyr Leu Lys Asp Tyr Ala Val  
370 375 380

Gln Gln Tyr Val Arg Asp Ser Arg Val His Gln Ile Leu Glu Gly Ser  
385 390 395 400

Asn Glu Val Met Arg Ile Leu Ile Ser Arg Ser Leu Leu Gln Glu

405

410

415

<210> 131  
<211> 6735  
<212> DNA  
<213> human organism

<400> 131	
gcctgcagag agaggcactt tgcaccacag acagatagca agaagggaaa gacagagagt	60
gagaaaaaaag aggagtcagt cgctcctggg gaagggagag agtgagactg ggagaaaagag	120
aagcacagaa agtgtgtgta aaacggagta aagaaagaaaa aaaaaaaaaac tacccttaaa	180
gcacattaa aaaaaaaaaa ctctggcaat tcaagaaaaga aacaggctac gtttaaagag	240
catagagaca atgaaaggct aaagaaaatt ttaaaatctc tgccacagtc tcataagggtgc	300
ttggaaatga aagtagaaact gcctgtcttt aacggactct gacagaggta actggattag	360
ggacgagtac gccagctttt ttttttttt ttttttttt tttaacatct taaatcctga	420
aaaaaaaaaa aaaaaaaaaa aaaaggcagc agctccgaat tgaatgaatt gatggcaca	480
ctccaactgc tgggctggag agactggact tagtcttgcc atttctgctt cttgaaaga	540
ggagacaact tgggcttcct tttaatttag tttttttcc cttctcccc caaccccaa	600
cttccccct tacctcccccc accccctta tcaccacccc cttttaaat aagagggtga	660
aggggaacca gagcgcacaa gggactgac tcaggaggca gagaagatgg gcacccctcg	720
cgttagacttg ctgatcacac tgcaaattct gccagttttt ttctccaact gcctcttcct	780
ggctctctat gactcggtca ttctgctcaa gcacgtggtg ctgctgtga gcccgtccaa	840
gtccactcgc ggagagtggc ggcgcgtgct gacccagag ggactgcgct gcgtctggaa	900
gagcttcctc ctcgatgcct acaaacaggt gaaattgggt gaggatgccccc ccaattccag	960
tgtggtgcat gtctccagta cagaaggagg tgacaacagt ggcaatggta cccaggagaa	1020
gatactgag ggagccacat gccaccccttct tgactttgcc agccctgagc gcccactagt	1080
ggtaacttt ggctcagcca cttgaccccttcc tttcacgagc cagctgccag cttccgcaa	1140
actggtgaa gagttctcct cagtggctga cttccctgctg gtctacattt atgaggctca	1200
tccatcagat ggctgggcga taccggggga ctccttttgc tcttttgggg tgaagaagca	1260
ccagaaccag gaagatcgat gtgcagcagc ccagcagctt ctggagcgtt tctccttgcc	1320
gccccagtcg ctagttgtgg ctgaccgcattt ggacaataac gccaacatacg cttacgggg	1380
agcccttgaa cgtgtgtgca ttgtgcagag acagaaaatt gcttatctgg gagggaaaggg	1440

cccccttctcc tacaaccttc aagaagtccg gcattggctg gagaagaatt tcagcaagag 1500  
atgaaagaaa actagattag ctggtaaag gtatgattat aagagagctt attgtttaa 1560  
aaagttatat aaaggcaagg aaattaagaa ctgaatccat attcaacag agccctattg 1620  
gcttactgaa agacaggagt ttatctatcg gaagaacatg aatctctaac agctccatac 1680  
ttcttcact actcaaatgg cattgggctg agtaagtaac catatcacct ctcttcttag 1740  
taaaaagccc tatgtaaaaa gatccaaga tggagagaa gaaacgctaa ttcagcatgt 1800  
gttcattctg cattgagaag gaactgatac atctgatgca tgcttgaga ccagaagaaa 1860  
agacttacct gaataattac tacattaggg aagctactgt ctacgtaag ataaaggta 1920  
ttgccttggc tctatttggc atggatggag cccagttgga aaattcccaa atattacaac 1980  
aagtccctga acccaggcca tgtggtaga cgttggtagt aaggtagac cttatgttag 2040  
agtcatattct gatgttccag cttctagcca tgttagtgctc tcagtcttca tacccagaa 2100  
attattggta tattttaga taccgagaat gatcccttag tctgagaggt tagaatgatc 2160  
atctgtatac tgagggtaa tttctaggca ggtggagaga gtggtaaaaa agaaatgaaa 2220  
ttgacaagct aggaaagagg aggcagaaag atttggaaaa ttcacagagt ttcaccctta 2280  
agctgttagag agtgggtcac atttggtagc cacggaaaca tagaaacata cacaaggcca 2340  
gaaaaagaag aaggagctca actaaaagtg gcatagagaa tacacatata aaaacaatat 2400  
atttgcata tgctcctaga gaggagaaag gggtgattga aagaaaaaaaa aatacttaaa 2460  
tatttgtaat tgtgaggggt ttctttggaa aataattact tttgaaccat gtatgtggta 2520  
tgtatattt cagtgggtta attatacccc atgataccta ttaaaggaaa accagtgggt 2580  
ctggtggtgc tggcttttc ctccccattc ctacaatttc tatgtggccc aagtattcc 2640  
taatcttggc ctctatagca gtgttctctc tgaatgctga gctgaagaaa ttatacgtac 2700  
atacacacat acatacatac atacaaatat atgtatatac attctcagct gctgcgggag 2760  
gtaggtacca tggccattca gcacagcctt gatttcctcc caaagttagt gagctatagt 2820  
gaagaatagg tgcaaacaaa caagcttact tccattgcaa aatagaagaa gaggaagtt 2880  
gagataattc tgatcaatca ttttggaggc tttgttataa ggcaaccccc ggtatatcat 2940  
ggaatttcca ttgacatttgc aatttggact tggatcttcc cttggtccca ttagctgagg 3000  
tttagtaatc taaagtccct atagtatatg attataatgc tattttaaaa aatatatata 3060  
taaaatattt ttttctttt aaaatagaca ctatagttt acccataagt aatatttaaa 3120  
gattatagct cccaaaagaa tggaccaacc actttcgat cataattct ttttggtaaa 3180

tatgagacta ttatgaaatc atagtatatg attgtattta aaggtacaat caaaggatct 3240  
tttgtccatt ccattaataa ctgaataaaa aataaataaa atggatagaa aaaaactaaa 3300  
gttggaaaata cattcttaaa ctagttgtct gaaatgagaa aagagtgaga actaggtgtg 3360  
caagaaccaa acgtatttta ttttattttt taaatggag caacatatca gtcgtgtcac 3420  
cagctggtat attgtgtaaa tattaaagct ccattggac tgattttca tggcaacatc 3480  
agctttctaa tggcttaaat tctataaaaa ccacccacaa agaaacaaag caaatttcat 3540  
tatctaata gttgctggaa aatcatattg agaataatta tttcagattc ctcagttgtt 3600  
aacttctaca ttcaagggct tatctctgcc cccattgatt tttAACCTCA aaatggtg 3660  
agatttactg tggAACCTA aagcagtaaa ataaaaaacc tggtgcagc acattcacac 3720  
tgggttcctt aaaattcccc tttttctct atgtacgata aagtaacagt atgtacgata 3780  
agccgggtggg gggatgagat taggctgagg cagtcttagt caactggggg aaaaggatga 3840  
tggaaaaatc acccagttgt gctatattt taaagaagga ggTCGTTTGT gtgtgcagac 3900  
aattctccct gaggttagcc caatggagaa atgaagcaga ggaaggaaac atagaaagac 3960  
atgggctatc agggaggaag atgttcaata gaacatgcaa gaatttctgg aagaaaggct 4020  
gtggaaaggc caatggagaa aatgaatgga caaagctcag gaatccctac gctatgtaga 4080  
atgttcttgg tgTTATCAGG gTTAGCCCT gtaattatgt aacctattta tcgcaacatg 4140  
aattttatg atttcttgc atgtattctt ttatgaaatt aacaagaact cattattttg 4200  
aggtagagga aaatcaatgc ttatctgat atgctgagaa attattagat tgccaatact 4260  
catgtgcgtt tcatgtgttt tataagggtt gttccttga agaattgttag ttcttagtcc 4320  
cacagggaaa tgtgtatcta tttatataatc atagtataaa tctatgatat atttatata 4380  
tatataaaaag tctgagttct ctttcttagt ccctaatacat gtttctccca taggctgtgt 4440  
ttacatggag ctatcggtt agcctttaa gcttcattag cttgtctatt attgaaatag 4500  
tttccaagaa attttagata ttatcataac atctgggtct actcaaacac ttattgtttg 4560  
aaagacttat gtcttggacc tatcaaaaac tgactttatt tattgcttag tgaaaatact 4620  
agtggatca acaatgattt tcttgaatgg gcatgaatgg agatgccccgc acagtaatgt 4680  
agaaatgttt catacagcta taaaatgta actgacccctcc ttagaggcag attagtaact 4740  
gttcctactt tgtatacgta agtgacagtc acttaactta catgactttc tttttcaca 4800  
ttgggtctct ggtcctgtgt ctccacccatca tttatagcact gtccttga tttttggtag 4860

tatcaacttc ccagtatct gttcagttaa gttcttctcc cgtaaccag gaagtgccta 4920  
ttctctcatc acagtggaa gaatagccta ttgtcttca tttgcctga gtgtattta 4980  
ctatttggc tctgaaataa aaattatgaa atatggtag gtcacatgtt ggtgctgcct 5040  
tgctgcataa aattctagga gggcaggta ggagacagtt atgtatggcc tttcggaaa 5100  
attcaaaggg tgggattaca agggtgttcc tcaggcatgc ccctatggc cctatgtgga 5160  
agcaagaaga attgactgat ttacaggact tctcttatg tcaatcttaa gaggatggat 5220  
gaatctggac atttgttcca cccgacctct gactgatggt ttggaaaata actttaatta 5280  
ggatcatatg accattgaaa aaggaaaaat gtagactctg acttccgtcc cactgaagga 5340  
ttaatgaaaa cctttaactag catttagagc tttcagaac atccccactg tcatgtgtct 5400  
cagcagtgga gactgcaagt aaggcttta attttaggag gttttttttt tttttttttt 5460  
ttcccctaaa tggtatggcc aaaagtcaaa gttaaaatat atatagttttag attccaactt 5520  
cctccttcac tctaaaaata gaatccaaac ccactcttca tatatgcttc cagaatgggg 5580  
cttaagtacc aatctctgct ttgcaatggg cacaatcttgc gtcatgtcct gaggctct 5640  
aagaaaaagag aggatctagg atgggagagc tagaaagtttgc ctaactggga agaacaaggc 5700  
cctgaggggt tggtctacca atctgggaag atttggaaaac aaacttctcg caactgaagg 5760  
aaggctgaag gctgctgaa gtcattgagt gacttttagga tgagcaaaac attgggccac 5820  
ttcctaattgc cctatgtgttta tagtaccaga agcaaggcttgc cagacttaac agaccagct 5880  
ctgttccaaag gtgagtcgttgc accaatagaa agcaaaacatg tgcaaatatc caaacaagac 5940  
tgctcatgca agtcggggct ggctacccttgc cttaggcagc aacagcagag ctccagggag 6000  
cttattcaat atttactgag acttcgaaga cccagcagat gtttaatgaa gtcactattt 6060  
tggctcaaacc cctccacttc tccccctccc ctcaaaaagc caacaggtaa acacataaaat 6120  
gaaagaaaacc cacagaaggg gatgggaaat aaagaaaatt ctctcaagac ttctccaggc 6180  
ccatgtcact ggtcagcgttgc gtttttatgt gtattaggat tggggatgt gaagaaataa 6240  
gtatccagta ctttataacc aaagcaatta aatgatatttgc gggtagggaa tggtggccag 6300  
ttttgttttag ttttgccttc acattgtcact ccagacctca cctagccccca agtaatcggtt 6360  
cgcccccaag agggagacag agatgtgcca gagttgaccc agtgtgcggta tgataactac 6420  
tgacgaaaga gtcatcgacc tcaatgttgc gttggatgttgc ctcacattttttgccttc 6480  
cccatcttttgc tctccctggc aaggagaata tgcgggacat gatgctaaga gccctgggtt 6540  
aatgtggtga gaatgcacgc gtgcataatgc tacacatatg tgcttctcag ttgcagaaaa 6600

tgaactgctt tgggagatta tcagtagaaaa gagtgttatac atattggtgc tgagtgtat 6660  
gttgcttat acaatttggtt ctgttatttt aataaaacttt gaataaaaaga ataaaaaaaaa 6720  
aaaaaaaaaaa aaaaa 6735

<210> 132  
<211> 273  
<212> PRT  
<213> human organism

<220>  
<221> misc\_feature  
<222> (133)..(133)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> misc\_feature  
<222> (266)..(266)  
<223> Xaa can be any naturally occurring amino acid

<400> 132

Met Gly Ile Leu Ser Val Asp Leu Leu Ile Thr Leu Gln Ile Leu Pro  
1 5 10 15

Val Phe Phe Ser Asn Cys Leu Phe Leu Ala Leu Tyr Asp Ser Val Ile  
20 25 30

Leu Leu Lys His Val Val Leu Leu Ser Arg Ser Lys Ser Thr Arg  
35 40 45

Gly Glu Trp Arg Arg Met Leu Thr Ser Glu Gly Leu Arg Cys Val Trp  
50 55 60

Lys Ser Phe Leu Leu Asp Ala Tyr Lys Gln Val Lys Leu Gly Glu Asp  
65 70 75 80

Ala Pro Asn Ser Ser Val Val His Val Ser Ser Thr Glu Gly Gly Asp  
85 90 95

Asn Ser Gly Asn Gly Thr Gln Glu Lys Ile Ala Glu Gly Ala Thr Cys  
100 105 110

His Leu Leu Asp Phe Ala Ser Pro Glu Arg Pro Leu Val Val Asn Phe  
115 120 125

Gly Ser Ala Thr Xaa Pro Pro Phe Thr Ser Gln Leu Pro Ala Phe Arg  
130 135 140

Lys Leu Val Glu Glu Phe Ser Ser Val Ala Asp Phe Leu Leu Val Tyr  
145 150 155 160

Ile Asp Glu Ala His Pro Ser Asp Gly Trp Ala Ile Pro Gly Asp Ser  
165 170 175

Ser Leu Ser Phe Glu Val Lys Lys His Gln Asn Gln Glu Asp Arg Cys  
180 185 190

Ala Ala Ala Gln Gln Leu Leu Glu Arg Phe Ser Leu Pro Pro Gln Cys  
195 200 205

Arg Val Val Ala Asp Arg Met Asp Asn Asn Ala Asn Ile Ala Tyr Gly  
210 215 220

Val Ala Phe Glu Arg Val Cys Ile Val Gln Arg Gln Lys Ile Ala Tyr  
225 230 235 240

Leu Gly Gly Lys Gly Pro Phe Ser Tyr Asn Leu Gln Glu Val Arg His  
245 250 255

Trp Leu Glu Lys Asn Phe Ser Lys Arg Xaa Lys Lys Thr Arg Leu Ala  
260 265 270

Gly

<210> 133  
<211> 2685  
<212> DNA  
<213> human organism

<400> 133  
caggcgtgtc ccagggggag ccccgctctg cagccctgtg cgccgttagag agctggactt 60  
aggctggcag catggccgag ttcagggtca gggtgtccac cggagaagcc ttccgggctg 120  
gcacatggga caaatgtct gtcagcatcg tggggacccg gggagagagc cccccactgc 180  
ccctggacaa tctcgcaag gagttcaactg cgggcgtga ggaggacttc cagtgacgc 240  
tcccgagga cgtaggccga gtgctgctgc tgcgcgtgca caaggcgccc ccagtgctgc 300

ccctgctggg gcccctggcc ccggatgcct ggttctgccg ctgggtccag ctgacaccgc 360  
cgccccggcgg ccacccctc ttccccctgct accagtggct ggagggggcg gggaccctgg 420  
tgctgcagga gggtaacagcc aagggtgtcct gggcagacca ccaccctgtg ctccagcaac 480  
agcgccagga ggagcttcag gcccgccagg agatgtacca gtgaaaggct tacaacccag 540  
gttggcctca ctgcctggat gaaaagacag tggaagactt ggagctaat atcaaatact 600  
ccacagccaa gaatgccaac ttttatctac aagctggctc tgctttgca gagatgaaaa 660  
tcaagggtt gctggaccgc aaggggctct ggaggagtct gaatgagatg aaaaggatct 720  
tcaacttccg gaggacccca gcagctgagc acgcattga gcactggcag gaggatgcct 780  
tcttcgcctc ccagttcctg aatggtctca accctgtcct gatccgcccgc tgtcactacc 840  
tcccaaagaa cttcccgctc actgatgcc a tggtggcctc attgttgggt cctggacca 900  
gcttgcaggc tgagcttagag aagggtctcc tggtcttgggt ggatcacggc atcctctctg 960  
gcatccagac caatgtcatt aatgggaagc cgca gtttctc tgccggccca atgaccctgc 1020  
tataccagag cccaggctgc gggccgctgc tgcctctcgc catccagctc agccagaccc 1080  
ccggcccaaa cagccccatc ttccctgcccc ctgatgacaa gtgggactgg ttgctggcca 1140  
agacctgggt gcgcaatgcc gagttctcct tccatgaggc cctcacgcac ctgctgcact 1200  
cacatctgct gcctgaggc ttcaccctgg ctaccctgcg tcagctgccc cactgccacc 1260  
ctctcttcaa gctgctgatc ccgcacaccc gatacaccct gcacatcaac acactcgccc 1320  
gggagctgct tatcgtgcc a gggcagggtgg tggacaggc cacaggcattc ggcattgaag 1380  
gcttctctga gttgatacag aggaacatga agcagctgaa ctattctctc ctgtgtctgc 1440  
ctgaggatat ccggacccga ggagttgaag acatcccagg ctactactac cgtgatgatg 1500  
ggatgcagat ttggggtgca gtggAACGCT ttgtctctga aatcatcggt atctactacc 1560  
caagtgtga gtctgtccaa gatgacagag agctccaggc ctgggtcaga gagatcttct 1620  
ccaagggtttt cctaaaccag gagagctcag gtatcccttc ctcactggag acccgaaag 1680  
ccctggtgca gtatgtcacc atggtgatat tcacccctgc agccaaagcat gcggctgtca 1740  
gtgcaggcgtt gtttgactcc tggcttggta tgcccaacct gccacccagg atgcagctgc 1800  
caccacccac ctccaaaggc ctggcaacat gcgagggtttt catagccacc ctcccacctg 1860  
tcaatgccac atgtgtatgtc atccttgcctc tctgggtgct gagcaaggag cctggagacc 1920  
aaaggccctt gggcacctat ccggatgagc acttcacaga ggaggccctt cggcggagca 1980  
tcggccacccctt ccagagccgc ctggcccaaga tctcgagggg catccaggag cggaaccggg 2040

gcctgggtgct gcccctacacc tacctagacc ctccccatcgat cgagaacacgc gtctccatct 2100  
aaatcccagg ggaacacacagg cccagatgac atcccttga ccacatcgct ctaggataac 2160  
tggcacccag agaaaaggac tcctcagaaa aaacaggccc ccatgtgcct ctcctggac 2220  
aaccagactc tgtaactcac ccccaccacc atacacacac acaaaaaacag aaacaaaatc 2280  
aaaacagaga aagcagaaaaa tctaccaaga acagagtctc aggacagaac cactgagtct 2340  
tttggaggct ccaaggctca aagtgcgcgc agagccacc ttgagggttt tgctagttgg 2400  
ttttgttttgcgatggggggc agcacataat cccgcggcag ggcccaactag 2460  
catccactga ttggaccta tggtcaccca actcaaggac agccaccaag aagtggctgc 2520  
caaagagact gggcgcagtg gctcatgccc ataatccag cactttgggat gatggaggcg 2580  
ggaaaaatcat ttgaggtcag aagttcaagg ccagcctgga cgacatagcg agactccacc 2640  
tctaccaaaa aataaaaaatt aaaaaacaaa aaaaaaaaaa aaaaa 2685

<210> 134

<211> 676

<212> PRT

<213> human organism

<400> 134

Met Ala Glu Phe Arg Val Arg Val Ser Thr Gly Glu Ala Phe Gly Ala  
1 5 10 15

Gly Thr Trp Asp Lys Val Ser Val Ser Ile Val Gly Thr Arg Gly Glu  
20 25 30

Ser Pro Pro Leu Pro Leu Asp Asn Leu Gly Lys Glu Phe Thr Ala Gly  
35 40 45

Ala Glu Glu Asp Phe Gln Val Thr Leu Pro Glu Asp Val Gly Arg Val  
50 55 60

Leu Leu Leu Arg Val His Lys Ala Pro Pro Val Leu Pro Leu Leu Gly  
65 70 75 80

Pro Leu Ala Pro Asp Ala Trp Phe Cys Arg Trp Phe Gln Leu Thr Pro  
85 90 95

Pro Arg Gly Gly His Leu Leu Phe Pro Cys Tyr Gln Trp Leu Glu Gly  
100 105 110

Ala Gly Thr Leu Val Leu Gln Glu Gly Thr Ala Lys Val Ser Trp Ala  
115 120 125

Asp His His Pro Val Leu Gln Gln Arg Gln Glu Glu Leu Gln Ala  
130 135 140

Arg Gln Glu Met Tyr Gln Trp Lys Ala Tyr Asn Pro Gly Trp Pro His  
145 150 155 160

Cys Leu Asp Glu Lys Thr Val Glu Asp Leu Glu Leu Asn Ile Lys Tyr  
165 170 175

Ser Thr Ala Lys Asn Ala Asn Phe Tyr Leu Gln Ala Gly Ser Ala Phe  
180 185 190

Ala Glu Met Lys Ile Lys Gly Leu Leu Asp Arg Lys Gly Leu Trp Arg  
195 200 205

Ser Leu Asn Glu Met Lys Arg Ile Phe Asn Phe Arg Arg Thr Pro Ala  
210 215 220

Ala Glu His Ala Phe Glu His Trp Gln Glu Asp Ala Phe Phe Ala Ser  
225 230 235 240

Gln Phe Leu Asn Gly Leu Asn Pro Val Leu Ile Arg Arg Cys His Tyr  
245 250 255

Leu Pro Lys Asn Phe Pro Val Thr Asp Ala Met Val Ala Ser Leu Leu  
260 265 270

Gly Pro Gly Thr Ser Leu Gln Ala Glu Leu Glu Lys Gly Ser Leu Phe  
275 280 285

Leu Val Asp His Gly Ile Leu Ser Gly Ile Gln Thr Asn Val Ile Asn  
290 295 300

Gly Lys Pro Gln Phe Ser Ala Ala Pro Met Thr Leu Leu Tyr Gln Ser  
305 310 315 320

Pro Gly Cys Gly Pro Leu Leu Pro Leu Ala Ile Gln Leu Ser Gln Thr  
325 330 335

Pro Gly Pro Asn Ser Pro Ile Phe Leu Pro Thr Asp Asp Lys Trp Asp  
340 345 350

Trp Leu Leu Ala Lys Thr Trp Val Arg Asn Ala Glu Phe Ser Phe His  
355 360 365

Glu Ala Leu Thr His Leu Leu His Ser His Leu Leu Pro Glu Val Phe  
370 375 380

Thr Leu Ala Thr Leu Arg Gln Leu Pro His Cys His Pro Leu Phe Lys  
385 390 395 400

Leu Leu Ile Pro His Thr Arg Tyr Thr Leu His Ile Asn Thr Leu Ala  
405 410 415

Arg Glu Leu Leu Ile Val Pro Gly Gln Val Val Asp Arg Ser Thr Gly  
420 425 430

Ile Gly Ile Glu Gly Phe Ser Glu Leu Ile Gln Arg Asn Met Lys Gln  
435 440 445

Leu Asn Tyr Ser Leu Leu Cys Leu Pro Glu Asp Ile Arg Thr Arg Gly  
450 455 460

Val Glu Asp Ile Pro Gly Tyr Tyr Arg Asp Asp Gly Met Gln Ile  
465 470 475 480

Trp Gly Ala Val Glu Arg Phe Val Ser Glu Ile Ile Gly Ile Tyr Tyr  
485 490 495

Pro Ser Asp Glu Ser Val Gln Asp Asp Arg Glu Leu Gln Ala Trp Val  
500 505 510

Arg Glu Ile Phe Ser Lys Gly Phe Leu Asn Gln Glu Ser Ser Gly Ile  
515 520 525

Pro Ser Ser Leu Glu Thr Arg Glu Ala Leu Val Gln Tyr Val Thr Met  
530 535 540

Val Ile Phe Thr Cys Ser Ala Lys His Ala Ala Val Ser Ala Gly Gln  
545 550 555 560

Phe Asp Ser Cys Ala Trp Met Pro Asn Leu Pro Pro Ser Met Gln Leu  
565 570 575

Pro Pro Pro Thr Ser Lys Gly Leu Ala Thr Cys Glu Gly Phe Ile Ala  
580 585 590

Thr Leu Pro Pro Val Asn Ala Thr Cys Asp Val Ile Leu Ala Leu Trp  
595 600 605

Leu Leu Ser Lys Glu Pro Gly Asp Gln Arg Pro Leu Gly Thr Tyr Pro  
610 615 620

Asp Glu His Phe Thr Glu Glu Ala Pro Arg Arg Ser Ile Ala Thr Phe  
625 630 635 640

Gln Ser Arg Leu Ala Gln Ile Ser Arg Gly Ile Gln Glu Arg Asn Arg  
645 650 655

Gly Leu Val Leu Pro Tyr Thr Tyr Leu Asp Pro Pro Leu Ile Glu Asn  
660 665 670

Ser Val Ser Ile  
675

<210> 135  
<211> 3742  
<212> DNA  
<213> human organism

<400> 135  
gaattccttc tctcctccctc ctcgccccttc tcctcgccct cctcctccctc ctcgcccctcc 60  
cctcccgatc ctcatccccct tgccctcccc cagcccaaggg actttccgg aaagtttta 120  
ttttccgtct gggctctcgg agaaaagaagc tcctggctca gcggctgcaa aactttcctg 180  
ctgccgcgcc gccagcccccc gccctccgct gcccggccct gcgcggccgc gagcgatgag 240  
cgccccctccg gtcctgcggc cgccccagtcc gctgctgccc gtggcggcgg cagctgccgc 300  
agcggccgcgc gcactggtcc cagggtccgg gcccggggccc gcgccgttct tggctcctgt 360  
cgcgcccccg gtcggggca tctcggttcca tctgcagatc ggcctgagcc gtgagccgg 420  
gctgctgctg caggactcgt ccggggacta cagcctggcg cacgtccgcg agatggcttg 480  
ctccattgtc gaccagaagt tccctgaatg tggttctac ggaatgtatg ataagatcct 540  
gcttttcgc catgacccta cctctgaaaa catccttcag ctggtgaaag cggccagtga 600

tatccaggaa ggcgatctta ttgaagtggc cttgtcacgt tccgccacct ttgaagactt 660  
tcagattcgt cccccacgctc tctttgttca ttcatacaga gctccagctt tctgtgatca 720  
ctgtggagaa atgctgtggg ggctggtagc tcaaggtctt aaatgtgaag ggtgtggct 780  
gaattaccat aagagatgtg catttaaat acccaacaat tgcaagcggtg tgaggcggag 840  
aaggctctca aacgtttccc tcactgggt cagcaccatc cgcacatcat ctgctgaact 900  
ctctacaagt gcccctgatg agccccttct gcaaaaatca ccatcagagt cgtttattgg 960  
tcgagagaag aggtcaaatt ctcaatcata cattggacga ccaattcacc ttgacaagat 1020  
tttgcgtct aaagttaaag tgccgcacac atttgcgtatc cactcctaca cccggccac 1080  
agtgtgccag tactgcaaga agcttctgaa ggggctttc aggcaaggct tgcagtgcaa 1140  
agattgcaga ttcaactgcc ataaacgttg tgcaccgaaa gtaccaaaca actgccttgg 1200  
cgaagtgacc attaatggag atttgcttag ccctggggca gagtctgatg tggcatgga 1260  
agaaggagt gatgacaatg atagtgaaag gaacagtggg ctcatggatg atatgaaaga 1320  
agcaatggtc caagatgcag agatggcaat ggcagagtgc cagaacgaca gtggcgagat 1380  
gcaagatcca gacccagacc acgaggacgc caacagaacc atcagtccat caacaagcaa 1440  
caatatccca ctcatgaggg tagtgcagtc tgtcaaacac acgaagagga aaagcagcac 1500  
agtcatgaaa gaaggatgga tggccacta caccagcaag gacacgctgc ggaaacggca 1560  
ctattggaga ttggatagca aatgttattac cctcttcag aatgacacag gaagcaggta 1620  
ctacaaggaa attcctttat ctgaaatttt gtctctggaa ccagtaaaaa cttcagcttt 1680  
aattcctaatt gggccaatc ctcattgttt cgaaatcaact acggcaaatg tagtgtatta 1740  
tgtggagaa aatgtggta atccttccag cccatcacca aataacagtg ttctcaccag 1800  
tggcggttgt gcagatgtgg ccaggatgtg ggagatagcc atccagcatg cccttatgcc 1860  
cgtcattccc aagggttcct ccgtgggtac aggaaccaac ttgcacagag atatctctgt 1920  
gagtatttca gtatcaaatt gccagattca agaaaatgtg gacatcagca cagtatatca 1980  
gattttcct gatgaagtac tgggttctgg acagttggc attgtttatg gagaaaaaca 2040  
tcgtaaaaca ggaagagatg tagctattaa aatcattgac aaattacgat ttccaacaaa 2100  
acaagaaaagc cagttcgta atgagggtgc aattctacag aaccttcatc accctgggt 2160  
tgtaaatttgc gagtgtatgt ttgagacgccc tgaaagagtg tttgttgtt tgaaaaact 2220  
ccatggagac atgctggaaa tgatcttgc aagtggaaag ggcaggtgc cagagcacat 2280

aacgaagttt	ttaattactc	agataactcgt	ggctttgcgg	cacccattt	ttaaaaaat	2340
cgttcactgt	gacctaaac	cagaaaatgt	gttgctagcc	tcagctgatc	ctttcctca	2400
ggtgaaacctt	tgtgattttg	gtttgcccgg	gatcatggaa	gagaagtctt	tccggaggtc	2460
agtggtggtt	accccgctt	acctggctcc	tgaggtccta	aggaacaagg	gctacaatcg	2520
ctctctagac	atgtggtctg	ttggggtcat	catctatgt	agcctaagcg	gcacattccc	2580
attnaatgaa	gatgaagaca	tacacgacca	aattcagaat	gcagcttca	tgtatccacc	2640
aaatccctgg	aaggaaatat	ctcatgaagc	cattgatctt	atcaacaatt	tgctgcaagt	2700
aaaaatgaga	aagcgctaca	gtgtggataa	gaccttgagc	cacccttggc	tacaggacta	2760
tcagacctgg	ttagatttgc	gagagctgga	atgcaaaatc	ggggagcgct	acatcaccca	2820
tgaaagtgtat	gacctgaggt	gggagaagta	tgcaggcgag	cagcggctgc	agtacccac	2880
acacctgatc	aatccaagtg	ctagccacag	tgacactcct	gagactgaag	aaacagaaat	2940
gaaagccctc	ggtgagcgtg	tcagcatcct	ctgagttcca	tctcctataaa	tctgtcaaaa	3000
cactgtggaa	ctaataaata	catacggta	ggttaacat	ttgccttgca	gaactgccat	3060
tatttctgt	cagatgagaa	caaagctgtt	aaactgttag	cactgttgat	gtatctgagt	3120
tgccaagaca	aatcaacaga	agcatttgc	ttttgtgtga	ccaaactgtgt	tgtattaaca	3180
aaagttccct	gaaacacgaa	acttgttatt	gtgaatgatt	catgttatat	ttaatgcatt	3240
aaacctgtct	ccactgtgcc	tttgc当地	agtgttttc	ttactggagc	ttcat	3300
taagagacag	aatgtatctg	tgaagtagtt	ctgtttggtg	tgtcccattt	gtgttgtcat	3360
tgtaaacaaa	ctcttgaaga	gtcgattatt	tccagtgttc	tatgaacaac	tccaaaaccc	3420
atgtggaaaa	aaaatgaatg	aggagggtag	ggaataaaaat	cctaagacac	aaatgcata	3480
acaagtttta	atgtatagtt	ttgaatcctt	tgccctgcctg	gtgtgcctca	gtatattaa	3540
actcaagaca	atgcacccat	ctgtgcaaga	cctagtgtc	ttaagcctaa	atgcctttaga	3600
aatgtaaact	gccatatata	acagatacat	ttccctctt	tttataatac	tctgttgtac	3660
tatggaaaaat	cagctgctca	gcaacccccc	acccccc	atccccc	atccccc	3720
attcttgtca	aaaaaaaaaa	aaaaaa	aaaaaa	aaaaaa	aaaaaa	3742

<210> 136  
 <211> 912  
 <212> PRT  
 <213> human organism

<400> 136

Met Ser Ala Pro Pro Val Leu Arg Pro Pro Ser Pro Leu Leu Pro Val  
1 5 10 15

Ala Ala Ala Ala Ala Ala Ala Ala Leu Val Pro Gly Ser Gly  
20 25 30

Pro Gly Pro Ala Pro Phe Leu Ala Pro Val Ala Ala Pro Val Gly Gly  
35 40 45

Ile Ser Phe His Leu Gln Ile Gly Leu Ser Arg Glu Pro Val Leu Leu  
50 55 60

Leu Gln Asp Ser Ser Gly Asp Tyr Ser Leu Ala His Val Arg Glu Met  
65 70 75 80

Ala Cys Ser Ile Val Asp Gln Lys Phe Pro Glu Cys Gly Phe Tyr Gly  
85 90 95

Met Tyr Asp Lys Ile Leu Leu Phe Arg His Asp Pro Thr Ser Glu Asn  
100 105 110

Ile Leu Gln Leu Val Lys Ala Ala Ser Asp Ile Gln Glu Gly Asp Leu  
115 120 125

Ile Glu Val Val Leu Ser Arg Ser Ala Thr Phe Glu Asp Phe Gln Ile  
130 135 140

Arg Pro His Ala Leu Phe Val His Ser Tyr Arg Ala Pro Ala Phe Cys  
145 150 155 160

Asp His Cys Gly Glu Met Leu Trp Gly Leu Val Arg Gln Gly Leu Lys  
165 170 175

Cys Glu Gly Cys Gly Leu Asn Tyr His Lys Arg Cys Ala Phe Lys Ile  
180 185 190

Pro Asn Asn Cys Ser Gly Val Arg Arg Arg Leu Ser Asn Val Ser  
195 200 205

Leu Thr Gly Val Ser Thr Ile Arg Thr Ser Ser Ala Glu Leu Ser Thr  
210 215 220

Ser Ala Pro Asp Glu Pro Leu Leu Gln Lys Ser Pro Ser Glu Ser Phe  
225   230   235   240

Ile Gly Arg Glu Lys Arg Ser Asn Ser Gln Ser Tyr Ile Gly Arg Pro  
245   250   255

Ile His Leu Asp Lys Ile Leu Met Ser Lys Val Lys Val Pro His Thr  
260   265   270

Phe Val Ile His Ser Tyr Thr Arg Pro Thr Val Cys Gln Tyr Cys Lys  
275   280   285

Lys Leu Leu Lys Gly Leu Phe Arg Gln Gly Leu Gln Cys Lys Asp Cys  
290   295   300

Arg Phe Asn Cys His Lys Arg Cys Ala Pro Lys Val Pro Asn Asn Cys  
305   310   315   320

Leu Gly Glu Val Thr Ile Asn Gly Asp Leu Leu Ser Pro Gly Ala Glu  
325   330   335

Ser Asp Val Val Met Glu Glu Gly Ser Asp Asp Asn Asp Ser Glu Arg  
340   345   350

Asn Ser Gly Leu Met Asp Asp Met Glu Glu Ala Met Val Gln Asp Ala  
355   360   365

Glu Met Ala Met Ala Glu Cys Gln Asn Asp Ser Gly Glu Met Gln Asp  
370   375   380

Pro Asp Pro Asp His Glu Asp Ala Asn Arg Thr Ile Ser Pro Ser Thr  
385   390   395   400

Ser Asn Asn Ile Pro Leu Met Arg Val Val Gln Ser Val Lys His Thr  
405   410   415

Lys Arg Lys Ser Ser Thr Val Met Lys Glu Gly Trp Met Val His Tyr  
420   425   430

Thr Ser Lys Asp Thr Leu Arg Lys Arg His Tyr Trp Arg Leu Asp Ser  
435   440   445

Lys Cys Ile Thr Leu Phe Gln Asn Asp Thr Gly Ser Arg Tyr Tyr Lys

450                    455                    460  
Glu Ile Pro Leu Ser Glu Ile Leu Ser Leu Glu Pro Val Lys Thr Ser  
465                    470                    475                    480  
  
Ala Leu Ile Pro Asn Gly Ala Asn Pro His Cys Phe Glu Ile Thr Thr  
485                    490                    495  
  
Ala Asn Val Val Tyr Tyr Val Gly Glu Asn Val Val Asn Pro Ser Ser  
500                    505                    510  
  
Pro Ser Pro Asn Asn Ser Val Leu Thr Ser Gly Val Gly Ala Asp Val  
515                    520                    525  
  
Ala Arg Met Trp Glu Ile Ala Ile Gln His Ala Leu Met Pro Val Ile  
530                    535                    540  
  
Pro Lys Gly Ser Ser Val Gly Thr Gly Thr Asn Leu His Arg Asp Ile  
545                    550                    555                    560  
  
Ser Val Ser Ile Ser Val Ser Asn Cys Gln Ile Gln Glu Asn Val Asp  
565                    570                    575  
  
Ile Ser Thr Val Tyr Gln Ile Phe Pro Asp Glu Val Leu Gly Ser Gly  
580                    585                    590  
  
Gln Phe Gly Ile Val Tyr Gly Gly Lys His Arg Lys Thr Gly Arg Asp  
595                    600                    605  
  
Val Ala Ile Lys Ile Ile Asp Lys Leu Arg Phe Pro Thr Lys Gln Glu  
610                    615                    620  
  
Ser Gln Leu Arg Asn Glu Val Ala Ile Leu Gln Asn Leu His His Pro  
625                    630                    635                    640  
  
Gly Val Val Asn Leu Glu Cys Met Phe Glu Thr Pro Glu Arg Val Phe  
645                    650                    655  
  
Val Val Met Glu Lys Leu His Gly Asp Met Leu Glu Met Ile Leu Ser  
660                    665                    670  
  
Ser Glu Lys Gly Arg Leu Pro Glu His Ile Thr Lys Phe Leu Ile Thr  
675                    680                    685

Gln Ile Leu Val Ala Leu Arg His Leu His Phe Lys Asn Ile Val His  
690 695 700

Cys Asp Leu Lys Pro Glu Asn Val Leu Leu Ala Ser Ala Asp Pro Phe  
705 710 715 720

Pro Gln Val Lys Leu Cys Asp Phe Gly Phe Ala Arg Ile Ile Gly Glu  
725 730 735

Lys Ser Phe Arg Arg Ser Val Val Gly Thr Pro Ala Tyr Leu Ala Pro  
740 745 750

Glu Val Leu Arg Asn Lys Gly Tyr Asn Arg Ser Leu Asp Met Trp Ser  
755 760 765

Val Gly Val Ile Ile Tyr Val Ser Leu Ser Gly Thr Phe Pro Phe Asn  
770 775 780

Glu Asp Glu Asp Ile His Asp Gln Ile Gln Asn Ala Ala Phe Met Tyr  
785 790 795 800

Pro Pro Asn Pro Trp Lys Glu Ile Ser His Glu Ala Ile Asp Leu Ile  
805 810 815

Asn Asn Leu Leu Gln Val Lys Met Arg Lys Arg Tyr Ser Val Asp Lys  
820 825 830

Thr Leu Ser His Pro Trp Leu Gln Asp Tyr Gln Thr Trp Leu Asp Leu  
835 840 845

Arg Glu Leu Glu Cys Lys Ile Gly Glu Arg Tyr Ile Thr His Glu Ser  
850 855 860

Asp Asp Leu Arg Trp Glu Lys Tyr Ala Gly Glu Gln Arg Leu Gln Tyr  
865 870 875 880

Pro Thr His Leu Ile Asn Pro Ser Ala Ser His Ser Asp Thr Pro Glu  
885 890 895

Thr Glu Glu Thr Glu Met Lys Ala Leu Gly Glu Arg Val Ser Ile Leu  
900 905 910

<210>	137	
<211>	3903	
<212>	DNA	
<213>	human organism	
<400>	137	
aatggtcagt caatacatta taacataata caccaaatgc tagaatagaa ggggaggggg	60	
gcacacataa tgactcactg ctggaagaag ggtgcatcg tgaattaaaa aatgtccctc	120	
ccctcttcag cactcagcgc gcagctattt cttctgccca gtctcttga actctggatc	180	
tttgcttttg ctgcgtgctc tcctgtttt cattctccac atttctcaa tcctcttct	240	
ttatccttag ccaccctgct ttttcctcc tttttaaaa aatcgagat ttgcgtttaa	300	
aatgatttgt cttccttacc ttgcgtccatt tcaacactga aggctgcaaa gaacttcacc	360	
tttcccctag tggattttaa aaattctcaa tccgtaaaaa gtcttttga aaggcaaagg	420	
aacaggaccc agaccctctc gacacccttg atccgagtca gatctgcact agcaaccaga	480	
actaatattt catttaaccc accaaaaggg ggaggcgaga ggagccagaa gcaaacttca	540	
tctgtctcag acggatccgt gttcctaca tttggaggag ccgcgtgtca gaaggcgtag	600	
gaccggcaagg ggggacaagg aggactcccg agtctccctt ctccgctctc cgagaccgaa	660	
gaggtggact gagccgctcg ggacagcggc accggaggag gctcgagaa gatgcggggc	720	
tcggggcccc ggggtgcggg acaccggcg cccccaagcg gccggcggcga caccggatc	780	
accccaagcgt ccctggccgg ctgctactct gcacctcgac gggctccctt ctggacgtgc	840	
cttctcctgt gcgccgact ccggaccctc ctggccagcc ccagcaacga agtgaattta	900	
ttggattcac gcactgtcat gggggacctg ggatggattt ctttccaaa aaatgggtgg	960	
gaagagattt gtgaagtggaa tgaaaattat gcccstatcc acacatacca agtatgc当地	1020	
gtgatggAAC agaatcagaa taactggctt ttgaccagtt ggatctccaa tgaagggtct	1080	
tccagaatct tcatagaact caaatttacc ctgcggact gcaacagcct tcctggagga	1140	
ctggggacct gtaaggaaac cttaatatg tattactttt agtcagatga tcagaatggg	1200	
agaaaacatca aggaaaacca atacatcaa attgatacca ttgctgccga tgaaagctt	1260	
acagaactt acatgggtga ccgtgttatg aaactgaata cagaggtcg agatgttagga	1320	
cctctaagca aaaaggatt ttatcttgc tttcaagatg ttgggtctt cattgctctg	1380	
gtttctgtgc gtgtatacta taaaaatgc cttctgtgg tacgacactt ggctgtttc	1440	
cctgacaccca tcactggagc tgattcttcc caattgctcg aagtgtcagg ctcctgtgtc	1500	

aaccattctg tgaccgatga acctccaaa atgcactgca gcgccgaagg ggagtggctg 1560  
gtgccatcg ggaaatgcat gtgcaaggca ggatatgaag agaaaaatgg cacctgtcaa 1620  
gtgtcagac ctggttctt caaagcctca cctcacatcc agagctgcgg caaatgtcca 1680  
cctcacagtt atacccatga ggaagcttca acctcttgc tctgtaaaa ggattatttc 1740  
aggagagagt ctgatccacc cacaatggca tgcacaagac ccccctctgc tcctcgaaat 1800  
gcatctcaa atgttaatga aactagtgtc ttcttgcggat ggattccgccc tgctgacact 1860  
ggtggaaagga aagacgtgtc atattatatt gcatgcaaga agtgcaactc ccatgcaggt 1920  
gtgtgtgagg agtgtggcgg tcatgtcagg taccttcccc ggcaaagcgg cctgaaaaac 1980  
acctctgtca tcatgggaa tctactcgct cacacaaact ataccttgc gattgaggca 2040  
gtgaatggag tgtccgactt gagcccagga gccggcagt atgtgtctgt aaatgttaacc 2100  
acaaatcaag cagctccatc tccagtcacc aatgtaaaa aagggaaaat tgcaaaaaac 2160  
agcatctctt tgtcttggca agaaccagat cgtcccaatg gaatcatcct agagtatgaa 2220  
atcaagcatt ttgaaaagga ccaagagacc agtacacga ttatcaaatt taaagagaca 2280  
actattactg cagagggctt gaaaccagct tcagttatg tcttccaaat tcgagcacgt 2340  
acagcagcag gctatgggt cttcagtcga agatttgagt ttgaaaccac cccagtggtt 2400  
gcagcatcca gcgatcaaag ccagattcct gtaattgctg tgtctgtgac agtaggagtc 2460  
attttgtgg cagtggttat cggcgtcctc ctcagtgaa gttgctgcga atgtggctgt 2520  
gggagggctt cttccctgtg cgctgttgcc catccaaatcc taatatggcg gtgtggctac 2580  
agcaaagcaa aacaagatcc agaagaggaa aagatgcatt ttcataatgg gcacattaaa 2640  
ctgccaggag taagaactta cattgatcca catacctatg aggatccaa tcaagctgtc 2700  
cacgaatttg ccaaggagat agaagcatca tgtatcacca ttgagagagt tattggagca 2760  
ggtaatttg gtgaagttt tagtggacgt ttgaaactac cagaaaaaag agaattacct 2820  
gtggctatca aaacccttaa agtaggctat actgaaaagc aacgcagaga tttccttaggt 2880  
gaagcaagta tcatggaca gtttgatcat cctaacatca tccatttgcg aggtgtggtg 2940  
acccaaaatgt aaccagtgtat gatcgtgaca ggttatatgg agaatggctc ttttagataca 3000  
tttttgaaga aaaacgatgg gcagttcact gtgattcagc ttgttggcat gctgagaggt 3060  
atctctgcag gaatgaagta ctttctgac atgggctatg tgcatacgaga tcttgcgtcc 3120  
agaaacatct taatcaacag taaccttgc tgcatacgatgt ctgactttgg actttccgg 3180  
gtactgaaag atgatcccgaa ggcagcctac accacaaggg gaggaaaaat tccaaatcaga 3240

tggactgcc	cagaagcaat	agcttccga	aagttactt	ctgccagtga	tgtctggagt	3300
tatggaatag	taatgtgg	agttgtgt	tatggagaga	gaccctactg	ggagatgacc	3360
aatcaagatg	tgattaaagc	ggttagaggaa	ggctatcg	tgccaagccc	catggattgt	3420
cctgctgctc	tctatcagtt	aatgctggat	tgctggcaga	aagagcgaaa	tagcaggccc	3480
aagtttgatg	aaatagtcaa	catgttggac	aagctgatac	gtaacccaag	tagtctgaag	3540
acgctggta	atgcac	cagagtatct	aatttattgg	cagaacatag	cccactagga	3600
tctgggcct	acagatcagt	aggtgaatgg	ctagaggcaa	tcaagatggg	ccggtat	3660
gagatttca	tggaaaatgg	atacagttca	atggacgctg	tggctcaggt	gaccttggag	3720
gatttgagac	ggcttggagt	gactcttgc	ggtcaccaga	agaagatcat	gaacagcctt	3780
caagaaatga	aggtgcagct	ggtaaacgg	atggtccat	tgtaacttca	tgtaaatgtc	3840
gcttcttcaa	gtgaatgatt	ctgcacttt	taaacagcac	ttagattat	tttaacaaaa	3900
aaa						3903

<210> 138  
 <211> 1037  
 <212> PRT  
 <213> human organism

<400> 138

Met	Arg	Gly	Ser	Gly	Pro	Arg	Gly	Ala	Gly	His	Arg	Arg	Pro	Pro	Ser
1				5				10				15			

Gly	Gly	Gly	Asp	Thr	Pro	Ile	Thr	Pro	Ala	Ser	Leu	Ala	Gly	Cys	Tyr
20					25							30			

Ser	Ala	Pro	Arg	Arg	Ala	Pro	Leu	Trp	Thr	Cys	Leu	Leu	Leu	Cys	Ala
35					40						45				

Ala	Leu	Arg	Thr	Leu	Leu	Ala	Ser	Pro	Ser	Asn	Glu	Val	Asn	Leu	Leu
50					55					60					

Asp	Ser	Arg	Thr	Val	Met	Gly	Asp	Leu	Gly	Trp	Ile	Ala	Phe	Pro	Lys
65					70				75		80				

Asn	Gly	Trp	Glu	Glu	Ile	Gly	Glu	Val	Asp	Glu	Asn	Tyr	Ala	Pro	Ile
85					90						95				

His Thr Tyr Gln Val Cys Lys Val Met Glu Gln Asn Gln Asn Asn Trp  
100 105 110

Leu Leu Thr Ser Trp Ile Ser Asn Glu Gly Ala Ser Arg Ile Phe Ile  
115 120 125

Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Gly Leu  
130 135 140

Gly Thr Cys Lys Glu Thr Phe Asn Met Tyr Tyr Phe Glu Ser Asp Asp  
145 150 155 160

Gln Asn Gly Arg Asn Ile Lys Glu Asn Gln Tyr Ile Lys Ile Asp Thr  
165 170 175

Ile Ala Ala Asp Glu Ser Phe Thr Glu Leu Asp Leu Gly Asp Arg Val  
180 185 190

Met Lys Leu Asn Thr Glu Val Arg Asp Val Gly Pro Leu Ser Lys Lys  
195 200 205

Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile Ala Leu Val  
210 215 220

Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Ser Val Val Arg His Leu  
225 230 235 240

Ala Val Phe Pro Asp Thr Ile Thr Gly Ala Asp Ser Ser Gln Leu Leu  
245 250 255

Glu Val Ser Gly Ser Cys Val Asn His Ser Val Thr Asp Glu Pro Pro  
260 265 270

Lys Met His Cys Ser Ala Glu Gly Glu Trp Leu Val Pro Ile Gly Lys  
275 280 285

Cys Met Cys Lys Ala Gly Tyr Glu Glu Lys Asn Gly Thr Cys Gln Val  
290 295 300

Cys Arg Pro Gly Phe Phe Lys Ala Ser Pro His Ile Gln Ser Cys Gly  
305 310 315 320

Lys Cys Pro Pro His Ser Tyr Thr His Glu Glu Ala Ser Thr Ser Cys

325

330

335

Val Cys Glu Lys Asp Tyr Phe Arg Arg Glu Ser Asp Pro Pro Thr Met  
340 345 350

Ala Cys Thr Arg Pro Pro Ser Ala Pro Arg Asn Ala Ile Ser Asn Val  
355 360 365

Asn Glu Thr Ser Val Phe Leu Glu Trp Ile Pro Pro Ala Asp Thr Gly  
370 375 380

Gly Arg Lys Asp Val Ser Tyr Tyr Ile Ala Cys Lys Lys Cys Asn Ser  
385 390 395 400

His Ala Gly Val Cys Glu Cys Gly His Val Arg Tyr Leu Pro  
405 410 415

Arg Gln Ser Gly Leu Lys Asn Thr Ser Val Met Met Val Asp Leu Leu  
420 425 430

Ala His Thr Asn Tyr Thr Phe Glu Ile Glu Ala Val Asn Gly Val Ser  
435 440 445

Asp Leu Ser Pro Gly Ala Arg Gln Tyr Val Ser Val Asn Val Thr Thr  
450 455 460

Asn Gln Ala Ala Pro Ser Pro Val Thr Asn Val Lys Lys Gly Lys Ile  
465 470 475 480

Ala Lys Asn Ser Ile Ser Leu Ser Trp Gln Glu Pro Asp Arg Pro Asn  
485 490 495

Gly Ile Ile Leu Glu Tyr Glu Ile Lys His Phe Glu Lys Asp Gln Glu  
500 505 510

Thr Ser Tyr Thr Ile Ile Lys Ser Lys Glu Thr Thr Ile Thr Ala Glu  
515 520 525

Gly Leu Lys Pro Ala Ser Val Tyr Val Phe Gln Ile Arg Ala Arg Thr  
530 535 540

Ala Ala Gly Tyr Gly Val Phe Ser Arg Arg Phe Glu Phe Glu Thr Thr  
545 550 555 560

Pro Val Phe Ala Ala Ser Ser Asp Gln Ser Gln Ile Pro Val Ile Ala  
565 570 575

Val Ser Val Thr Val Gly Val Ile Leu Leu Ala Val Val Ile Gly Val  
580 585 590

Leu Leu Ser Gly Ser Cys Cys Glu Cys Gly Cys Gly Arg Ala Ser Ser  
595 600 605

Leu Cys Ala Val Ala His Pro Ile Leu Ile Trp Arg Cys Gly Tyr Ser  
610 615 620

Lys Ala Lys Gln Asp Pro Glu Glu Glu Lys Met His Phe His Asn Gly  
625 630 635 640

His Ile Lys Leu Pro Gly Val Arg Thr Tyr Ile Asp Pro His Thr Tyr  
645 650 655

Glu Asp Pro Asn Gln Ala Val His Glu Phe Ala Lys Glu Ile Glu Ala  
660 665 670

Ser Cys Ile Thr Ile Glu Arg Val Ile Gly Ala Gly Glu Phe Gly Glu  
675 680 685

Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Lys Arg Glu Leu Pro Val  
690 695 700

Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg Arg Asp  
705 710 715 720

Phe Leu Gly Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile  
725 730 735

Ile His Leu Glu Gly Val Val Thr Lys Ser Lys Pro Val Met Ile Val  
740 745 750

Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Thr Phe Leu Lys Lys Asn  
755 760 765

Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile  
770 775 780

Ser Ala Gly Met Lys Tyr Leu Ser Asp Met Gly Tyr Val His Arg Asp  
785 790 795 800

Leu Ala Ala Arg Asn Ile Leu Ile Asn Ser Asn Leu Val Cys Lys Val  
805 810 815

Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Ala  
820 825 830

Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu  
835 840 845

Ala Ile Ala Phe Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr  
850 855 860

Gly Ile Val Met Trp Glu Val Val Ser Tyr Gly Glu Arg Pro Tyr Trp  
865 870 875 880

Glu Met Thr Asn Gln Asp Val Ile Lys Ala Val Glu Glu Gly Tyr Arg  
885 890 895

Leu Pro Ser Pro Met Asp Cys Pro Ala Ala Leu Tyr Gln Leu Met Leu  
900 905 910

Asp Cys Trp Gln Lys Glu Arg Asn Ser Arg Pro Lys Phe Asp Glu Ile  
915 920 925

Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Ser Ser Leu Lys Thr  
930 935 940

Leu Val Asn Ala Ser Cys Arg Val Ser Asn Leu Leu Ala Glu His Ser  
945 950 955 960

Pro Leu Gly Ser Gly Ala Tyr Arg Ser Val Gly Glu Trp Leu Glu Ala  
965 970 975

Ile Lys Met Gly Arg Tyr Thr Glu Ile Phe Met Glu Asn Gly Tyr Ser  
980 985 990

Ser Met Asp Ala Val Ala Gln Val Thr Leu Glu Asp Leu Arg Arg Leu  
995 1000 1005

Gly Val Thr Leu Val Gly His Gln Lys Lys Ile Met Asn Ser Leu  
1010 1015 1020

Gln Glu Met Lys Val Gln Leu Val Asn Gly Met Val Pro Leu  
1025 1030 1035

<210> 139  
<211> 1282  
<212> DNA  
<213> human organism

<400> 139  
ctgcgatccc gcagggcagc gacgcgactc tggtgccggc cgtcttcttc cccccgagct 60  
ggcgctgcgc ggccgcaatg aactgggagc tgctgctgtg gctgctggtg ctgtgcgcgc 120  
tgctcctgtc cttggtgcaag ctgctgcgtc tcctgagggc tgacggcgac ctgacgctac 180  
tatgggccga gtggcaggga cgacgcccag aatgggagct gactgatatg gtggtgtggg 240  
tgactggagc ctcgagtgga attggtgagg agctggctta ccagttgtct aaactaggag 300  
tttctcttgt gctgtcagcc agaagagtgc atgagctgga aagggtgaaa agaagatgcc 360  
tagagaatgg caattaaaaaa gaaaaagata tacttgtttt gcccccttgac ctgaccgaca 420  
ctggttccca tgaagcggct accaaagctg ttctccagga gtttggtaga atcgacattc 480  
tggtaacaa tggtgaaatg tcccagcggt ctctgtgcat ggataccagc ttggatgtct 540  
acagaaagct aatagagctt aactacttag ggacgggtgc cttgacaaaaa tgtgttctgc 600  
ctcacatgtatcgaggaag caaggaaaga ttgttactgt gaatagcatc ctgggtatca 660  
tatctgtacc tctttccatt ggatactgtg ctagcaagca tgctctccgg ggtttttta 720  
atggccttcg aacagaacctt gcccacatacc caggtataat agtttctaacc atttgcccag 780  
gacctgtgca atcaaataattt gtggagaatt ccctagctgg agaagtcaca aagactata 840  
gcaataatgg agaccagtcc cacaagatga caaccagtgc ttgtgtggg ctgatgttaa 900  
tcagcatggc caatgatttg aaagaagttt ggatctcaga acaaccttc ttgttagtaa 960  
catatttgc gcaatacatg ccaacctggg cctgggtggat aaccaacaag atggggaaaga 1020  
aaaggattga gaactttaag agtgggtgtgg atgcagactc ttcttatttt aaaatctta 1080  
agacaaaaca tgactgaaaaa gagcacctgt actttcaag ccactggagg gagaatgga 1140  
aaacatgaaa acagcaatct tcttatgctt ctgaataatc aaagactaat ttgtgatttt 1200  
acttttaat agatatgact ttgcttccaa catggaatga aataaaaaat aaataataaa 1260  
agattgccat gaatcttgca aa 1282

<210> 140  
<211> 339  
<212> PRT  
<213> human organism

<400> 140

Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu  
1 5 10 15

Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu  
20 25 30

Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu  
35 40 45

Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu  
50 55 60

Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser  
65 70 75 80

Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu  
85 90 95

Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu  
100 105 110

Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu  
115 120 125

Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly Met Ser Gln Arg  
130 135 140

Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg Lys Leu Ile Glu  
145 150 155 160

Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His  
165 170 175

Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu  
180 185 190

Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His  
195 200 205

Ala Leu Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr  
210 215 220

Pro Gly Ile Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn  
225 230 235 240

Ile Val Glu Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn  
245 250 255

Asn Gly Asp Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu  
260 265 270

Met Leu Ile Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu  
275 280 285

Gln Pro Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp  
290 295 300

Ala Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe  
305 310 315 320

Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys Thr  
325 330 335

Lys His Asp

<210> 141  
<211> 1740  
<212> DNA  
<213> human organism

<400> 141  
atgagcagct gcaggtacaa cgggggcgtc atgcggccgc tcagcaactt gagcgcgtcc 60  
cgccggaacc tgcacgagat ggactcagag ggcgcagcccc tgcagcccc cgcgtctgtc 120  
ggaggaggta gccccgcgtc ctccccgtct gcagccgctg ccgcgcgcgc cgctgtttcg 180  
tcctcagccc ccgagatcgt ggtgtctaag cccgagcaca acaactccaa caacctggcg 240  
ctctatggaa ccggcggcgg aggcagcact ggaggaggcg gcggcgggtgg cgggagcggg 300  
cacggcagca gcagtggcac caagtccagc aaaaagaaaa accagaacat cggctacaag 360

ctggccacc	ggcgccccct	gttcgaaaag	cgcaagcggc	tcagcgacta	cgcgcatac	420
ttcgcatgt	tcggcatcgt	ggtcatggtc	atcgagaccg	agctgtcgta	gggcgcctac	480
gacaaggcgt	cgctgtattc	cttagctctg	aatgcctta	tcagtctctc	cacgatcatc	540
ctgctcggtc	tgatcatcgt	gtaccacgcc	aggaaatac	agttgttcat	ggtggacaat	600
ggagcagatg	actggagaat	agccatgact	tatgagcgta	ttttcttcat	ctgcttgaa	660
atactggtgt	gtgctattca	tcccataacct	gggaattata	cattcacatg	gacggcccg	720
cttgccctct	cctatgcccc	atccacaacc	accgctgatg	tggatattat	tttatctata	780
ccaatgttct	taagactcta	tctgattgcc	agagtcatgc	ttttacatag	caaactttc	840
actgatgcct	cctctagaag	cattggagca	cttaataaga	taaacttcaa	tacacgttt	900
gttatgaaga	ctttaatgac	tatatgccca	ggaactgtac	tcttggttt	tagtatctca	960
ttatggataa	ttgcccgcatg	gactgtccga	gcttgtgaaa	ggtaccatga	tcaacaggat	1020
gttactagca	acttccttgg	aggatgtgg	ttgatatcaa	taactttct	ctccattgg	1080
tatggtgaca	tggcacctaa	cacatactgt	ggaaaaggag	tctgcttact	tactggaatt	1140
atgggtgctg	gttgcacagc	cctgggtgta	gctgtagtgg	caaggaagct	agaacttacc	1200
aaagcagaaa	aacacgtgca	caatttcatg	atggatactc	agctgactaa	aagagtaaaa	1260
aatgcagctg	ccaatgtact	cagggaaaca	tggctaattt	acaaaaatac	aaagctagtg	1320
aaaaagatag	atcatgcaaa	agtaagaaaa	catcaacgaa	aattcctgca	agctattcat	1380
caattaagaa	gtgtaaaaat	ggagcagagg	aaactgaatg	accaagcaaa	cacttggtg	1440
gacttggcaa	agacccagaa	catcatgtat	gatatgattt	ctgacttaaa	cgaaaggagt	1500
gaagacttcg	agaagaggat	tgttaccctg	gaaacaaaac	tagagacttt	gattggtagc	1560
atccacgccc	tccctgggct	cataagccag	accatcaggc	agcagcagag	agatttcatt	1620
gaggctcaga	tggagagcta	cgacaagcac	gtcacttaca	atgctgagcg	gtcccggtcc	1680
tcgtccagga	ggcgccggtc	ctcttccaca	gcaccaccaa	cttcatcaga	gagtagctag	1740

<210> 142  
 <211> 579  
 <212> PRT  
 <213> human organism

<400> 142

Met Ser Ser Cys Arg Tyr Asn Gly Gly Val Met Arg Pro Leu Ser Asn  
 1 5 10 15

Leu Ser Ala Ser Arg Arg Asn Leu His Glu Met Asp Ser Glu Ala Gln  
20 25 30

Pro Leu Gln Pro Pro Ala Ser Val Gly Gly Gly Gly Ala Ser Ser  
35 40 45

Pro Ser Ala Ala Ala Ala Ala Ala Ala Val Ser Ser Ser Ala Pro  
50 55 60

Glu Ile Val Val Ser Lys Pro Glu His Asn Asn Ser Asn Asn Leu Ala  
65 70 75 80

Leu Tyr Gly Thr Gly Gly Gly Ser Thr Gly Gly Gly Gly Gly Gly  
85 90 95

Gly Gly Ser Gly His Gly Ser Ser Gly Thr Lys Ser Ser Lys Lys  
100 105 110

Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly His Arg Arg Ala Leu Phe  
115 120 125

Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala Leu Ile Phe Gly Met Phe  
130 135 140

Gly Ile Val Val Met Val Ile Glu Thr Glu Leu Ser Trp Gly Ala Tyr  
145 150 155 160

Asp Lys Ala Ser Leu Tyr Ser Leu Ala Leu Lys Cys Leu Ile Ser Leu  
165 170 175

Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile Val Tyr His Ala Arg Glu  
180 185 190

Ile Gln Leu Phe Met Val Asp Asn Gly Ala Asp Asp Trp Arg Ile Ala  
195 200 205

Met Thr Tyr Glu Arg Ile Phe Phe Ile Cys Leu Glu Ile Leu Val Cys  
210 215 220

Ala Ile His Pro Ile Pro Gly Asn Tyr Thr Phe Thr Trp Thr Ala Arg  
225 230 235 240

Leu Ala Phe Ser Tyr Ala Pro Ser Thr Thr Thr Ala Asp Val Asp Ile  
245 250 255

Ile Leu Ser Ile Pro Met Phe Leu Arg Leu Tyr Leu Ile Ala Arg Val  
260 265 270

Met Leu Leu His Ser Lys Leu Phe Thr Asp Ala Ser Ser Arg Ser Ile  
275 280 285

Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr Arg Phe Val Met Lys Thr  
290 295 300

Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe Ser Ile Ser  
305 310 315 320

Leu Trp Ile Ile Ala Ala Trp Thr Val Arg Ala Cys Glu Arg Tyr His  
325 330 335

Asp Gln Gln Asp Val Thr Ser Asn Phe Leu Gly Ala Met Trp Leu Ile  
340 345 350

Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met Val Pro Asn Thr  
355 360 365

Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile Met Gly Ala Gly  
370 375 380

Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys Leu Glu Leu Thr  
385 390 395 400

Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Thr Gln Leu Thr  
405 410 415

Lys Arg Val Lys Asn Ala Ala Asn Val Leu Arg Glu Thr Trp Leu  
420 425 430

Ile Tyr Lys Asn Thr Lys Leu Val Lys Lys Ile Asp His Ala Lys Val  
435 440 445

Arg Lys His Gln Arg Lys Phe Leu Gln Ala Ile His Gln Leu Arg Ser  
450 455 460

Val Lys Met Glu Gln Arg Lys Leu Asn Asp Gln Ala Asn Thr Leu Val  
465 470 475 480

Asp Leu Ala Lys Thr Gln Asn Ile Met Tyr Asp Met Ile Ser Asp Leu  
485 490 495

Asn Glu Arg Ser Glu Asp Phe Glu Lys Arg Ile Val Thr Leu Glu Thr  
500 505 510

Lys Leu Glu Thr Leu Ile Gly Ser Ile His Ala Leu Pro Gly Leu Ile  
515 520 525

Ser Gln Thr Ile Arg Gln Gln Gln Arg Asp Phe Ile Glu Ala Gln Met  
530 535 540

Glu Ser Tyr Asp Lys His Val Thr Tyr Asn Ala Glu Arg Ser Arg Ser  
545 550 555 560

Ser Ser Arg Arg Arg Ser Ser Ser Thr Ala Pro Pro Thr Ser Ser  
565 570 575

Glu Ser Ser

<210> 143  
<211> 1896  
<212> DNA  
<213> human organism

<400> 143  
atgcgcgccc tgccgtgcc cggcccgctc ctggcgctgc tgctgctcgc gtcctggcc 60  
gctcccgccg cccgcgccag cagagccgag tccgtctccg cgccgtggcc cgaacccgag 120  
cgcgagtcgc ggccaccgcc cggcccgggg cccggaaaca ccacccgggtt tgggtctggg 180  
gcggcgggccc gcagcggcag ctccagctcc aacagcagtgc gcgacgcctt ggtgacccgc 240  
atttccatcc tcctccgcga cctacccacc ctcaaggcag ccgtgatcgt ggcgttcgcc 300  
tttaccaccc tcctcatcgc ctgcctgctg ctgcgcgtct tcaggtcggg aaagaggta 360  
aagaagacac gcaagtatga tatcatcacc actccagcag agcgagtggaa atggcgcca 420  
ctaaatgaag aggatgatga agatgaggac tccacagttat tcgacatcaa atacagagtgc 480  
tccttgcggg ctgcactgag acgtcagctg ccagggtgcc agacgctact gacagttcct 540  
gtgcccccac ctttcatcct cgacattgac cttccagcaa gatgcagtgg aaggcctgat 600

ggtggaatca gacctggtaa aacctgtttc ccagcctggt ggcacccctgt ggaaagtgg	660
tcagctgcaa cctgggggtgt gaaggactgg acctggaaagc cctcttgcggt cgagggtgtt	720
gaaaccaaaa cgaacgttat gtataaaacc ccagctccat cgtgcgtgtc aggcacatgtc	780
tcagactgtc actggcaagc tcgtttccac gtcaccacaa tggagttgct tctgccaccc	840
tttgggcattc cctttaaagt gccccctact tctactcccc atggtttgc acaactgcag	900
ctgaatctca tggaaaagct ggattcctct gccttacgca gaaacacccg ggctccatct	960
gccaggtgct tgccactggt cctggcagaa atggcggctg ctgaaagtga cttccaaat	1020
ccttggtggc acttcagcgc cacaggctct ccaataaaaaa ccctttacac acaaaccatg	1080
agtaccttgg gcttggatgt tttctgtggt gccggccagc gggcacctt ttgtgaagac	1140
agagcagtga ctaaggtct ccaggtagc tctttctcca aacagctgcg ctggaaagcca	1200
gccctagaga gtgggtttcc ccatcatctc aggcttctca gagagtgtcc tccgctgagc	1260
accatcctg tcaggttggc tcgttcagat gcccggggac aagccagcct gacggggagg	1320
agggtgttgc ggctcccgcg gcagtctctg catggcggag gtcagcggg taccgcaact	1380
tgcctttgg ttttgaagat tctgttgagg cgccatcctc accttgaccc ttctacaaa	1440
atctgtctcc cctgctgtgc cgtggAACAC ctacggaaag ccaagagaag ctcagtgact	1500
gtccttgcgt cattttagca gagcccacaa aaggcagctg ctgcccacgg ggagccctgtc	1560
aaacgagggc ccagtggca attgaccaga cacacatgcc ctggctgggg gatcacacat	1620
gcgaacctgc agacaattcc agataccaa ggccaggaag gcccacgtga ggatgtcact	1680
caccctggag gagacttggc tgggtggca aatttctatt tggaggaaga gggttccag	1740
gatggcagat gccagaagat ggctctgatg tctgaggaag ggccacctag tttgacagga	1800
tgtgagaggc tcacagggttc ccatcaacttc tccagccatt ccaagtcttgc tcccttcctt	1860
tccccccgac agccctgtt tctgtccagg ccctga	1896

<210> 144  
 <211> 631  
 <212> PRT  
 <213> human organism  
  
 <400> 144

Met	Arg	Ala	Val	Pro	Leu	Pro	Ala	Pro	Leu	Leu	Pro	Leu	Leu	Leu	Leu
1				5					10						15

Ala Leu Leu Ala Ala Pro Ala Ala Arg Ala Ser Arg Ala Glu Ser Val  
20 25 30

Ser Ala Pro Trp Pro Glu Pro Glu Arg Glu Ser Arg Pro Pro Pro Gly  
35 40 45

Pro Gly Pro Gly Asn Thr Thr Arg Phe Gly Ser Gly Ala Ala Gly Gly  
50 55 60

Ser Gly Ser Ser Ser Ser Asn Ser Ser Gly Asp Ala Leu Val Thr Arg  
65 70 75 80

Ile Ser Ile Leu Leu Arg Asp Leu Pro Thr Leu Lys Ala Ala Val Ile  
85 90 95

Val Ala Phe Ala Phe Thr Thr Leu Leu Ile Ala Cys Leu Leu Leu Arg  
100 105 110

Val Phe Arg Ser Gly Lys Arg Leu Lys Lys Thr Arg Lys Tyr Asp Ile  
115 120 125

Ile Thr Thr Pro Ala Glu Arg Val Glu Met Ala Pro Leu Asn Glu Glu  
130 135 140

Asp Asp Glu Asp Glu Asp Ser Thr Val Phe Asp Ile Lys Tyr Arg Val  
145 150 155 160

Ser Leu Pro Ala Ala Leu Arg Arg Gln Leu Pro Gly Cys Gln Thr Leu  
165 170 175

Leu Thr Val Pro Val Pro Pro Phe Ile Leu Asp Ile Asp Leu Pro  
180 185 190

Ala Arg Cys Ser Gly Arg Pro Asp Gly Gly Ile Arg Pro Gly Lys Thr  
195 200 205

Cys Phe Pro Ala Trp Trp His Pro Val Glu Ser Trp Ser Ala Ala Thr  
210 215 220

Trp Gly Val Lys Asp Trp Thr Trp Lys Pro Ser Cys Val Gly Gly Val  
225 230 235 240

Glu Thr Lys Thr Asn Val Met Tyr Lys Thr Pro Ala Pro Ser Cys Val

245

250

255

Ser Gly Ile Cys Ser Asp Cys His Trp Gln Ala Arg Phe His Val Thr  
260 265 270

Thr Met Glu Leu Leu Pro Pro Phe Gly His Pro Phe Lys Val Pro  
275 280 285

Pro Thr Ser Thr Pro His Gly Phe Arg Gln Leu Gln Leu Asn Leu Met  
290 295 300

Glu Lys Leu Asp Ser Ser Ala Leu Arg Arg Asn Thr Arg Ala Pro Ser  
305 310 315 320

Ala Arg Cys Leu Pro Leu Val Leu Ala Glu Met Ala Ala Ala Glu Ser  
325 330 335

Asp Leu Pro Asn Pro Trp Trp His Phe Ser Ala Thr Gly Ser Pro Ile  
340 345 350

Lys Thr Leu Tyr Thr Gln Thr Met Ser Thr Leu Gly Leu Asp Val Phe  
355 360 365

Cys Gly Ala Gly Gln Arg Gly Thr Phe Cys Glu Asp Arg Ala Val Thr  
370 375 380

Lys Val Leu Gln Gly Ser Ser Phe Ser Lys Gln Leu Arg Trp Lys Pro  
385 390 395 400

Ala Leu Glu Ser Gly Phe Pro His His Leu Arg Leu Leu Arg Glu Cys  
405 410 415

Pro Pro Leu Ser Thr His Pro Val Arg Leu Ala Arg Ser Asp Ala Arg  
420 425 430

Gly Gln Ala Ser Leu Thr Gly Arg Arg Val Phe Arg Arg Pro Arg Gln  
435 440 445

Ser Leu His Gly Gly Ser Ala Gly Thr Ala Thr Cys Leu Leu Val  
450 455 460

Leu Lys Ile Leu Leu Arg Arg His Pro His Leu Asp Leu Phe Tyr Lys  
465 470 475 480

Ile Cys Leu Pro Cys Cys Ala Val Glu His Leu Arg Glu Ala Lys Arg  
485 490 495

Ser Ser Val Thr Val Leu Ala Ser Phe Glu Gln Ser Pro Gln Lys Ala  
500 505 510

Ala Ala Ala His Gly Glu Pro Val Lys Arg Gly Pro Ser Gly Gln Leu  
515 520 525

Thr Arg His Thr Cys Pro Gly Trp Gly Ile Thr His Ala Asn Leu Gln  
530 535 540

Thr Ile Pro Asp Thr Gln Gly Gln Glu Gly Pro Arg Glu Asp Val Thr  
545 550 555 560

His Pro Gly Gly Asp Leu Asp Gly Val Ala Asn Phe Tyr Leu Glu Glu  
565 570 575

Glu Gly Phe Gln Asp Gly Arg Cys Gln Lys Met Val Leu Met Ser Glu  
580 585 590

Glu Gly Pro Pro Ser Leu Thr Gly Cys Glu Arg Leu Thr Gly Ser His  
595 600 605

His Phe Ser Ser His Ser Lys Ser Trp Ser Phe Leu Ser Pro Arg Gln  
610 615 620

Pro Leu Phe Leu Ser Arg Pro  
625 630

<210> 145  
<211> 5133  
<212> DNA  
<213> human organism

<400> 145  
ggctgggctg cgaatagcgt gttcctctcc ggcggAACAC acacACCCGG cttggggct 60  
gttcctgaa gtccttcct ccacggagag cgctgagcgc cgccggaaat tccatcccac 120  
cgtagggcacg cagtcttgg aggtccccgg cgcaGACGC tcgggtgtccc cacactgcag 180  
caagacagag accccgggg aaccttgagc ttggAACAAAC cttgagcct ctgcagtccg 240  
aagagtggc gcagcagccc agcggaggcc aggcgcgcaa cctcgggcgc cggggcaagg 300

agagagtgc gggaggcgca gtcaggcgc ccggctcagg agcgggagga agttctcgcg 360  
gcgccgggag cgccgtggac gcgcctggg cgcacgccc ggcagcattc tccctggccc 420  
tcggactgt cctcggcgg caaggaggag cttgctggag tcttagaggc catccagagc 480  
cagcgagcag gagcgctgca tctccgcct cagctaggaa gggggagtgg cgctggcagg 540  
ctggagctgg gaacccagcg agcgcctgac cttcctcctc ctcttcctga ccctcttcgc 600  
gtcttggct ccggaggaag gttctagcgg ctgcaggagg tccccagacc catttccta 660  
gaaggctggt gatggatctg ctgctcctgc cgccgcccgg gcacttggag cgacccggcg 720  
gcgcgtgagc tgggctttgc tctccaccgc cctggcaaa ccccgccca gccccgcctg 780  
gcaccttgc ctgagtcctt ttcggttccc gacccaaagc caccagcgca cagggaggga 840  
ggaggaggtg gtcctcaggt gcagccccgc cgagatgtcc ggcgcagagcc tgctccacag 900  
cgtcttcctcc tgttcctcgc ccgcttcaag tagcgcggcc tggccaagg gcttctccaa 960  
gaggaagctg cgccagaccc gcagcctgga cccggccctg atcggcggct gcgggagcga 1020  
cgaggcgggc gcggagggca gtgcgcgggg agccacggcg ggccgcctct actccccatc 1080  
actccccagcc gagagtctcg gccctcgctt ggcttcctct tcccggggtc cgccccccag 1140  
ggccaccagg ctaccgcctc ctggacctct ttgctcgtcc ttctccacac ccagcacccc 1200  
gcaggagaag tcaccatccg gcagcttca ctttgactat gaggtcccc tgggtcgcgg 1260  
cgccctcaag aagagcatgg cctggaccc gccttctgtc ctggccgggc cagccagtag 1320  
ccgaagcgct tccagcatcc tctgttcatc cgggggaggc ccaatggca tttcgcttc 1380  
tcctaggagg tggctccagc agaggaagtt ccagtcctt cccgacagtc gcgggcaccc 1440  
ctacgtcgtg tggaaatccg agggtgattt cacctggaac agcatgtcag gccgcagtgt 1500  
gcggctgagg tcagtcctt cccagagtct ctcagagctg gagagggccc ggctgcagga 1560  
agtgcctttt tatcagttgc aacaggactg tgacctgagc tgtcagatca ccattccaa 1620  
agatggacaa aagagaaaga aatcttaag aaagaaactg gattcaactg gaaaggagaa 1680  
aaacaaagac aaagaattca tcccacaggc atttggaatg cccttatccc aagtcatgc 1740  
gaatgacagg gcctataaac tcaagcagga cttgcagagg gacgagcaga aagatgcattc 1800  
tgactttgtg gcttcctcc tcccatgg aaataaaaga caaaacaaag aactctcaag 1860  
cagtaactca tctctcagct caacctcaga aacaccgaat gagtcaacgt ccccaaacac 1920  
cccgaaaccg gtcctcggg ctaggaggag gggtgccatg tcagtggatt ctatcaccga 1980

tcttgatgac aatcagtctc gactactaga agctttacaa ctttccttgc ctgctgaggc 2040  
tcaaagtaaa aaggaaaaag ccagagataa gaaactcagt ctgaatccta tttacagaca 2100  
ggtcccttagg ctggtgacca gctgctgtca gcacctagaa aaacatggcc tccagacagt 2160  
ggggatattc cgagttggaa gctaaaaaaaaa gagagtgaga caattacgtg aggaatttga 2220  
ccgtgggatt gatgtctctc tggaggagga gcacagtgtt catgatgtgg cagccttgc 2280  
gaaagagttc ctgagggaca tgccagaccc ctttcacc accggagctgt acacagctt 2340  
catcaacact ctcttggg aggccggagga acagctggc accttgcagc tcctcatata 2400  
ccttctacct ccctgcaact gcgcacccct ccaccgcctg ctacagttcc tctccatcgt 2460  
ggccaggcat gccgatgaca acatcagcaa agatggcaa gaggtcactg ggaataaaat 2520  
gacatctcta aacttagcca ccatatttgg acccaacctg ctgcacaaggc agaagtcattc 2580  
agacaaagaa ttctcagttc agagttcagc ccgggctgag gagagcacgg ccatcatcg 2640  
tgttgcaaa aagatgattt aaaaattatga agccctgttc atggcccc cagatctcca 2700  
gaacgaagtg ctgatcagcc tggtagagac cgatcctgat gtcgtggact atttactcag 2760  
aagaaaggct tcccaatcat caagccctga catgctgcag tcggaagttt cttttccgt 2820  
gggagggagg cattcatcta cagactccaa caaggcctcc agcggagaca tctccccta 2880  
tgacaacaac tccccagtgc tgtctgagcg ctccctgctg gctatgcaag aggacgcggc 2940  
cccggggggc tcggagaagc ttacagagt gccaggcag tttatgctgg tggccactt 3000  
gtcgctgtca aagtcaaggg aaagttctcc tggaccaagg cttggaaag atctgtcaga 3060  
ggagccttgc gatatctggg gaacttggca ttcaacatta aaaagcggat ccaaagaccc 3120  
aggaatgaca gttcccttg gagacattt tgaaagcagc tccctaagag cggggccctg 3180  
ctcccttct caaggaaacc tgtccccaaa ttggcctcg tggcagggga gccccgcaga 3240  
gctggacagc gacacgcagg gggctcgag gactcaggcc gcagcccccg cgacggaggg 3300  
cagggcccac cctgcgtgt cgcgccctg cagcacgccc cacgtccagg tggcagggaa 3360  
agccgagcgg cccacggcca ggtcgagca gtacttgacc ctgagcggcg cccacgacct 3420  
cagcgagagt gagctggatg tggccggct gcagagccgg gccacacctc agtgc当地 3480  
accccatggg agtggggagg atgacaagcg gccccgcct ccataccgg gcccaggaa 3540  
gcccgccgca gcggcagcct ggatccagg gccccggaa ggcgtggaga cacccacgg 3600  
ccagggaggc caagcagccg agcgagagca gcaggtcacf cagaaaaaac tgagcagcgc 3660  
caactccctg ccagcggcg agcaggacag tccgcgcctg gggacgctg gctggctcga 3720

ctggcagaga gagcgctggc agatctggg gctcctgtcg accgacaacc ccgatgccct	3780
gcccggagacg ctggtctgag cccgcaccca gccgagcccc ccctgccccg agccccccgc	3840
cctccagccc aggggggacc gtgggtggtg gccactggca cacttagtgt tcttcattca	3900
cacttctcaa aagtgacaca agagaaatcc agttcaccta cagaggtaga gcactcacgc	3960
ccccggcatt gagaataagg ttccattgcg tagccagcct tagaaaaaac aaacagaacc	4020
caaaccagat ggcaatgtcc aatctaaaaa cgtcccttggctctataa tataagatac	4080
aactcttgct tggtagtgc taaccgtatt tatgtgtctt cggtttgac tattgtgtat	4140
tctgtacat attatgtata atcatatatg atatattcac aaagagaaaa caaaaggaac	4200
ttttaaaaaa aaaatcactt cacttatatt aagcaatgag atatactaaa caatgagatt	4260
ctatagaatg ttctagaatg tgccacaagcg gggttctgtg cttttgccat agcttataa	4320
ctggggataa cccttccttc gataccaaac actaacaaga ggaaggcagaa tatgagaagc	4380
catatttta cataggagtc agataaaaaa agaaaaatca ctgaatgctt ttagatattg	4440
aatacgtttt cagaaaaatg ctaaatctga tagattacga aatataattt tagaacttgt	4500
tttagaaagga ttcaatgttac caaacaagaa aaaggcagtgc ctcacaaag aaattaagaa	4560
gttgtccgtc ccacgttaca tcaaatttcag ttttatata gccatataata atatataattt	4620
ataatgtata attttatgt attttcaaa actacaaact ggaatccaac tataaagtgt	4680
ttaagaatct acacagaata ttcaaaattt agaacatgtt tttccctt gccccataat	4740
cagtatttgc caaattacat gcaattcctt aaaaactaaa tcacattggt aaaaggccta	4800
cagctttgtt cttacattgtt gccaaaggctt gaggaaatgtt tttctttcga attttatgt	4860
gtattgtaaa atgttctacc gtacttttagt agtttgaagt tttcaagtgc ataactattt	4920
ttgaccagca gaaggcgata cgcttcagta ttttatgcaaa tttttttca cttcgaaggg	4980
aaagtgtatt ataaaaaaaaa atttttttt tttaaaacat gctactctta attttcatgt	5040
tgggtatgaa attcccaatgtt gtgtttctta aggttctatc ttgtgccatg atgaataaaa	5100
agttaagcaa aaaaaaaaaa aaaaaaaaaa aaa	5133

<210> 146  
 <211> 974  
 <212> PRT  
 <213> human organism

<400> 146

Met Ser Ala Gln Ser Leu Leu His Ser Val Phe Ser Cys Ser Ser Pro  
1 5 10 15

Ala Ser Ser Ser Ala Ala Ser Ala Lys Gly Phe Ser Lys Arg Lys Leu  
20 25 30

Arg Gln Thr Arg Ser Leu Asp Pro Ala Leu Ile Gly Gly Cys Gly Ser  
35 40 45

Asp Glu Ala Gly Ala Glu Gly Ser Ala Arg Gly Ala Thr Ala Gly Arg  
50 55 60

Leu Tyr Ser Pro Ser Leu Pro Ala Glu Ser Leu Gly Pro Arg Leu Ala  
65 70 75 80

Ser Ser Ser Arg Gly Pro Pro Pro Arg Ala Thr Arg Leu Pro Pro Pro  
85 90 95

Gly Pro Leu Cys Ser Ser Phe Ser Thr Pro Ser Thr Pro Gln Glu Lys  
100 105 110

Ser Pro Ser Gly Ser Phe His Phe Asp Tyr Glu Val Pro Leu Gly Arg  
115 120 125

Gly Gly Leu Lys Lys Ser Met Ala Trp Asp Leu Pro Ser Val Leu Ala  
130 135 140

Gly Pro Ala Ser Ser Arg Ser Ala Ser Ser Ile Leu Cys Ser Ser Gly  
145 150 155 160

Gly Gly Pro Asn Gly Ile Phe Ala Ser Pro Arg Arg Trp Leu Gln Gln  
165 170 175

Arg Lys Phe Gln Ser Pro Pro Asp Ser Arg Gly His Pro Tyr Val Val  
180 185 190

Trp Lys Ser Glu Gly Asp Phe Thr Trp Asn Ser Met Ser Gly Arg Ser  
195 200 205

Val Arg Leu Arg Ser Val Pro Ile Gln Ser Leu Ser Glu Leu Glu Arg  
210 215 220

Ala Arg Leu Gln Glu Val Pro Phe Tyr Gln Leu Gln Gln Asp Cys Asp

225                    230                    235                    240

Leu Ser Cys Gln Ile Thr Ile Pro Lys Asp Gly Gln Lys Arg Lys Lys  
245                    250                    255

Ser Leu Arg Lys Lys Leu Asp Ser Leu Gly Lys Glu Lys Asn Lys Asp  
260                    265                    270

Lys Glu Phe Ile Pro Gln Ala Phe Gly Met Pro Leu Ser Gln Val Ile  
275                    280                    285

Ala Asn Asp Arg Ala Tyr Lys Leu Lys Gln Asp Leu Gln Arg Asp Glu  
290                    295                    300

Gln Lys Asp Ala Ser Asp Phe Val Ala Ser Leu Leu Pro Phe Gly Asn  
305                    310                    315                    320

Lys Arg Gln Asn Lys Glu Leu Ser Ser Ser Asn Ser Ser Leu Ser Ser  
325                    330                    335

Thr Ser Glu Thr Pro Asn Glu Ser Thr Ser Pro Asn Thr Pro Glu Pro  
340                    345                    350

Ala Pro Arg Ala Arg Arg Arg Gly Ala Met Ser Val Asp Ser Ile Thr  
355                    360                    365

Asp Leu Asp Asp Asn Gln Ser Arg Leu Leu Glu Ala Leu Gln Leu Ser  
370                    375                    380

Leu Pro Ala Glu Ala Gln Ser Lys Lys Glu Lys Ala Arg Asp Lys Lys  
385                    390                    395                    400

Leu Ser Leu Asn Pro Ile Tyr Arg Gln Val Pro Arg Leu Val Asp Ser  
405                    410                    415

Cys Cys Gln His Leu Glu Lys His Gly Leu Gln Thr Val Gly Ile Phe  
420                    425                    430

Arg Val Gly Ser Ser Lys Lys Arg Val Arg Gln Leu Arg Glu Glu Phe  
435                    440                    445

Asp Arg Gly Ile Asp Val Ser Leu Glu Glu Glu His Ser Val His Asp  
450                    455                    460

Val Ala Ala Leu Leu Lys Glu Phe Leu Arg Asp Met Pro Asp Pro Leu  
465 470 475 480

Leu Thr Arg Glu Leu Tyr Thr Ala Phe Ile Asn Thr Leu Leu Leu Glu  
485 490 495

Pro Glu Glu Gln Leu Gly Thr Leu Gln Leu Leu Ile Tyr Leu Leu Pro  
500 505 510

Pro Cys Asn Cys Asp Thr Leu His Arg Leu Leu Gln Phe Leu Ser Ile  
515 520 525

Val Ala Arg His Ala Asp Asp Asn Ile Ser Lys Asp Gly Gln Glu Val  
530 535 540

Thr Gly Asn Lys Met Thr Ser Leu Asn Leu Ala Thr Ile Phe Gly Pro  
545 550 555 560

Asn Leu Leu His Lys Gln Lys Ser Ser Asp Lys Glu Phe Ser Val Gln  
565 570 575

Ser Ser Ala Arg Ala Glu Glu Ser Thr Ala Ile Ile Ala Val Val Gln  
580 585 590

Lys Met Ile Glu Asn Tyr Glu Ala Leu Phe Met Val Pro Pro Asp Leu  
595 600 605

Gln Asn Glu Val Leu Ile Ser Leu Leu Glu Thr Asp Pro Asp Val Val  
610 615 620

Asp Tyr Leu Leu Arg Arg Lys Ala Ser Gln Ser Ser Ser Pro Asp Met  
625 630 635 640

Leu Gln Ser Glu Val Ser Phe Ser Val Gly Gly Arg His Ser Ser Thr  
645 650 655

Asp Ser Asn Lys Ala Ser Ser Gly Asp Ile Ser Pro Tyr Asp Asn Asn  
660 665 670

Ser Pro Val Leu Ser Glu Arg Ser Leu Leu Ala Met Gln Glu Asp Ala  
675 680 685

Ala Pro Gly Gly Ser Glu Lys Leu Tyr Arg Val Pro Gly Gln Phe Met  
690 695 700

Leu Val Gly His Leu Ser Ser Ser Lys Ser Arg Glu Ser Ser Pro Gly  
705 710 715 720

Pro Arg Leu Gly Lys Asp Leu Ser Glu Glu Pro Phe Asp Ile Trp Gly  
725 730 735

Thr Trp His Ser Thr Leu Lys Ser Gly Ser Lys Asp Pro Gly Met Thr  
740 745 750

Gly Ser Ser Gly Asp Ile Phe Glu Ser Ser Ser Leu Arg Ala Gly Pro  
755 760 765

Cys Ser Leu Ser Gln Gly Asn Leu Ser Pro Asn Trp Pro Arg Trp Gln  
770 775 780

Gly Ser Pro Ala Glu Leu Asp Ser Asp Thr Gln Gly Ala Arg Arg Thr  
785 790 795 800

Gln Ala Ala Ala Pro Ala Thr Glu Gly Arg Ala His Pro Ala Val Ser  
805 810 815

Arg Ala Cys Ser Thr Pro His Val Gln Val Ala Gly Lys Ala Glu Arg  
820 825 830

Pro Thr Ala Arg Ser Glu Gln Tyr Leu Thr Leu Ser Gly Ala His Asp  
835 840 845

Leu Ser Glu Ser Glu Leu Asp Val Ala Gly Leu Gln Ser Arg Ala Thr  
850 855 860

Pro Gln Cys Gln Arg Pro His Gly Ser Gly Arg Asp Asp Lys Arg Pro  
865 870 875 880

Pro Pro Pro Tyr Pro Gly Pro Gly Lys Pro Ala Ala Ala Ala Trp  
885 890 895

Ile Gln Gly Pro Pro Glu Gly Val Glu Thr Pro Thr Asp Gln Gly Gly  
900 905 910

Gln Ala Ala Glu Arg Glu Gln Gln Val Thr Gln Lys Lys Leu Ser Ser  
915 920 925

Ala Asn Ser Leu Pro Ala Gly Glu Gln Asp Ser Pro Arg Leu Gly Asp  
930 935 940

Ala Gly Trp Leu Asp Trp Gln Arg Glu Arg Trp Gln Ile Trp Glu Leu  
945 950 955 960

Leu Ser Thr Asp Asn Pro Asp Ala Leu Pro Glu Thr Leu Val  
965 970

<210> 147

<211> 2397

<212> DNA

<213> human organism

<400> 147

cccccgagcc ggcggcggc tgccgccc gcagcgctc cgctccgcca actccgccc 60

cttaaattgg actccttagat ccgcgagggc gcggcgac cgagcagcgg ctcttcagc 120

atggcaacc ccaggggcc aatattccca cttagccaca gctccagcat cctctctgtg 180

ggctgttcac caactgtaca accaccattt cactgtggac attactccct cttacagata 240

tgggagacat gggagatcca ccaaaaaaaa aacgtctgat ttccctatgt gttgggtcg 300

gcaatcagat tcacgatcag tatattctga gggttctcc ggatttggaa tggcatgcgg 360

catgtttgaa atgtgcggag tctaattcagt atttggacga gagctgtaca tgctttgtt 420

gggatggaa aacctactgt aaaagagatt atatcagggt gtacgggatc aaatgcgcc 480

agtgcagcat cggcttcagc aagaacgact tcgtgatgcg tgccgctcc aaggtgtatc 540

acatcgagtg tttccgtgt gtggcctgca gccgcccagct catccctggg gacgaattt 600

cgcttcggga ggacggtctc ttctgcccag cagaccacga tgtggtggag agggccagtc 660

taggcgctgg cgaccggctc agtccccctgc atccagcgcg gccactgcaa atggcagcgg 720

agcccatctc cgccaggcag ccagccctgc ggccccacgt ccacaagcag ccggagaaga 780

ccaccccggt gcggactgtg ctgaacgaga agcagctgca caccttgcgg acctgctacg 840

ccgcaaaacc cggccagat gcgcctatga aggagcaact ggttagagatg acgggcctca 900

gtccccgtgt gatccgggtc tggttcaaa acaagcggtg caaggacaag aagcgaagca 960

tcatgatgaa gcaactccag cagcagcagc ccaatgacaa aactaatatc cagggatga 1020

caggaactcc catggtggt ggcagtccag agagacacga cggtggtt caggctaacc 1080

cagtggaaat	acaaaggttac	cagccacctt	ggaaagtact	gagcgacttc	gccttcaga	1140
gtgacataga	tcagcctgct	tttcagcaac	tggtaattt	ttcagaagga	ggaccggct	1200
ctaattccac	tggcagtgaa	gtagcatcaa	tgtcctctca	acttccagat	acacctaaaca	1260
gcatggtagc	cagtcctatt	gaggcatgag	gaacattcat	tctgtatTTT	tttccctgt	1320
tggagaaaat	gggaaattat	aatgtcgaac	tctgaaacaa	aagtatTTA	cgaccaggc	1380
aatgaaaact	gaatcaagaa	atgaatgctc	catgaaatgc	acgaagtctg	tttaatgac	1440
aaggtagat	ggttagcaaca	ctgtgaagac	aatcatggg	ttttactaga	attaaacaac	1500
aaacaaaacg	caaaaacccag	tatATGCTAT	tcaatgatct	tagaagtact	aaaaaaa	1560
gacgtttta	aaacgttagag	gatttatatt	caaggatctc	aaagaaagca	ttttcatttc	1620
actgcacatc	tagagaaaaa	caaaaataga	aaattttcta	gtccatccta	atctgaatgg	1680
tgctgtttct	atattggtca	ttgccttgcc	aaacaggagc	tccagcaaaa	gcgcaggaag	1740
agagactggc	ctccttggct	gaaagagtcc	tttcaggaag	gtggagctgc	attggttga	1800
tatgtttaaa	gttgacttta	acaaggggtt	aattgaaatc	ctgggtctct	ttgcctgtcc	1860
tgttagctgg	ttatTTTTA	cttgcccccc	tccccacttt	tttgagatc	catcctttat	1920
caagaagtct	gaagcgacta	taaaggTTTT	tgaattcaga	tttaaaaacc	aacttataaaa	1980
gcattgcaac	aaggTTACCT	ctatTTGCC	acaaggGTCT	cgggattgtg	tttgacttgt	2040
gtctgtccaa	gaactttcc	ccaaagatg	tgtatagtta	ttggTTaaaa	tgactgttt	2100
ctctctctat	ggaaataaaa	aggaaaaaaa	aaaggaaact	tttttgttt	gctcttgcatt	2160
tgcaaaaatt	ataaaagtaat	ttattattta	ttgtcggaag	acttgcact	tttcatgtca	2220
tttgacattt	tttggTTGCT	gaagtgaaaa	aaaaagataa	aggttgtacg	gtggTCTTG	2280
aattatatgt	ctaattctat	gtgtttgtc	ttttcttaa	atattatgtg	aaatcaaagc	2340
gccatatgt	gaattatatc	ttcaggacta	tttcactaat	aaacatttgg	catagat	2397

<210> 148  
 <211> 346  
 <212> PRT  
 <213> human organism

<400> 148

Met	Gly	Asp	Pro	Pro	Lys	Lys	Arg	Leu	Ile	Ser	Leu	Cys	Val	Gly
1					5			10				15		

Cys Gly Asn Gln Ile His Asp Gln Tyr Ile Leu Arg Val Ser Pro Asp  
20 25 30

Leu Glu Trp His Ala Ala Cys Leu Lys Cys Ala Glu Cys Asn Gln Tyr  
35 40 45

Leu Asp Glu Ser Cys Thr Cys Phe Val Arg Asp Gly Lys Thr Tyr Cys  
50 55 60

Lys Arg Asp Tyr Ile Arg Leu Tyr Gly Ile Lys Cys Ala Lys Cys Ser  
65 70 75 80

Ile Gly Phe Ser Lys Asn Asp Phe Val Met Arg Ala Arg Ser Lys Val  
85 90 95

Tyr His Ile Glu Cys Phe Arg Cys Val Ala Cys Ser Arg Gln Leu Ile  
100 105 110

Pro Gly Asp Glu Phe Ala Leu Arg Glu Asp Gly Leu Phe Cys Arg Ala  
115 120 125

Asp His Asp Val Val Glu Arg Ala Ser Leu Gly Ala Gly Asp Pro Leu  
130 135 140

Ser Pro Leu His Pro Ala Arg Pro Leu Gln Met Ala Ala Glu Pro Ile  
145 150 155 160

Ser Ala Arg Gln Pro Ala Leu Arg Pro His Val His Lys Gln Pro Glu  
165 170 175

Lys Thr Thr Arg Val Arg Thr Val Leu Asn Glu Lys Gln Leu His Thr  
180 185 190

Leu Arg Thr Cys Tyr Ala Ala Asn Pro Arg Pro Asp Ala Leu Met Lys  
195 200 205

Glu Gln Leu Val Glu Met Thr Gly Leu Ser Pro Arg Val Ile Arg Val  
210 215 220

Trp Phe Gln Asn Lys Arg Cys Lys Asp Lys Lys Arg Ser Ile Met Met  
225 230 235 240

Lys Gln Leu Gln Gln Gln Pro Asn Asp Lys Thr Asn Ile Gln Gly

245

250

255

Met Thr Gly Thr Pro Met Val Ala Ala Ser Pro Glu Arg His Asp Gly  
260 265 270

Gly Leu Gln Ala Asn Pro Val Glu Val Gln Ser Tyr Gln Pro Pro Trp  
275 280 285

Lys Val Leu Ser Asp Phe Ala Leu Gln Ser Asp Ile Asp Gln Pro Ala  
290 295 300

Phe Gln Gln Leu Val Asn Phe Ser Glu Gly Gly Pro Gly Ser Asn Ser  
305 310 315 320

Thr Gly Ser Glu Val Ala Ser Met Ser Ser Gln Leu Pro Asp Thr Pro  
325 330 335

Asn Ser Met Val Ala Ser Pro Ile Glu Ala  
340 345

<210> 149

<211> 1886

<212> DNA

<213> human organism

<400> 149

gcggagctct gccttgaga ttctcagtgc tgccgatcat gtccctaagg ggcagcctct 60

cgcgtctcct ccagacgcga gtgcattcca tcctgaagaa atccgtccac tccgtggctg 120

tgataggagc cccgttctca caagggcaga aaagaaaagg agtggagcat ggtcccgtg 180

ccataagaga agctggcttg atgaaaaggc tctccagttt gggctgccac ctaaaagact 240

ttggagattt gagtttact ccagtccccca aagatgatct ctacaacaac ctgatagtga 300

atccacgctc agtgggtctt gccaaccagg aactggctga ggtggtagc agagctgtgt 360

cagatggcta cagctgtgtc acactggag gagaccacag cctggcaatc ggtaccatta 420

gtggccatgc ccgacactgc ccagaccttt gtgttgtctg ggttgatgcc catgctgaca 480

tcaacacacc ccttaccact tcatcaggaa atctccatgg acagccagg tcatttctcc 540

tcagagaact acaggataag gtaccacaac tcccaggatt ttcctggatc aaaccttgc 600

tctcttctgc aagtattgtg tatattggtc tgagagacgt ggaccctcct gaacattta 660

ttttaaagaa ctatgatatc cagtattttt ccatgagaga tattgatcga cttggatcc 720

agaaggtcat ggaacgaaca tttgatctgc tgattggcaa gagacaaaga ccaatccatt	780
ttagtttga tattgatgca tttgacccta cactggctcc agccacagga actcctgttg	840
tcggggact aacctatcga gaaggcatgt atattgctga ggaaatacac aatacagggt	900
tgctatcagc actggatctt gttgaagtca atcctcagtt ggccacactca gaggaagagg	960
cgaagactac agctaacctg gcagtagatg tgattgcttc aagcttttgt cagacaagag	1020
aaggagggca tattgtctat gaccaacttc ctactcccag ttcaccagat gaatcagaaa	1080
atcaagcacg tgtgagaatt taggagacac tgtgcactga catgtttcac aacaggcatt	1140
ccagaattat gaggcattga gggatagat gaatactaaa tggttgtctg ggtcaatact	1200
gccttaatga gaacatttac acatttcac aattgtaaag tttccctct atttgggtga	1260
ccaatactac tgtaaatgta ttgggtttt tgcagttcac agggtattaa tatgctacag	1320
tactatgtaa atttaaagaa gtcataaaca gcatttatta cttggtata tcatactgg	1380
cttggttgtg ttgttccttc acatthaagt ggttttcat cttccctccc tcctcccaca	1440
gcctggctat acagtgcac cttgaactgt cagccacag cagcaatatg cttattctat	1500
ccacatccct aacatcatgc attcacaagg tcaaagttct ggtccacaaa ccctcccta	1560
tagaagttca atggctgcga aagaatttgt agtaaaccag gcctcccagg atggcgagct	1620
ccagtaagat gataatggaa agcagcagct tggataacc ttccttctaa acattgggg gtagacctg	1680
agtggggagt agtcagaagt ttggataacc ttccttctaa acattgggg gtagacctg	1740
ggaccacggc tggataactct gaggctgtat gttgatcac acagccactt agcaggaagt	1800
actcataagg ttcttagct gtcacttagg gataacactg tctacactac agaaatgtta	1860
aactgagaca ataaaaccca aagcat	1886

<210> 150  
 <211> 354  
 <212> PRT  
 <213> human organism

<400> 150

Met Ser Leu Arg Gly Ser Leu Ser Arg Leu Leu Gln Thr Arg Val His			
1	5	10	15

Ser Ile Leu Lys Lys Ser Val His Ser Val Ala Val Ile Gly Ala Pro		
20	25	30

Phe Ser Gln Gly Gln Lys Arg Lys Gly Val Glu His Gly Pro Ala Ala

35

40

45

Ile Arg Glu Ala Gly Leu Met Lys Arg Leu Ser Ser Leu Gly Cys His  
50 55 60

Leu Lys Asp Phe Gly Asp Leu Ser Phe Thr Pro Val Pro Lys Asp Asp  
65 70 75 80

Leu Tyr Asn Asn Leu Ile Val Asn Pro Arg Ser Val Gly Leu Ala Asn  
85 90 95

Gln Glu Leu Ala Glu Val Val Ser Arg Ala Val Ser Asp Gly Tyr Ser  
100 105 110

Cys Val Thr Leu Gly Gly Asp His Ser Leu Ala Ile Gly Thr Ile Ser  
115 120 125

Gly His Ala Arg His Cys Pro Asp Leu Cys Val Val Trp Val Asp Ala  
130 135 140

His Ala Asp Ile Asn Thr Pro Leu Thr Thr Ser Ser Gly Asn Leu His  
145 150 155 160

Gly Gln Pro Val Ser Phe Leu Leu Arg Glu Leu Gln Asp Lys Val Pro  
165 170 175

Gln Leu Pro Gly Phe Ser Trp Ile Lys Pro Cys Ile Ser Ser Ala Ser  
180 185 190

Ile Val Tyr Ile Gly Leu Arg Asp Val Asp Pro Pro Glu His Phe Ile  
195 200 205

Leu Lys Asn Tyr Asp Ile Gln Tyr Phe Ser Met Arg Asp Ile Asp Arg  
210 215 220

Leu Gly Ile Gln Lys Val Met Glu Arg Thr Phe Asp Leu Leu Ile Gly  
225 230 235 240

Lys Arg Gln Arg Pro Ile His Leu Ser Phe Asp Ile Asp Ala Phe Asp  
245 250 255

Pro Thr Leu Ala Pro Ala Thr Gly Thr Pro Val Val Gly Gly Leu Thr  
260 265 270

Tyr Arg Glu Gly Met Tyr Ile Ala Glu Glu Ile His Asn Thr Gly Leu  
275 280 285

Leu Ser Ala Leu Asp Leu Val Glu Val Asn Pro Gln Leu Ala Thr Ser  
290 295 300

Glu Glu Glu Ala Lys Thr Thr Ala Asn Leu Ala Val Asp Val Ile Ala  
305 310 315 320

Ser Ser Phe Gly Gln Thr Arg Glu Gly Gly His Ile Val Tyr Asp Gln  
325 330 335

Leu Pro Thr Pro Ser Ser Pro Asp Glu Ser Glu Asn Gln Ala Arg Val  
340 345 350

Arg Ile

<210> 151  
<211> 1554  
<212> DNA  
<213> human organism

<400> 151	
aattatataat ttttactcta tgggtttttt tctttccgtt gctggcggaa	60
gaggcacgtg cgctgctgaa tggagctggg cgctgggtgc tacgagcagg tcctctttgg	120
gttcgctgta cacccggagc ccaaggcttg cggcgaccac gagcaatgga ctcttgtggc	180
tgacttcact caccatgctc acactgcctc cttgtcagca gtagctgtaa atagtcgttt	240
tgtggtcact gggagcaaag atgaaacaat tcacattt gacataaaaa agaagattga	300
gcatggggct ctagtgcattt acagtggtagtac aataacttgc ctgaaattct atggcaacag	360
gcatttaatc agtggagcgg aagatggact catctgtatc tggatgcaa agaaatggga	420
atgcctgaag tcaattaaag ctcacaaaagg acaggtgacc ttcccttctt ttcacccatc	480
tggcaagttt gcccctgtcgg ttggtaga taaaacttta agaacgtgga atctttaga	540
aggaagatca gcattcataa aaaatataaa acaaaaatgct cacatagtag aatggcccc	600
aagaggagag cagtagttag ttatcataca gaataaaata gacatctatc agcttgacac	660
tgcattccattt agtggcacca tcacaaaatga aaagagaattt ccctctgtta aatttcttcc	720
agagtctgtc cttgcagtgg ctggagatga agaagttata aggtttttt actgtgattc	780

actagtgtgc ctctgcgaat tttaagctca tgaaaacagg gtaaaggaca tgttcagttt	840
tgaaattcca gagcatcatg ttattgttc agcatcgagt gatggttca tcaaaatgtg	900
gaagcttaag caggataaga aagttccccc atcttactc tgtgaaataa acactaatgc	960
caggctgacg tgtcttggag tgtggctaga caaagtggca gacatgaaaaa gccttcctcc	1020
agctgcagag ctttctcctg taagtaaaga acagtccaaa attggcaaaa aggagcctgg	1080
tgacacagtg cacaaagaag aaaagcggtc aaaacctaac acaaagaaac gcggttAAC	1140
aggtgacagt aagaaagcaa caaaagaaag tggcctgata tcaaccaaga agagaaaaat	1200
ggtagaaatg ttggaaaaga agaggaaaaa gaagaaaata aaaacaatgc agtgaatcac	1260
agatgtctcc tgaaagaact cttagatg aaatcattct actcaaatgt accttaattt	1320
ttttttcc ctgagtaaaa gcaagaaaatt tcttccttg gaaaaaatat atatattaaa	1380
aaaccactt tagatggttt ttttaaaaa aaaaaaaaaa actggtaaaa ttactttgg	1440
cagacagtgt ttatgaatt atgtatcatg ttgatatata atatgttaat gtgtcatgta	1500
attttactt tgtacaaagc aaataaagat ctttctcaaa aaaaaaaaaa aaaa	1554

<210> 152

<211> 391

<212> PRT

<213> human organism

<400> 152

Met Glu Leu Val Ala Gly Cys Tyr Glu Gln Val Leu Phe Gly Phe Ala			
1	5	10	15

Val His Pro Glu Pro Lys Ala Cys Gly Asp His Glu Gln Trp Thr Leu			
20	25	30	

Val Ala Asp Phe Thr His His Ala His Thr Ala Ser Leu Ser Ala Val			
35	40	45	

Ala Val Asn Ser Arg Phe Val Val Thr Gly Ser Lys Asp Glu Thr Ile			
50	55	60	

His Ile Tyr Asp Met Lys Lys Ile Glu His Gly Ala Leu Val His			
65	70	75	80

His Ser Gly Thr Ile Thr Cys Leu Lys Phe Tyr Gly Asn Arg His Leu			
85	90	95	

Ile Ser Gly Ala Glu Asp Gly Leu Ile Cys Ile Trp Asp Ala Lys Lys  
100 105 110

Trp Glu Cys Leu Lys Ser Ile Lys Ala His Lys Gly Gln Val Thr Phe  
115 120 125

Leu Ser Ile His Pro Ser Gly Lys Leu Ala Leu Ser Val Gly Thr Asp  
130 135 140

Lys Thr Leu Arg Thr Trp Asn Leu Val Glu Gly Arg Ser Ala Phe Ile  
145 150 155 160

Lys Asn Ile Lys Gln Asn Ala His Ile Val Glu Trp Ser Pro Arg Gly  
165 170 175

Glu Gln Tyr Val Val Ile Ile Gln Asn Lys Ile Asp Ile Tyr Gln Leu  
180 185 190

Asp Thr Ala Ser Ile Ser Gly Thr Ile Thr Asn Glu Lys Arg Ile Ser  
195 200 205

Ser Val Lys Phe Leu Ser Glu Ser Val Leu Ala Val Ala Gly Asp Glu  
210 215 220

Glu Val Ile Arg Phe Phe Asp Cys Asp Ser Leu Val Cys Leu Cys Glu  
225 230 235 240

Phe Lys Ala His Glu Asn Arg Val Lys Asp Met Phe Ser Phe Glu Ile  
245 250 255

Pro Glu His His Val Ile Val Ser Ala Ser Ser Asp Gly Phe Ile Lys  
260 265 270

Met Trp Lys Leu Lys Gln Asp Lys Lys Val Pro Pro Ser Leu Leu Cys  
275 280 285

Glu Ile Asn Thr Asn Ala Arg Leu Thr Cys Leu Gly Val Trp Leu Asp  
290 295 300

Lys Val Ala Asp Met Lys Ser Leu Pro Pro Ala Ala Glu Pro Ser Pro  
305 310 315 320

Val Ser Lys Glu Gln Ser Lys Ile Gly Lys Lys Glu Pro Gly Asp Thr  
325 330 335

Val His Lys Glu Glu Lys Arg Ser Lys Pro Asn Thr Lys Lys Arg Gly  
340 345 350

Leu Thr Gly Asp Ser Lys Ala Thr Lys Glu Ser Gly Leu Ile Ser  
355 360 365

Thr Lys Lys Arg Lys Met Val Glu Met Leu Glu Lys Lys Arg Lys Lys  
370 375 380

Lys Lys Ile Lys Thr Met Gln  
385 390

<210> 153  
<211> 5285  
<212> DNA  
<213> human organism

<400> 153  
gatgtcttgg acatgctctg gctggctaat ctccatgttc tagccgactg aaaatacggt 60  
ggccaagtgg atggtgtgct tatttgcaat ctaaaagaaat ttccctttga tgtggcagaa 120  
aatcgaggat gtggagtgga gaccccagac ttacttggag ctggagggtc tgccttgcatt 180  
cctgatcttc agtggatgg acccgcatgg ggagtccttgc ccgaggtctt tgaggtaactg 240  
tgacctgcga ttgataaact cctcctgctt ggtgagaaca gccttggagc aggagctggg 300  
cctggctgcc tactttgtga gcaacgaggt tcccttggag aagggggcta ggaacgaggc 360  
cttggagagt gatgctgaga agctgagcag cacagacaac gaggatgagg agctggggac 420  
agaaggctct acctcggaga agagaagccc catgaaaagg gagaggtccc gctcccacga 480  
ctcagcatcc tcataccctct cctccaaggc ttcccggttca gcgctcggtg gcgagtcctc 540  
ggctcagccc acagcactcc cccagggaga gcatgccagg tcgccccagc cccgtggccc 600  
cgcagaggag ggcagagccc ctggtgagaa acagaggccc cgggcaagtc aggggccacc 660  
ctcggccatc agcaggcaca gtcccgccgac gacgccccag cccgactgttgcgcctcaggac 720  
cggccagagg agcgtccagg tgtcggtcac ctcgtcgtgc tccctcggttgcctc 780  
gggctcatcc tcctcatccg tggcgccccgc tgccggcacg tgggtcctgc aggccctccca 840  
gtgctccttgc accaaggcct gccggccagcc acccattgtc ttcttgcacc agctcgtgttgc 900

cgacatggtt gtgtccactg acagcagtgg cctgcccaag gcccgcctcc tcctgccctc	960
ccccctcggtc atgtgggcca gctcttccg cccccctgctc agcaagacca tgacatccac	1020
cgagcagtcc ctctactacc ggcagtggac ggtgccccgg cccagccaca tggactacgg	1080
caaccgggcc gagggccgcg tggacggctt ccaccccccgc aggctgctgc tcagcggccc	1140
ccctcagatc gggaaagacag gtgcctacct gcagttcctc agtgcctgt ccaggatgct	1200
tgttcggctc acagaagtgg atgtctatga cgaggaggag atcaatatca acctcagaga	1260
agaatctgac tggcattatc tccagcttag cgaccctgg ccagacctgg agctgttcaa	1320
gaagttgccc tttgactaca tcattcacga cccgaagtat gaagatgccca gcctgatttg	1380
ttcgcactat cagggtataa agagtgaaga cagaggatg tcccgaaagc cggaggacct	1440
ttatgtgcgg cgtcagacgg cacggatgag actgtccaag tacgcagcgt acaacactta	1500
ccaccactgt gagcagtgcc accagtacat gggcttccac ccccgctacc agctgtatga	1560
gtccaccctg cacgccttgc cttctctta ctccatgcta ggagaggaga tccagctgca	1620
ttcatcatc cccaagtcca aggagcacca ctttgtcttc agccaacctg gaggccagct	1680
ggagagcatg cgactacccc tctgtacaga caagagccat gaatatataa aaagtccgac	1740
attcactcca accacccggcc gtcacgaaca tgggctctt aatctgtacc acgcaatgga	1800
cgggccagc catttgcacg tctgggtgtt caaggaatac gagatggcaa ttataagaa	1860
atattggccc aaccacatca tgctggtgct cccagatc ttcaacagtg ctggagttgg	1920
tgctgctcat ttccatcatca aggagctgtc ctaccataac ctggagctcg agcggaaaccg	1980
gcaggaggag ctggaatca agccgcagga catctggcct ttcattgtga tctctgtatga	2040
ctcctgcgtg atgtggAACG tggggatgtt caactctgtt ggggagagaa gcaggagtt	2100
ctcctggcgtg gaaaggaacg tgtctttgaa gcacatcatg cagcacatcg aggccggccc	2160
cgacatcatg cactacgccc tctgggcct gcggaaagtgg tccagcaaga cccggccag	2220
cgaggtgcaa gagcccttct cccgctgcca cgtgcacaac ttcatcatcc tgaacgtgga	2280
cctgacccag aacgtgcagt acaaccagaa ccggttcctg tgtgacgtatg tagacttcaa	2340
cctgccccgt cacagcgcgg gcctcctgtt ctggccggttc aaccgcttca gcgtgtatga	2400
gaagcagatc gtgggtggcg gccacaggatc cttccacatc acatccaagg tgtctgataa	2460
ctctgccccgt gtcgtgcgg cccagatcatc ctgtggcccg gacagcaagc acacgttct	2520
cgcagcgcggcc gcccagctcc tgctggagaa gttcctgcag caccacagcc acctcttctt	2580
cccgctgtcc ctgaagaacc atgaccaccc agtgctgtct gtcgactgtt acctgaacct	2640

gggatctcag atttctgttt gctatgttag ctccaggccc cactcttaa acatcagctg 2700  
ctcggaacttg ctgttcagtgg ggcgtgtgt gtacctctgt gactctttt tgggagctag 2760  
ctttttgaaa aagtttcatt ttctgaaagg tgcgacgttg tgtgtcatct gtcaggaccg 2820  
gagctcaactg cgccagacgg tcgtccgcct ggagctcgag gacgagtggc agttccggct 2880  
gcgcgatgag ttccagacccg ccaatgccag ggaagacccgg ccgcctttt ttctgacggg 2940  
acgacacatc tgaggaagac agcggcgagt tttctgaaga gatgagtgtc cagagccctc 3000  
atgctgttga ggctaaaggg aggccctggaa cgggtggcg tttgactgga atggacccca 3060  
gggactgtcc aggtgcagcc cctcctagta cacatggcc cccgaggccg tggcctggg 3120  
agccaggaag actccgcagt gggtgagaat gaaaacttga gactcccaag ttctggcca 3180  
gccccattgtcttggctgtt ttaaagccca tttcacgagg aacaaagatt tacttcctgt 3240  
cctgccattc gtgtgcttcc atggacaaac ctgattttt tctcttagtt ctaaagaatc 3300  
ttgggttatt ttgttagcggt gccagtattt cagtagatgg gatttcagcc aagtaggttc 3360  
ccctgttaacc tcctacaaag caatattcca aaggaacatt ttaactgtaa aggctggaga 3420  
caagaaaaaa taagtagatc gtttaataa caattattta attgcctata agtttgctgt 3480  
ttcagaggct agcccaaagg catcaaattt aataaagtta aacaaatttga tttacttcag 3540  
agcaaatatg atcctattaa aataatatag ggttaatacc ctaccttta gaaaggcga 3600  
aaatgcaaag aagctttctt taaaactaaa agggttttt gggggggag ttggcgggga 3660  
ggaaataagg ctaacagagg ttgacctaaa attagcctta caaaggagaa aggaccacat 3720  
tgcttacttg aaacagacaa tgaaaacaac caaagtgata tataaaatag ttgatgagaa 3780  
ctagacttat gactgttagtt tactagagtt tagtttcag ttgctgaagt agtcatttt 3840  
ctcttactaa tgtttggttc ctcagggaaag aatctcaactt gactagagag gaggtggaa 3900  
cagaagagag aaggaggcag ggagatgtat ttcttagggc tcaccccttc acagactgac 3960  
agaatggttt tgtttggtt tgtttggtt tgtttggtt ttgagatgga ctctagctct 4020  
gtcacccagg ctggagtgca gtgggtgcgtat ctgcggctcac tgcaagctcc gcctccggg 4080  
ttctcaccat tctcctgcct cagcctcccg agtagctggg actacaggcg cccaccacca 4140  
cgcccggtca atttttgtta ttttttagta gagacgggggt ttcaccatgt tagccaggat 4200  
ggtctcgatc tcctgacccctc gtgatccgccc cgcctegggcc tcccaaagtgc tggttggattac 4260  
aggcgtgagc caccgtgcct gccccagaat ggttttaaa gccacagttg agaggccacc 4320

cattgcccgg cgcctggaca gtgatcatct tggatcatctt gttcagtcct ttcttgttg	4380
attggaaatta ttcatccctt ttgaaagatg agaagggttga gatgcaaaga gtctaccttt	4440
ccaagttctc actgctggaa agagctagaa gcacagttca aagttctggc ttctggactc	4500
tgcagtccag gtctcccttc tcccacttgc ctaccctcaa tgccacactg tttttaaagt	4560
ggcccataac ttgaaggaaa agttaaaga cagttcaatt taatcatcag aatgcattct	4620
tttttttc ggagacggag tttcactctt gctgcccagg ctggagtgca atggtgcaat	4680
gatctcggtt cactgcaacc tctgcctcct gggttcaagt gattctccag cctcagcctc	4740
ccgagtagct gggattatgg gcgcccacca ccatgcccag ctaatttttgc tattttttt	4800
ttttagtaga gatggggttt cgccaggttg gccaggctgg tcttgtgaac tcctggcctc	4860
aggtagatctg cccacctcat cttccaaaag tgctggatt acaggcatga gccactgcgc	4920
ctggcctcag aatgcattct tacacatcta tccttagacat ttataagcac tctaattggat	4980
aacaatccaa gaataaatga ttgtaaaaga tgatgccaa gagttgatgt caatctttt	5040
ttcctaagaa aaaaagtccg cgagtattaa atatttagat caatgtttat aaaaatgatta	5100
ctttagtatat ctcattattc ctatggaa ataaaaactg accttcttta atcatatact	5160
tgtctttgt aaatagcagc ttttgtgtca ttctccccac tttatttagtt aattttaaatt	5220
ggaaaaaaacc ctcaaactaa tattcttgc tgttccagtc ttataaataa aacttataat	5280
gcattg	5285

<210> 154  
 <211> 947  
 <212> PRT  
 <213> human organism

<400> 154

Met Trp Gln Lys Ile Glu Asp Val Glu Trp Arg Pro Gln Thr Tyr Leu			
1	5	10	15

Glu Leu Glu Gly Leu Pro Cys Ile Leu Ile Phe Ser Gly Met Asp Pro			
20	25	30	

His Gly Glu Ser Leu Pro Arg Ser Leu Arg Tyr Cys Asp Leu Arg Leu			
35	40	45	

Ile Asn Ser Ser Cys Leu Val Arg Thr Ala Leu Glu Gln Glu Leu Gly			
50	55	60	

Leu Ala Ala Tyr Phe Val Ser Asn Glu Val Pro Leu Glu Lys Gly Ala  
65 70 75 80

Arg Asn Glu Ala Leu Glu Ser Asp Ala Glu Lys Leu Ser Ser Thr Asp  
85 90 95

Asn Glu Asp Glu Glu Leu Gly Thr Glu Gly Ser Thr Ser Glu Lys Arg  
100 105 110

Ser Pro Met Lys Arg Glu Arg Ser Arg Ser His Asp Ser Ala Ser Ser  
115 120 125

Ser Leu Ser Ser Lys Ala Ser Gly Ser Ala Leu Gly Gly Glu Ser Ser  
130 135 140

Ala Gln Pro Thr Ala Leu Pro Gln Gly Glu His Ala Arg Ser Pro Gln  
145 150 155 160

Pro Arg Gly Pro Ala Glu Glu Gly Arg Ala Pro Gly Glu Lys Gln Arg  
165 170 175

Pro Arg Ala Ser Gln Gly Pro Pro Ser Ala Ile Ser Arg His Ser Pro  
180 185 190

Gly Pro Thr Pro Gln Pro Asp Cys Ser Leu Arg Thr Gly Gln Arg Ser  
195 200 205

Val Gln Val Ser Val Thr Ser Ser Cys Ser Gln Leu Ser Ser Ser Ser  
210 215 220

Gly Ser Ser Ser Ser Val Ala Pro Ala Ala Gly Thr Trp Val Leu  
225 230 235 240

Gln Ala Ser Gln Cys Ser Leu Thr Lys Ala Cys Arg Gln Pro Pro Ile  
245 250 255

Val Phe Leu Pro Lys Leu Val Tyr Asp Met Val Val Ser Thr Asp Ser  
260 265 270

Ser Gly Leu Pro Lys Ala Ala Ser Leu Leu Pro Ser Pro Ser Val Met  
275 280 285

Trp Ala Ser Ser Phe Arg Pro Leu Leu Ser Lys Thr Met Thr Ser Thr  
290 295 300

Glu Gln Ser Leu Tyr Tyr Arg Gln Trp Thr Val Pro Arg Pro Ser His  
305 310 315 320

Met Asp Tyr Gly Asn Arg Ala Glu Gly Arg Val Asp Gly Phe His Pro  
325 330 335

Arg Arg Leu Leu Leu Ser Gly Pro Pro Gln Ile Gly Lys Thr Gly Ala  
340 345 350

Tyr Leu Gln Phe Leu Ser Val Leu Ser Arg Met Leu Val Arg Leu Thr  
355 360 365

Glu Val Asp Val Tyr Asp Glu Glu Glu Ile Asn Ile Asn Leu Arg Glu  
370 375 380

Glu Ser Asp Trp His Tyr Leu Gln Leu Ser Asp Pro Trp Pro Asp Leu  
385 390 395 400

Glu Leu Phe Lys Lys Leu Pro Phe Asp Tyr Ile Ile His Asp Pro Lys  
405 410 415

Tyr Glu Asp Ala Ser Leu Ile Cys Ser His Tyr Gln Gly Ile Lys Ser  
420 425 430

Glu Asp Arg Gly Met Ser Arg Lys Pro Glu Asp Leu Tyr Val Arg Arg  
435 440 445

Gln Thr Ala Arg Met Arg Leu Ser Lys Tyr Ala Ala Tyr Asn Thr Tyr  
450 455 460

His His Cys Glu Gln Cys His Gln Tyr Met Gly Phe His Pro Arg Tyr  
465 470 475 480

Gln Leu Tyr Glu Ser Thr Leu His Ala Phe Ala Phe Ser Tyr Ser Met  
485 490 495

Leu Gly Glu Glu Ile Gln Leu His Phe Ile Ile Pro Lys Ser Lys Glu  
500 505 510

His His Phe Val Phe Ser Gln Pro Gly Gln Leu Glu Ser Met Arg

515

520

525

Leu Pro Leu Val Thr Asp Lys Ser His Glu Tyr Ile Lys Ser Pro Thr  
530 535 540

Phe Thr Pro Thr Thr Gly Arg His Glu His Gly Leu Phe Asn Leu Tyr  
545 550 555 560

His Ala Met Asp Gly Ala Ser His Leu His Val Leu Val Val Lys Glu  
565 570 575

Tyr Glu Met Ala Ile Tyr Lys Tyr Trp Pro Asn His Ile Met Leu  
580 585 590

Val Leu Pro Ser Ile Phe Asn Ser Ala Gly Val Gly Ala Ala His Phe  
595 600 605

Leu Ile Lys Glu Leu Ser Tyr His Asn Leu Glu Leu Glu Arg Asn Arg  
610 615 620

Gln Glu Glu Leu Gly Ile Lys Pro Gln Asp Ile Trp Pro Phe Ile Val  
625 630 635 640

Ile Ser Asp Asp Ser Cys Val Met Trp Asn Val Val Asp Val Asn Ser  
645 650 655

Ala Gly Glu Arg Ser Arg Glu Phe Ser Trp Ser Glu Arg Asn Val Ser  
660 665 670

Leu Lys His Ile Met Gln His Ile Glu Ala Ala Pro Asp Ile Met His  
675 680 685

Tyr Ala Leu Leu Gly Leu Arg Lys Trp Ser Ser Lys Thr Arg Ala Ser  
690 695 700

Glu Val Gln Glu Pro Phe Ser Arg Cys His Val His Asn Phe Ile Ile  
705 710 715 720

Leu Asn Val Asp Leu Thr Gln Asn Val Gln Tyr Asn Gln Asn Arg Phe  
725 730 735

Leu Cys Asp Asp Val Asp Phe Asn Leu Arg Val His Ser Ala Gly Leu  
740 745 750

Leu Leu Cys Arg Phe Asn Arg Phe Ser Val Met Lys Lys Gln Ile Val  
755 760 765

Val Gly Gly His Arg Ser Phe His Ile Thr Ser Lys Val Ser Asp Asn  
770 775 780

Ser Ala Ala Val Val Pro Ala Gln Tyr Ile Cys Ala Pro Asp Ser Lys  
785 790 795 800

His Thr Phe Leu Ala Ala Pro Ala Gln Leu Leu Leu Glu Lys Phe Leu  
805 810 815

Gln His His Ser His Leu Phe Phe Pro Leu Ser Leu Lys Asn His Asp  
820 825 830

His Pro Val Leu Ser Val Asp Cys Tyr Leu Asn Leu Gly Ser Gln Ile  
835 840 845

Ser Val Cys Tyr Val Ser Ser Arg Pro His Ser Leu Asn Ile Ser Cys  
850 855 860

Ser Asp Leu Leu Phe Ser Gly Leu Leu Leu Tyr Leu Cys Asp Ser Phe  
865 870 875 880

Val Gly Ala Ser Phe Leu Lys Lys Phe His Phe Leu Lys Gly Ala Thr  
885 890 895

Leu Cys Val Ile Cys Gln Asp Arg Ser Ser Leu Arg Gln Thr Val Val  
900 905 910

Arg Leu Glu Leu Glu Asp Glu Trp Gln Phe Arg Leu Arg Asp Glu Phe  
915 920 925

Gln Thr Ala Asn Ala Arg Glu Asp Arg Pro Leu Phe Phe Leu Thr Gly  
930 935 940

Arg His Ile  
945

<210> 155  
<211> 1167  
<212> DNA

<213> human organism

<400> 155  
atgacagcct ccgtgctcct ccaccccccgc tggatcgagc ccaccgtcat gtttctctac 60  
gacaacggcg gcggccttgtt ggccgacgag ctcaacaaga acatgaaagg ggccggccgc 120  
gctgcagcag cggctgcagc ggcggccgc gcccggccg gggggccgggg cttcccccac 180  
ccggccggctg cggcggcagg gggcaacttc tcgggtggcgg cccggccgc ggctgcggcg 240  
gccgcccggg ccaaccagtg ccgcaacctg atggcgcacc cggcgccctt ggccgcagga 300  
gccgcgtccg cctacagcag cgcccccggg gagggcgcccc cgtcggctgc cgccgctgct 360  
gccgcggctg ccgctgcagc cggccgcgc gcccggcggt cgtcctcggg aggtccccggc 420  
ccggcggggcc cggcggccgc agaggcggcc aagcaatgca gcccctgctc ggccgcggcg 480  
cagagctcgt cggggccgcg cggcgtgccc tatggctact tcggcagcgg ctactacccg 540  
tgcccccgcga tgggcccccc ccccaacgccc atcaagtcgt gcccccaagcc cccctcgcc 600  
gccgcccggc cccgccttcgc ggacaagtac atggataccg cccggccagc tgccgaggag 660  
ttcagctccc gcgctaagga gttcgcgttc taccaccagg gctacgcagc cgggccttac 720  
caccaccatc agcccatgcc tggctacctg gatatgccag tggtgccggg cctcgggggc 780  
cccgccgagt cgcgcacga acccttgggt cttccatgg aaagctacca gcccctggcg 840  
ctgccaacg gctggaacgg ccaaattgtac tgccccaaag agcaggcgcgca gcctccccac 900  
ctctggaaatg ccactctgcc cgcgtggtc tcccatccct cggatgccag ctctatagg 960  
agggggagaa agaagcgcgt gccttataacc aaggtgcaat taaaagaact tgaacggaa 1020  
tacgccacga ataaattcat tactaaggac aaacggaggc ggatatcagc cacgacgaat 1080  
ctctctgagc ggcaggtcac aatctggttc cagaacagga gggtaaaga gaaaaaaagtc 1140  
atcaacaaac tgaaaaccac tagttaa 1167

<210> 156

<211> 388

<212> PRT

<213> human organism

<400> 156

Met	Thr	Ala	Ser	Val	Leu	Leu	His	Pro	Arg	Trp	Ile	Glu	Pro	Thr	Val
1				5				10				15			

Met	Phe	Leu	Tyr	Asp	Asn	Gly	Gly	Ley	Val	Ala	Asp	Glu	Leu	Asn
20						25						30		

Lys Asn Met Glu Gly Ala Ala Ala Ala Ala Ala Ala Ala Ala  
35 40 45

Ala Ala Ala Gly Ala Gly Gly Gly Phe Pro His Pro Ala Ala Ala  
50 55 60

Ala Ala Gly Gly Asn Phe Ser Val Ala Ala Ala Ala Ala Ala  
65 70 75 80

Ala Ala Ala Asn Gln Cys Arg Asn Leu Met Ala His Pro Ala Pro  
85 90 95

Leu Ala Pro Gly Ala Ala Ser Ala Tyr Ser Ser Ala Pro Gly Glu Ala  
100 105 110

Pro Pro Ser Ala  
115 120 125

Ala Ala Ala Ala Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Pro  
130 135 140

Ala Ala Ala Glu Ala Ala Lys Gln Cys Ser Pro Cys Ser Ala Ala Ala  
145 150 155 160

Gln Ser Ser Ser Gly Pro Ala Ala Leu Pro Tyr Gly Tyr Phe Gly Ser  
165 170 175

Gly Tyr Tyr Pro Cys Ala Arg Met Gly Pro Pro Pro Asn Ala Ile Lys  
180 185 190

Ser Cys Pro Gln Pro Pro Ser Ala Ala Ala Ala Ala Phe Ala Asp  
195 200 205

Lys Tyr Met Asp Thr Ala Gly Pro Ala Ala Glu Glu Phe Ser Ser Arg  
210 215 220

Ala Lys Glu Phe Ala Phe Tyr His Gln Gly Tyr Ala Ala Gly Pro Tyr  
225 230 235 240

His His His Gln Pro Met Pro Gly Tyr Leu Asp Met Pro Val Val Pro  
245 250 255

Gly Leu Gly Gly Pro Gly Glu Ser Arg His Glu Pro Leu Gly Leu Pro  
260 265 270

Met Glu Ser Tyr Gln Pro Trp Ala Leu Pro Asn Gly Trp Asn Gly Gln  
275 280 285

Met Tyr Cys Pro Lys Glu Gln Ala Gln Pro Pro His Leu Trp Lys Ser  
290 295 300

Thr Leu Pro Asp Val Val Ser His Pro Ser Asp Ala Ser Ser Tyr Arg  
305 310 315 320

Arg Gly Arg Lys Lys Arg Val Pro Tyr Thr Lys Val Gln Leu Lys Glu  
325 330 335

Leu Glu Arg Glu Tyr Ala Thr Asn Lys Phe Ile Thr Lys Asp Lys Arg  
340 345 350

Arg Arg Ile Ser Ala Thr Thr Asn Leu Ser Glu Arg Gln Val Thr Ile  
355 360 365

Trp Phe Gln Asn Arg Arg Val Lys Glu Lys Lys Val Ile Asn Lys Leu  
370 375 380

Lys Thr Thr Ser  
385

<210> 157  
<211> 3004  
<212> DNA  
<213> human organism

<400> 157  
cccttatggc gattgggcgg ctgcagagac caggactcag ttcccctgcc ctagtctgag 60  
cctagtgggt gggactcagc tcagagtcaag ttttcagaag caggtttcag ttgcagagtt 120  
ttcctacact tttcctgcgc tagagcagcg agcagcctgg aacagaccca ggcggaggac 180  
acctgtgggg gagggagcgc ctggaggagc ttagagaccc cagccggcgc tgatctcacc 240  
atgtgcggat ttgcgaggcg cgccctggag ctgctagaga tccggaagca cagccccgag 300  
gtgtgcgaag ccaccaagac tgccgcttt ggagaaagcg tgagcagggg gccacccgccc 360  
tctccggcct gtctgcaccc tgtcgccctga gctgcctgac agtgacaatg acatcccagt 420

taccagtgtc cttgaattga tagtggcttc tgtttgcag tctcatataa gaactacagc 480  
tcatcaggag gagatcgtag cagggttaaga gacaccaaca ccatgttctg cacgaagctc 540  
aaggatctca agatcacagg agagtgtcct ttctccttac tggcaccagg tcaagttcct 600  
aacgagtctt cagaggaggc agcaggaagc tcagagagct gcaaagcaac cgtgcccattc 660  
tgtcaagaca ttccctgagaa gaacatacaa gaaagtcttc ctcaaagaaa aaccagtcgg 720  
agccgagtct atcttcacac tttggcagag agtatttgc aactgatttt cccagagttt 780  
gaacggctga atgttgcact tcagagaaca ttggcaaagc acaaaataaa agaaaggcagg 840  
aaatcttgg aaagagaaga ctttgaaaaa acaattgcag agcaagcagt gcagcagagt 900  
ccagtgaggat tatcaaagaa tctcttggtg aagaggttt taaaatatgt tacgaggaag 960  
atgaaaacat ctttgggtg gttggaggca cccttaaaga tttttaaaca gcttcagttac 1020  
ccttcgtaaa cagagcagcc attgccaaga agcaggaaaa aggggcagct tgaggacgcc 1080  
tccattctat gcctggataa ggaggatgtat tttctacatg tttactactt ctccctaag 1140  
agaaccacct ccctgattct tcccggcatc ataaaggcag ctgctcacgt attatatgaa 1200  
acggaagtgg aagtgtcgaa aatgcctccc tgcttccata atgattgcag cgagtttgc 1260  
aatcagccct acttgttgta ctccgttcac atgaaaagca ccaagccatc cctgtcccc 1320  
agcaaaccccc agtcctcgct ggtgattccc acatcgctat tctgcaagac atttccattc 1380  
catttcatgt ttgacaaaga tatgacaatt ctgcaatttg gcaatggcat cagaaggctg 1440  
atgaacagga gagacttca aggaaaggct aattttgaat actttgaaat tctgactcca 1500  
aaaatcaacc agacctttag cgggatcatg actatgtga atatgcagtt tggttacga 1560  
gtgaggagat gggacaactc tgtgaagaaa tcttcaaggg ttatggacct caaaggccaa 1620  
atgatctaca ttgttgaatc cagtgcatac ttgttttgg ggtcaccctg tgtggacaga 1680  
ttagaagatt ttacaggacg agggctctac ctctcagaca tcccaattca caatgcactg 1740  
aggatgtgg tcttaatagg ggaacaagcc cgagctcaag atggcctgaa gaagaggctg 1800  
gggaagctga aggctaccct tgagcaagcc caccaagccc tggaggagga gaagaaaaag 1860  
acagtagacc ttctgtgctc catatttccc tgtgaggttg ctcagcagct gtggcaaggg 1920  
caagttgtgc aagccaagaa gttcagtaat gtcaccatgc tcttctcaga catcggtgg 1980  
ttcactgcca tctgctccca gtgctcaccg ctgcaggatca tcaccatgct caatgcactg 2040  
tacactcgct tcgaccagca gtgtggagag ctggatgtct acaaggtgga gaccattgcg 2100  
atgcctattg tgtggcttgg gggattacac aaagagagtg atactcatgc tggtcagata 2160

gcgctgatgg ccctgaagat gatggagctc tctgatgaag ttatgtctcc ccatggagaa	2220
cctatcaaga tgcgaattgg actgcactct ggatcagttt ttgctggcgt cgttggagtt	2280
aaaatgcccc gttactgtct tttggaaac aatgtcaactc tggctaacaa atttgagtcc	2340
tgcagtgtac cacgaaaaat caatgtcagc ccaacaactt acagattact caaagactgt	2400
cctggtttcg tgtttacccc tcgatcaagg gaggaacttc caccaaactt ccctagtgaa	2460
atccccggaa tctgccattt tctggatgct taccaacaag gaacaaactc aaaaccatgc	2520
ttccaaaaga aagatgtgga agatgcaagc caatttta ggcaaagcat caggaataga	2580
ttagcaacct atataccat ttataagtct ttggggttg actcattgaa gatgtgtaga	2640
gcctctgaaa gcactttagg gattgtagat ggctaacaag cagtattaaa atttcaggag	2700
ccaagtcaca atcttctcc tgTTAACAT gacaaaatgt actcaactca gtacttcagc	2760
tcttcaagaa aaaaaaaaaa acctaaaaaa gctactttg tgggagtatt tctattat	2820
aaccagcaact tactacctgt actcaaaatt cagcaccttg tacatatatc agataattgt	2880
agtcaattgt acaaaactgat ggagtcacct gcaatctcat atcctggtgg aatgccatgg	2940
ttattaaagt gtgttgtga tagttgtcgt caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	3000
aaaaa	3004

<210> 158

<211> 717

<212> PRT

<213> human organism

<400> 158

Met	Phe	Cys	Thr	Lys	Leu	Lys	Asp	Leu	Lys	Ile	Thr	Gly	Glu	Cys	Pro
1					5				10					15	

Phe	Ser	Leu	Leu	Ala	Pro	Gly	Gln	Val	Pro	Asn	Glu	Ser	Ser	Glu	Glu
					20			25				30			

Ala	Ala	Gly	Ser	Ser	Glu	Ser	Cys	Lys	Ala	Thr	Val	Pro	Ile	Cys	Gln
							35		40			45			

Asp	Ile	Pro	Glu	Lys	Asn	Ile	Gln	Glu	Ser	Leu	Pro	Gln	Arg	Lys	Thr
					50			55			60				

Ser	Arg	Ser	Arg	Val	Tyr	Leu	His	Thr	Leu	Ala	Glu	Ser	Ile	Cys	Lys
					65			70			75		80		

Leu Ile Phe Pro Glu Phe Glu Arg Leu Asn Val Ala Leu Gln Arg Thr  
85 90 95

Leu Ala Lys His Lys Ile Lys Glu Ser Arg Lys Ser Leu Glu Arg Glu  
100 105 110

Asp Phe Glu Lys Thr Ile Ala Glu Gln Ala Val Gln Gln Ser Pro Val  
115 120 125

Glu Leu Ser Lys Asn Leu Leu Val Lys Arg Phe Leu Lys Tyr Val Thr  
130 135 140

Arg Lys Met Lys Thr Ser Leu Gly Trp Leu Glu Ala Pro Leu Lys Ile  
145 150 155 160

Phe Lys Gln Leu Gln Tyr Pro Ser Glu Thr Glu Gln Pro Leu Pro Arg  
165 170 175

Ser Arg Lys Lys Gly Gln Leu Glu Asp Ala Ser Ile Leu Cys Leu Asp  
180 185 190

Lys Glu Asp Asp Phe Leu His Val Tyr Tyr Phe Phe Pro Lys Arg Thr  
195 200 205

Thr Ser Leu Ile Leu Pro Gly Ile Ile Lys Ala Ala Ala His Val Leu  
210 215 220

Tyr Glu Thr Glu Val Glu Val Ser Leu Met Pro Pro Cys Phe His Asn  
225 230 235 240

Asp Cys Ser Glu Phe Val Asn Gln Pro Tyr Leu Leu Tyr Ser Val His  
245 250 255

Met Lys Ser Thr Lys Pro Ser Leu Ser Pro Ser Lys Pro Gln Ser Ser  
260 265 270

Leu Val Ile Pro Thr Ser Leu Phe Cys Lys Thr Phe Pro Phe His Phe  
275 280 285

Met Phe Asp Lys Asp Met Thr Ile Leu Gln Phe Gly Asn Gly Ile Arg  
290 295 300

Arg Leu Met Asn Arg Arg Asp Phe Gln Gly Lys Pro Asn Phe Glu Tyr  
305 310 315 320

Phe Glu Ile Leu Thr Pro Lys Ile Asn Gln Thr Phe Ser Gly Ile Met  
325 330 335

Thr Met Leu Asn Met Gln Phe Val Val Arg Val Arg Arg Trp Asp Asn  
340 345 350

Ser Val Lys Lys Ser Ser Arg Val Met Asp Leu Lys Gly Gln Met Ile  
355 360 365

Tyr Ile Val Glu Ser Ser Ala Ile Leu Phe Leu Gly Ser Pro Cys Val  
370 375 380

Asp Arg Leu Glu Asp Phe Thr Gly Arg Gly Leu Tyr Leu Ser Asp Ile  
385 390 395 400

Pro Ile His Asn Ala Leu Arg Asp Val Val Leu Ile Gly Glu Gln Ala  
405 410 415

Arg Ala Gln Asp Gly Leu Lys Lys Arg Leu Gly Lys Leu Lys Ala Thr  
420 425 430

Leu Glu Gln Ala His Gln Ala Leu Glu Glu Glu Lys Lys Lys Thr Val  
435 440 445

Asp Leu Leu Cys Ser Ile Phe Pro Cys Glu Val Ala Gln Gln Leu Trp  
450 455 460

Gln Gly Gln Val Val Gln Ala Lys Lys Phe Ser Asn Val Thr Met Leu  
465 470 475 480

Phe Ser Asp Ile Val Gly Phe Thr Ala Ile Cys Ser Gln Cys Ser Pro  
485 490 495

Leu Gln Val Ile Thr Met Leu Asn Ala Leu Tyr Thr Arg Phe Asp Gln  
500 505 510

Gln Cys Gly Glu Leu Asp Val Tyr Lys Val Glu Thr Ile Ala Met Pro  
515 520 525

Ile Val Trp Leu Gly Gly Leu His Lys Glu Ser Asp Thr His Ala Val  
530 535 540

Gln Ile Ala Leu Met Ala Leu Lys Met Met Glu Leu Ser Asp Glu Val  
545 550 555 560

Met Ser Pro His Gly Glu Pro Ile Lys Met Arg Ile Gly Leu His Ser  
565 570 575

Gly Ser Val Phe Ala Gly Val Val Gly Val Lys Met Pro Arg Tyr Cys  
580 585 590

Leu Phe Gly Asn Asn Val Thr Leu Ala Asn Lys Phe Glu Ser Cys Ser  
595 600 605

Val Pro Arg Lys Ile Asn Val Ser Pro Thr Thr Tyr Arg Leu Leu Lys  
610 615 620

Asp Cys Pro Gly Phe Val Phe Thr Pro Arg Ser Arg Glu Glu Leu Pro  
625 630 635 640

Pro Asn Phe Pro Ser Glu Ile Pro Gly Ile Cys His Phe Leu Asp Ala  
645 650 655

Tyr Gln Gln Gly Thr Asn Ser Lys Pro Cys Phe Gln Lys Lys Asp Val  
660 665 670

Glu Asp Ala Ser Gln Phe Phe Arg Gln Ser Ile Arg Asn Arg Leu Ala  
675 680 685

Thr Tyr Ile Pro Ile Tyr Lys Ser Leu Gly Phe Asp Ser Leu Lys Met  
690 695 700

Cys Arg Ala Ser Glu Ser Thr Leu Gly Ile Val Asp Gly  
705 710 715

<210> 159  
<211> 2710  
<212> DNA  
<213> human organism

<400> 159  
cgccggcggg actggctctga agagacgcgg ggacaaagtg gcaacgactt ggacatctga 60  
gctgtcactg ccgaaaacag gccgcaagag agataatcaa tatgcatttc caagccttt 120

ggctatgtt gggtcttcg ttcatctcaa ttaatgcaga atttatggat gatgatgttg 180  
agacggaaga ctttgaagaa aattcagaag aaattgatgt taatgaaaagt gaacttcct 240  
cagagattaa atataagaca cctcaaccta taggagaagt atatttgca gaaaactttg 300  
atagtggaaag gttggctgga tgggtcttat caaaagcaaa gaaagatgac atggatgagg 360  
aaatttcaat atacgatgga agatggaaa ttgaagagtt gaaagaaaaac caggtacctg 420  
gtgacagagg actggtatta aaatctagag caaagcatca tgcaatatct gctgtattag 480  
caaaaccatt cattttgct gataaaccct tgatagttca atatgaagta aattttcaag 540  
atggtattga ttgtggaggt gcatacatta aactccctgc agacactgat gatttgattc 600  
tgaaaaactt ttatgataaa acatcctata tcattatggtt tggaccagat aaatgtggag 660  
aagattataa acttcatttt atcttcagac ataaacatcc caaaactgga gtttcgaag 720  
agaaacatgc caaacctcca gatgttagacc ttaaaaagtt ct当地agac aggaagactc 780  
atcttatac ctttgtgatg aatccagatg acacattga ggtgttagtt gatcaaacag 840  
ttgttaaaca aggaagcctc ctagaggatg tggttcctcc tatcaaacct cccaaagaaa 900  
ttgaagatcc caatgataaa aaacctgagg aatggatga aagagcaaaa attcctgatc 960  
cttctgccgt caaaccagaa gactggatg aaagtgaacc tgcccaata gaagattcaa 1020  
gtgttgtaa acctgctggc tggcttgatg atgaaccaaa atttacccct gatcctaattg 1080  
ctgaaaaacc tgatgactgg aatgaagaca cggatggaga atggaggca cctcagattc 1140  
ttaatccagc atgtcgattt ggggtgtggtg agtggaaacc tcccatgata gataacccaa 1200  
aatacaaagg agtatggaga cctccactgg tcgataatcc taactatcag ggaatctgga 1260  
gtcctcgaaa aattcctaatt ccagattatt tcgaagatga tcatccattt cttctgactt 1320  
cttcagtgc tcttggttt gagctttggc ctatgacctc tgatatctac tttgataatt 1380  
ttattatctg ttccggaaaag gaagtagcag atcactggc tgcagatggt tggagatgga 1440  
aaataatgtt agcaaatgct aataagcctg gtgtttaaaa acagttatg gcagctgctg 1500  
aaggcaccc atggcttggc ttgatttac ttgtgacagc aggagtgc当地 atagcattaa 1560  
ttacttcatt ttgttggcca agaaaaagtaa agaaaaaaca taaagataca ggtataaaa 1620  
aaaccgacat atgtatacca caaacaaaag ggtactaga gcaagaagaa aaggaagaga 1680  
aagcagccct ggaaaaacca atggacctgg aagaggaaaa aaagcaaaaat gatggtaaaa 1740  
tgcttgaaaa agaagaggaa agtgaacctg aggaaaagag tgaagaagaa attgaaatca 1800

tagaaggca agaagaaagt aatcaatcaa ataagtctgg gtcagaggat gagatgaaag	1860
aagcagatga gagcacagga tctggagatg ggccgataaa gtcagtacgc aaaagaagag	1920
tacgaaagga ctaaactaga ttgaaatatt ttaattccc gagaggatgt ttggcattgt	1980
aaaaatcagc atgccagacc tgaacttta tcagtctgca catcctgttt ctaatatcta	2040
gcaacattat attcttcag acatttattt tagccttca tttccgagga aaaagaagca	2100
actttgaagt tacctcatct ttgaatttag aataaaagtg gcacattaca tatcgatct	2160
aagagattaa taccattaga agttacacag ttttagtgt ttggagatag tttggtttg	2220
tacagaacaa aataatatgt agcagcttca ttgctattgg aaaaatcagt tattgaaatt	2280
tccacttaaa tggctataca acaatataac tggtagttct ataataaaaa tgagcatatg	2340
ttctgttgtg aagagctaaa tgcaataaaag tttctgtatg gttgtttgat tctatcaaca	2400
attgaaagtg ttgtatatga cccacattta cctagttgt gtcaaattat agttacagtg	2460
agtggttgc ttaaattata gattccttta aggacatgcc ttgttcataa aatcactgga	2520
ttatattgca gcatattta catttgaata caaggataat gggtttatac aaaacaaaat	2580
gatgtacaga tttttttca agttttata gttgctttat gccagagtgg tttacccat	2640
tcacaaaaatt tcttatgcat acattgctat tgaaaataaa atttaaatat ttttcatcc	2700
tgaaaaaaaaa	2710

<210> 160

<211> 610

<212> PRT

<213> human organism

<400> 160

Met His Phe Gln Ala Phe Trp Leu Cys Leu Gly Leu Leu Phe Ile Ser	
1	5
	10
	15

Ile Asn Ala Glu Phe Met Asp Asp Asp Val Glu Thr Glu Asp Phe Glu	
20	25
	30

Glu Asn Ser Glu Glu Ile Asp Val Asn Glu Ser Glu Leu Ser Ser Glu	
35	40
	45

Ile Lys Tyr Lys Thr Pro Gln Pro Ile Gly Glu Val Tyr Phe Ala Glu	
50	55
	60

Thr Phe Asp Ser Gly Arg Leu Ala Gly Trp Val Leu Ser Lys Ala Lys

65	70	75	80
Lys Asp Asp Met Asp Glu Glu Ile Ser Ile Tyr Asp Gly Arg Trp Glu			
85	90		95
Ile Glu Glu Leu Lys Glu Asn Gln Val Pro Gly Asp Arg Gly Leu Val			
100	105		110
Leu Lys Ser Arg Ala Lys His His Ala Ile Ser Ala Val Leu Ala Lys			
115	120		125
Pro Phe Ile Phe Ala Asp Lys Pro Leu Ile Val Gln Tyr Glu Val Asn			
130	135		140
Phe Gln Asp Gly Ile Asp Cys Gly Gly Ala Tyr Ile Lys Leu Leu Ala			
145	150		155
160			
Asp Thr Asp Asp Leu Ile Leu Glu Asn Phe Tyr Asp Lys Thr Ser Tyr			
165	170		175
Ile Ile Met Phe Gly Pro Asp Lys Cys Gly Glu Asp Tyr Lys Leu His			
180	185		190
Phe Ile Phe Arg His Lys His Pro Lys Thr Gly Val Phe Glu Glu Lys			
195	200		205
His Ala Lys Pro Pro Asp Val Asp Leu Lys Lys Phe Phe Thr Asp Arg			
210	215		220
Lys Thr His Leu Tyr Thr Leu Val Met Asn Pro Asp Asp Thr Phe Glu			
225	230		235
240			
Val Leu Val Asp Gln Thr Val Val Asn Lys Gly Ser Leu Leu Glu Asp			
245	250		255
Val Val Pro Pro Ile Lys Pro Pro Lys Glu Ile Glu Asp Pro Asn Asp			
260	265		270
Lys Lys Pro Glu Glu Trp Asp Glu Arg Ala Lys Ile Pro Asp Pro Ser			
275	280		285
Ala Val Lys Pro Glu Asp Trp Asp Glu Ser Glu Pro Ala Gln Ile Glu			
290	295		300

Asp Ser Ser Val Val Lys Pro Ala Gly Trp Leu Asp Asp Glu Pro Lys  
305 310 315 320

Phe Ile Pro Asp Pro Asn Ala Glu Lys Pro Asp Asp Trp Asn Glu Asp  
325 330 335

Thr Asp Gly Glu Trp Glu Ala Pro Gln Ile Leu Asn Pro Ala Cys Arg  
340 345 350

Ile Gly Cys Gly Glu Trp Lys Pro Pro Met Ile Asp Asn Pro Lys Tyr  
355 360 365

Lys Gly Val Trp Arg Pro Pro Leu Val Asp Asn Pro Asn Tyr Gln Gly  
370 375 380

Ile Trp Ser Pro Arg Lys Ile Pro Asn Pro Asp Tyr Phe Glu Asp Asp  
385 390 395 400

His Pro Phe Leu Leu Thr Ser Phe Ser Ala Leu Gly Leu Glu Leu Trp  
405 410 415

Ser Met Thr Ser Asp Ile Tyr Phe Asp Asn Phe Ile Ile Cys Ser Glu  
420 425 430

Lys Glu Val Ala Asp His Trp Ala Ala Asp Gly Trp Arg Trp Lys Ile  
435 440 445

Met Ile Ala Asn Ala Asn Lys Pro Gly Val Leu Lys Gln Leu Met Ala  
450 455 460

Ala Ala Glu Gly His Pro Trp Leu Trp Leu Ile Tyr Leu Val Thr Ala  
465 470 475 480

Gly Val Pro Ile Ala Leu Ile Thr Ser Phe Cys Trp Pro Arg Lys Val  
485 490 495

Lys Lys Lys His Lys Asp Thr Glu Tyr Lys Lys Thr Asp Ile Cys Ile  
500 505 510

Pro Gln Thr Lys Gly Val Leu Glu Gln Glu Glu Lys Glu Glu Lys Ala  
515 520 525

Ala Leu Glu Lys Pro Met Asp Leu Glu Glu Lys Lys Gln Asn Asp  
530 535 540

Gly Glu Met Leu Glu Lys Glu Glu Ser Glu Pro Glu Glu Lys Ser  
545 550 555 560

Glu Glu Glu Ile Glu Ile Glu Gly Gln Glu Glu Ser Asn Gln Ser  
565 570 575

Asn Lys Ser Gly Ser Glu Asp Glu Met Lys Glu Ala Asp Glu Ser Thr  
580 585 590

Gly Ser Gly Asp Gly Pro Ile Lys Ser Val Arg Lys Arg Arg Val Arg  
595 600 605

Lys Asp  
610

<210> 161  
<211> 2392  
<212> DNA  
<213> human organism .  
  
<400> 161  
gcggagcgcg cgctcccagc gaaagcagca gggcagggat ctgcgttgg a ggaaggact 60  
gctctggtgc tagaatgctg tgcgtcgaa ggctggcg cttggagcc agacgacgag 120  
ctctgccgcc ccgcccggcg ggccgggaa gcctcgaagc cggatccgg gcccgaagg 180  
tcagcaccag ctggtctccc gtggcgccg cttcaatgt caagccccag ggcagccgct 240  
tggacctgtt cggcgagcgg ggcgtcttt ttggagttcc tgagctgagt gccccagaag 300  
gattcata tgcacaagaa aaagcattga gaaagacaga attgcttgt gaccgtgcat 360  
gttccacccc acctgggccc cagaccgtgc tgcgttcga tgagctctcg gattcattat 420  
gcagagtggc cgacttggct gatgggtga aaatcgctca ccctgagcca gcattcagag 480  
aagctgcgga agaagcttgt agaagtattg gcaccatggt agagaagttg aacacaaatg 540  
tggattata tcaaagttt caaaaattac tagctgataa aaaacttgt gattcccttg 600  
atccagaaac aaggcgagt gctgaactgt ttatgttga ttttggaaatt agtggaaatcc 660  
atcttagacaa acaaaaagcgt aaaagagcag tggacctcaa tggatggatc ttggatttga 720  
gtagtacatt tcttatggga accaatttc ccaacaagat tgagaagcat ctcttaccag 780

aacacattcg tcgtaacttt acatctgctg gggatcatat cataattgat ggtctccacg 840  
cagaatcacc agatgacttg gtgcgagaag ctgcttataa aatttttctt tatcccaatg 900  
ctggtaatt gaaatgtta gaagaattgc tcagcagcag agatcttctg gcaaagttgg 960  
tgggttattc cacgtttct cacaggctc tccaaggaac gatagctaaa aatccagaga 1020  
ctgtcatgca gttccttgaa aaactatctg acaaacttgc tgaaagaact ctgaaagatt 1080  
ttgagatgat acgagggatg aaaatgaaac tgaatgctca aaattccgaa gtaatgccct 1140  
gggacccccc ttactacagt ggtgtattc gtgcagaaag gtataatatt gagcccagcc 1200  
tatattgccc gttttctct cttggagcat gcatggaagg cctgaatatt ttgcttaaca 1260  
gactgttggg gatttcatta tatgcagagc agcctgcaaa aggagaggtg tggagcgaag 1320  
atgtccgaaa actggctgtt gttcatgaat ctgaaggatt gttgggtac atttactgtg 1380  
atttttca gcgagcagac aaaccacatc aggattgcca tttcactatc cgtggaggca 1440  
gactaaagga agatggagac tatcaactcc cacttgttagt tcttatgctg aatctcccc 1500  
gttcctcaag gagttctcca actttgctaa ctcctggcat gatggaaaat cttttccatg 1560  
aaatggaca tgccatgcat tcaatgctag gacgtactcg ttaccaacac gtcactggga 1620  
ccaggtgccc tactgatttt gctgaggttc cttctattct gatggagtac tttgcaaatg 1680  
attatcgagt agttaaccaa tttgccagac attatcagac tggacagcca ctgccaaaaa 1740  
atatgggtc tcgtctttgt gaatctaaaa aggtttgtgc tgcagctgat atgcaacttc 1800  
aggctttta tgccactctg gatcaaatct accatggaa gcatcccctg aggaattcaa 1860  
ccacagacat tctcaaggaa acacaagaga aattctatgg cctaccatat gttccaaata 1920  
ctgcctggca gctgcgattc agccacctcg tgggttatgg tgctagatat tactcttacc 1980  
tcatgtccag agcggtcgccc tccatggttt ggaaggagtg ttttctacag gatccttca 2040  
acagggctgc cggggagcgc tatcgcaggg agatgctggc ccacggtgg a ggcaggagc 2100  
ccatgctcat ggttgaaggt atgcttcaga agtgccttc tggatgac ttgcgttgt 2160  
ccctcgtttc cgacttggat ctggacttcg aaactttcct catggattct gaataaaaaga 2220  
aacactctac acctctaatac aaggctatgt agtaatgact ttgttataaa tgctacagct 2280  
gtgagagctt gtttctgatt gtttcattgt tcgcttctgt aattctgaaa aactttaaac 2340  
tggtagaact tggataaaat aatttggttt aattaaaaaaa aaaaaaaaaaa aa 2392

<210> 162

<211> 713



<218> PRT  
<219> human organism

<400> 162

Met Leu Cys Val Gly Arg Leu Gly Gly Leu Gly Ala Arg Ala Ala Ala  
1 5 10 15

Leu Pro Pro Arg Arg Ala Gly Arg Gly Ser Leu Glu Ala Gly Ile Arg  
20 25 30

Ala Arg Arg Val Ser Thr Ser Trp Ser Pro Val Gly Ala Ala Phe Asn  
35 40 45

Val Lys Pro Gln Gly Ser Arg Leu Asp Leu Phe Gly Glu Arg Ala Arg  
50 55 60

Leu Phe Gly Val Pro Glu Leu Ser Ala Pro Glu Gly Phe His Ile Ala  
65 70 75 80

Gln Glu Lys Ala Leu Arg Lys Thr Glu Leu Leu Val Asp Arg Ala Cys  
85 90 95

Ser Thr Pro Pro Gly Pro Gln Thr Val Leu Ile Phe Asp Glu Leu Ser  
100 105 110

Asp Ser Leu Cys Arg Val Ala Asp Leu Ala Asp Phe Val Lys Ile Ala  
115 120 125

His Pro Glu Pro Ala Phe Arg Glu Ala Ala Glu Glu Ala Cys Arg Ser  
130 135 140

Ile Gly Thr Met Val Glu Lys Leu Asn Thr Asn Val Asp Leu Tyr Gln  
145 150 155 160

Ser Leu Gln Lys Leu Leu Ala Asp Lys Lys Leu Val Asp Ser Leu Asp  
165 170 175

Pro Glu Thr Arg Arg Val Ala Glu Leu Phe Met Phe Asp Phe Glu Ile  
180 185 190

Ser Gly Ile His Leu Asp Lys Gln Lys Arg Lys Arg Ala Val Asp Leu  
195 200 205

Asn Val Lys Ile Leu Asp Leu Ser Ser Thr Phe Leu Met Gly Thr Asn  
210 215 220

Phe Pro Asn Lys Ile Glu Lys His Leu Leu Pro Glu His Ile Arg Arg  
225 230 235 240

Asn Phe Thr Ser Ala Gly Asp His Ile Ile Ile Asp Gly Leu His Ala  
245 250 255

Glu Ser Pro Asp Asp Leu Val Arg Glu Ala Ala Tyr Lys Ile Phe Leu  
260 265 270

Tyr Pro Asn Ala Gly Gln Leu Lys Cys Leu Glu Glu Leu Leu Ser Ser  
275 280 285

Arg Asp Leu Leu Ala Lys Leu Val Gly Tyr Ser Thr Phe Ser His Arg  
290 295 300

Ala Leu Gln Gly Thr Ile Ala Lys Asn Pro Glu Thr Val Met Gln Phe  
305 310 315 320

Leu Glu Lys Leu Ser Asp Lys Leu Ser Glu Arg Thr Leu Lys Asp Phe  
325 330 335

Glu Met Ile Arg Gly Met Lys Met Lys Leu Asn Ala Gln Asn Ser Glu  
340 345 350

Val Met Pro Trp Asp Pro Pro Tyr Tyr Ser Gly Val Ile Arg Ala Glu  
355 360 365

Arg Tyr Asn Ile Glu Pro Ser Leu Tyr Cys Pro Phe Phe Ser Leu Gly  
370 375 380 385

Ala Cys Met Glu Gly Leu Asn Ile Leu Leu Asn Arg Leu Leu Gly Ile  
385 390 395 400

Ser Leu Tyr Ala Glu Gln Pro Ala Lys Gly Glu Val Trp Ser Glu Asp  
405 410 415

Val Arg Lys Leu Ala Val Val His Glu Ser Glu Gly Leu Leu Gly Tyr  
420 425 430

Ile Tyr Cys Asp Phe Phe Gln Arg Ala Asp Lys Pro His Gln Asp Cys

435

440

445

His Phe Thr Ile Arg Gly Gly Arg Leu Lys Glu Asp Gly Asp Tyr Gln  
450 455 460

Leu Pro Leu Val Val Leu Met Leu Asn Leu Pro Arg Ser Ser Arg Ser  
465 470 475 480

Ser Pro Thr Leu Leu Thr Pro Gly Met Met Glu Asn Leu Phe His Glu  
485 490 495

Met Gly His Ala Met His Ser Met Leu Gly Arg Thr Arg Tyr Gln His  
500 505 510

Val Thr Gly Thr Arg Cys Pro Thr Asp Phe Ala Glu Val Pro Ser Ile  
515 520 525

Leu Met Glu Tyr Phe Ala Asn Asp Tyr Arg Val Val Asn Gln Phe Ala  
530 535 540

Arg His Tyr Gln Thr Gly Gln Pro Leu Pro Lys Asn Met Val Ser Arg  
545 550 555 560

Leu Cys Glu Ser Lys Lys Val Cys Ala Ala Ala Asp Met Gln Leu Gln  
565 570 575

0

Val Phe Tyr Ala Thr Leu Asp Gln Ile Tyr His Gly Lys His Pro Leu  
580 585 590

Arg Asn Ser Thr Thr Asp Ile Leu Lys Glu Thr Gln Glu Lys Phe Tyr  
595 600 605

Gly Leu Pro Tyr Val Pro Asn Thr Ala Trp Gln Leu Arg Phe Ser His  
610 615 620

Leu Val Gly Tyr Gly Ala Arg Tyr Tyr Ser Tyr Leu Met Ser Arg Ala  
625 630 635 640

Val Ala Ser Met Val Trp Lys Glu Cys Phe Leu Gln Asp Pro Phe Asn  
645 650 655

Arg Ala Ala Gly Glu Arg Tyr Arg Arg Glu Met Leu Ala His Gly Gly  
660 665 670

Gly Arg Glu Pro Met Leu Met Val Glu Gly Met Leu Gln Lys Cys Pro  
675 680 685

Ser Val Asp Asp Phe Val Ser Ala Leu Val Ser Asp Leu Asp Leu Asp  
690 695 700

Phe Glu Thr Phe Leu Met Asp Ser Glu  
705 710

<210> 163  
<211> 3923  
<212> DNA  
<213> human organism

<400> 163  
acagaagaaa tagcaagtgc cgagaagctg gcatcagaaa aacagagggg agatttgt 60  
ggctgcagcc gagggagacc aggaagatct gcatggtggg aaggacctga tgatacagag 120  
gaattacaac acatataactt agtgtttcaa tgaacaccaa gataaataag tgaagagcta 180  
gtccgctgtg agtctcctca gtgacacagg gctggatcac catcgacggc actttctgag 240  
tactcagtgc agcaaagaaa gactacagac atctcaatgg caggggtgag aaataagaaa 300  
ggctgctgac tttaccatct gaggccacac atctgctgaa atggagataa ttaacatcac 360  
tagaaacagc aagatgacaa tataatgtct aagtagtgac atgttttgc acatttccag 420  
cccctttaaa tatccacaca cacaggaagc aaaaaaggaa gcacagagat ccctgggaga 480  
aatgccccggc cgccatcttgc ggtcatcgat gagcctcgcc ctgtgcctgg tcccgcttgt 540  
gagggaaagga cattagaaaa tgaattgatg tgcccttaa aggatggca ggaaaacaga 600  
tcctgttgtg gatatttatt tgaacggat tacagatttgc aaatgaagt acaaagttag 660  
cattaccaat gagaggaaaa cagacgagaa aatcttgatg gcttcacaag acatgcaaca 720  
aacaaaatgg aatactgtga tgacatgagg cagccaagct ggggaggaga taaccacggg 780  
gcagagggtc aggattctgg ccctgctgcc taaactgtgc gttcataacc aaatcatttc 840  
atatttctaa ccctcaaaac aaagctgttg taatatctga tctctacggt tccttctggg 900  
cccaacattc tccatatac cagccacact cattttaat atttagttcc cagatctgt 960  
ctgtgacctt tctacactgt agaataacat tactcatttt gttcaaagac cttcgtgtt 1020  
gctgcctaat atgttagctga ctgttttcc taaggagtgt tctggccag gggatctgtg 1080  
aacaggctgg gaagcatctc aagatcttc cagggttata cttactagca cacagcatga 1140

tcattacgga gtgaattatac taatcaacat catcctcagt gtctttgccccc atactgaaat 1200  
tcatttccca cttttgtgcc cattctcaag acctcaaaat gtcattccat taatatcaca 1260  
ggattaactt ttttttttaa cctggaagaa ttcaatgtta catgcagcta tggaattta 1320  
attacatatt ttgtttcca gtgcaaagat gactaagtcc tttatccctc ccctttgttt 1380  
gattttttt ccagtataaa gttaaaatgc ttagccttgt actgaggctg tatacagcac 1440  
agcctctccc catccctcca gccttatctg tcattaccat caaccctcc cataccacct 1500  
aaacaaaatc taacttgtaa ttccttgaac atgtcaggac atacattatt ctttctgcct 1560  
gagaagctct tccttgcctc ttaaatctag aatgtatgtaa agtttgaat aagttgacta 1620  
tcttacttca tgcaaagaag ggacacatat gagattcatc atcacatgag acagcaaata 1680  
ctaaaagtgt aatttgatta taagagtttata gataaatata taaaatgcaa gagccacaga 1740  
ggaaatgttt atggggcacg tttgttgcctc tggatgtga agcaaaggca gggAACCTCA 1800  
tagtatctta tataatatac ttcatttctc tatctctatc acaatatcca acaagctttt 1860  
cacagaattc atgcagtgc aatccccaaa ggtaacctttt atccatttca tggtgagtgc 1920  
gctttagaat ttggcaaat catactggtc acttatctca actttgagat gtgttgtcc 1980  
ttgttagttaa ttgaaagaaa tagggcactc ttgtgagcca cttagggtt cactcctggc 2040  
aataaagaat ttacaaagag ctactcagga ccagttgtta agagctctgt gtgtgtgtgt 2100  
gtgtgtgtgt gagtgtacat gccaaggatgt gcctctctctt cttgacccat tatttcagac 2160  
ttaaaacaag catgtttca aatggcacta tgagctgcca atgatgtatc accaccatat 2220  
ctcattattc tccagtaaat gtgataataa tgtcatctgt taacataaaa aaagttgac 2280  
ttcacaaaag cagctggaaa tggacaacca caatatgcat aaatctaact cctaccatca 2340  
gctacacact gcttgacata tattgttaga agcacctcgat atttgtgggt tctcttaagc 2400  
aaaatacttg cattaggtct cagctggggc tgtgcacatcag gcggttttagt aaatattcaa 2460  
ttctcagcag aagccagaat ttgaattccc tcattttta ggaatcattt accaggtttg 2520  
gagaggattc agacagctca ggtgcatttca ctaatgtctc tgaacttctg tccctctttg 2580  
tgttcatgga tagtccaata aataatgtta tctttgaact gatgctcata ggagagaata 2640  
taagaactct gagtgtatc aacatttaggg attcaaagaa atattagatt taagctcaca 2700  
ctggtaaaaa ggaaccaaga tacaaagaac tctgagctgt catcgcccccc atctctgtga 2760  
gccacacaacca acagcaggac ccaacgcacatc tctgagatcc taaaatcaag gaaaccagtg 2820

tcatgagttt aattctccta ttatggatgc tagcttctgg ccatctctgg ctctcccttt	2880
gacacatatt agcttcttagc ctttgcttcc acgactttta tctttctcc aacacatcg	2940
ttaccaatcc tctctctgct ctgttgcttt ggacttcccc acaagaattt caacgactct	3000
caagtctttt cttccatccc caccactaac ctgaatgcct agacccttat ttttattaat	3060
ttccaataga tgctgcctat gggctatatt gcttagatg aacattagat atttaaagct	3120
caagagggttc aaaatccaac tcattatctt ctcttctt cacctccctg ctcctctccc	3180
tatattactg attgcactga acagcatggt ccccaatgta gccatgcaa tgagaaaccc	3240
agtggctcct tgtggtacat gcatgcaaga ctgctgaagc cagaaggatg actgattacg	3300
cctcatgggt ggaggggacc actcctgggc cttcgtgatt gtcaggagca agacctgaga	3360
tgctccctgc cttagtgtc ctctgcatact ccccttctta atgaagatcc atagaatttg	3420
ctacatttga gaattccaat taggaactca catgtttat ctgccctatc aatttttaa	3480
acttgctgaa aattaagttt ttcaaaaatc tgtccttgta aattactttt tcttacagtg	3540
tcttggcata ctatatcaac ttgattctt tgttacaact ttcttactc ttttatcacc	3600
aaagtggctt ttattcttatt tattattattt atttctttt actactatac tacgttgtt	3660
ttattttgtt ctctatagta tcaattttatt tgattnattt tcaattttatt ttatgtctg	3720
actttaaaaa taagtgattc ggggggtggg agaacagggg agggagagca ttaggacaaa	3780
tacctaattgc atgtggact taaaacctag atgatgggtt gataggtgca gcaaaccact	3840
atggcacacg tataacctgtg taacaaacctt acacattctg cacatgtatc ccagaacgta	3900
aagtaaaatt taaaaaaaaag tga	3923

<210> 164  
 <211> 8488  
 <212> DNA  
 <213> human organism

<400> 164	
atgatgatga acgtccccgg cggaggagcg gccgcgggtga tgatgacggg ctacaataat	60
ggtcgctgtc cccggatttc tctctacagt gactgcatta ttgaggagaa gacgggtggc	120
ctgcagaaaaa aagacaatga gggctttgga ttctgtcttc gagggggccaa agctgacaca	180
cccatgttgg aattcacacc aacaccggct ttcccagccc tacagtacctt ggagtccgtg	240
gatgaagggtt ggggtggcgtg gcaaggccgga ctaaggaccg gggacttctt gattgagggtt	300
aacaatgaga atgttgtcaa agtcggccac aggcagggtgg tgaacatgtatccggcaggga	360

ggaaatcacc tggtccttaa ggtggtcacg gtgaccagga atctggaccc cgacgacacc 420  
gccaggaaga aagctcccc gcctccaaag cgggcaccga ccacagccct caccctgcgc 480  
tccaagtcca tgacctcgga gctggaggag ctctggata aagataaaacc cgaggagata 540  
gtcccggcct ccaagccctc cgcgcgtgct gagaacatgg ctgtggaacc gagggtgtggcg 600  
accatcaagc agcggccag cagccggtgc ttcccggcgg gctcagacat gaaactctgtg 660  
tacgaacgcc aaggaatcgc cgtgatgacg cccactgttc ctgggagccc aaaagccccg 720  
tttctggca tccctcgagg tacgatgcga aggcaaaaat caatagacag cagaatcttt 780  
ctatcaggaa taacagagga agagcggcag tttctggctc ctccaatgct gaagttcacc 840  
agaagcctgt ccatgcccga cacctctgag gacatccccctt ctccaccgcgca gtctgtgccc 900  
ccgtccccac caccacccctc cccaaacctactacaactgccc ccaagttccca aactccaaga 960  
gtctacggga cgattaagcc tgcgttcaat cagaattctg ccgccaagggt gtccccggcc 1020  
accagggtccg acaccgtggc caccatgatg agggagaagg ggatgtactt caggagagag 1080  
ctggaccgct actccttgga ctctgaagac ctctacagtc ggaatgcccgg cccgcaagcc 1140  
aacttccgca acaagagagg ccagatgcca gaaaacccat actcagaggt gggaaagatc 1200  
gccagcaaag ccgtctacgt ccccgccaaag cccgcccaggc ggaaggggat gctggtgaag 1260  
cagtccaaacg tggaggacag ccccgagaag acgtgttcca tccctatccc gaccatcatc 1320  
gtgaaggagc cgtccaccag cagcagcggc aagagcagcc agggcagcag catggagatc 1380  
gaccccccagg ccccgaggcc acccgagccag ctgcggcctg acgaaaggctt gaccgtcagc 1440  
agcccccttg ccggcccat cggccggagcc gtcccgaccc gttgagaagcg gctggaaagcc 1500  
aggaggaact ccccgccctt cctctccaca gacctggggg atgaggatgt gggcctgggg 1560  
ccacccggccc ccaggacgcg gcccctccatg ttcccccggagg agggggattt tgctgacgag 1620  
gacagcgctg agcagctgtc atccccatg ccgagtgcca cggccaggga gcccggaaaaac 1680  
catttcgtgg gtggcgccga ggccagtgtc ccgggtgagg ctgggaggcc gctgaattcc 1740  
acgtccaaag cccaggggcc cggagcagc ccagcagtc cctccgcggcag cagcggcaca 1800  
gccggccccc ggaattatgt ccacccactc acagggcggc tgcttgatcc cagctccccg 1860  
ctggccctgg cactctccgc aagggaccga gccatgaagg agtctcaaca gggacccaaa 1920  
ggggaggccc ccaaggccga cctcaacaaa cctctttaca ttgataccaa aatgcggccc 1980  
agcctggatg ccggcttccc tacggtcacc aggcagaaca cccggggacc cctgaggcgg 2040  
caggagacgg agaacaagta cgagaccgac ctggggcggag accggaaagg cgatgacaag 2100

aagaacatgc tgatcgacat catggacacg tcccagcaga agtcggctgg cctgctgatg 2160  
gtgcacaccg tggacgccac taagctggac aacgcctgc aggaagagga cgagaaggca 2220  
gaggtggaga tgaagccaga cagctgccc tccgaggtgc cagaaggtgt ttccgaaacc 2280  
gaaggtgctt tacagatctc cgctgcccc gagccacca ccgtgcccgg cagaaccatc 2340  
gtcgcgggtgg gctccatgga agaggcggtg attttgcatt tccgcattccc tcctccccct 2400  
ctggcatccg tggacttggta tgaggatttt attttacag agccattgcc tcctccctg 2460  
gaatttgc当地 atagtttgc当地 tatccccat gaccgggc当地 ct当地gtccc ggctctctca 2520  
gacttagtgc当地 agcagaagaa aagcgacacc cctcagtc当地 ct当地gtt当地aa ctccagccaa 2580  
ccaaccaact ctgcagacag caagaagccca gccagtc当地 cttactgtct gcctgc当地ca 2640  
ttctgccc当地 cccctgaaag ct当地tgc当地 gtc当地ccgact ct当地ggatc当地a ggagggtggac 2700  
agccggagta gcagc当地acca ccacctcgag acgaccagca ct当地tccac cgtgtctagc 2760  
atctccaccc tgc当地tccg当地 aggtggagag aatgtggaca cctgc当地acgt ct当地gc当地at 2820  
gggcaagcat ttatgggtgc当地 caaacccttca gtacctc当地ta agccaaaaat gaagcccatc 2880  
attcacaaaa gcaatgc当地act ttatcaagac ggc当地tc当地gtgg aagaagatgt agatac当地ttt 2940  
gttacccccc cggccgctcc cccgcccccc cccggc当地gtg cccagc当地tgg gatggcc当地ag 3000  
gttctccagc caaggacctc caagttgtgg ggc当地gacgtca cagagatcaa aagcccgatt 3060  
ctctcaggcc caaaggccaa cgttatttagt gaattgaact ct当地cttaca gcaaatgaac 3120  
cgagagaaaat tggcaaagcc gggggaaagga ctggattcac caatgggagc caagtccgccc 3180  
agcctcgctc caagaagccc ggagatcatg agcaccatct caggtacacg gagcacgacg 3240  
gtcaccttca ctgttgc当地cc cggcacctcc cagcccatca ccctgc当地agag ccggcccccc 3300  
gactatgaaa gcaggacctc aggaacaaga cgtgccccaa gccctgtggt ct当地gccaaca 3360  
gagatgaaca aagagaccct gcccggcccc ctgtctgctg ccaccgc当地tc tccttctccc 3420  
gctctctc当地ag atgtctttag cttccaaagc cagccccc当地t ct当地gggatct atttggctt当地g 3480  
aacccagc当地gg gacgc当地gtg gtc当地ccatcc ccctcgatc当地 tgcaacagcc aatctcaaata 3540  
aaggcccttta caactaaacc tgc当地ccacctg tggactaaac cagatgtggc cgattggctg 3600  
gaaagtctaa acttgggtgc当地 acataaagag gccttcatgg acaatgagat cgatggc当地gt 3660  
cacttaccaa acctgc当地gaa ggaggacctc atcgatctt当地g gggtaactcg agtccggc当地ac 3720  
agaatgaaca tagaaagggc当地 tttgaaacag ctgctggaca gataaggacg gctgctctcc 3780

acctcgcaga ctgctttgt tataagtaga gatgggctcg tgctgaaaca tctgaatgcc 3840  
aagcgaagtc tgtgagcatc aaccccactc catgggttg tctcctggta cccaaagaaa 3900  
tactgagttg tgtccacaac atggctgggt cttcagaccc ctggctcacc atgtgggtgt 3960  
cttggcagt ttctatcaca catggacaa ggggagggag ttttctaac atggaaaaag 4020  
attcccagcc tgccgcccag catgcaggta gcctcgctt gccgggtccg agaggctccc 4080  
cgtcaatttt gcacgggatc ctagctttg taggcagaca ccagtgcact ctagataacct 4140  
cctgagacct ccgtccctcg cttccgggc agctctcacc accccaggcc ccggcatgag 4200  
gccttcctc agtcctgtgg cctctcagag gacacctgat gtcacactgc cccttttct 4260  
cctgcacttg gcttgcagtg agatgctccc agatgcattt gtccagtgcc ccatcatggg 4320  
cctgaaaggc agagaaactt ttcctacac agatttttt ccccatctcc tcctgtggtt 4380  
tgcatccatg gctcttggc catgagggtc ctggcagtgc tggagttt gatggatcg 4440  
tgcccagctt tgcttagctt tcttatttc tgcaaatctg ttagcataat tccaaggtgg 4500  
ccaagcagat gtcacatgga gtttgtcaaa gcacaaagtc acgattccac aatggagggg 4560  
agacctggcc aaggagcca gccagcgtgc aactgccaa gctccaggc tccaggacaa 4620  
gagcagttgt ctgccccatgag cacccatcca ggatggagaa taagggcttc tctgcctc 4680  
agaattttt ttaatttgaag atgtctttagt ctctgcaaaatc atcagagcag gtgagcatcc 4740  
actttgacat gaaggacaag aagacgcattt gctcatggcg ggcacatgcg gtcgcagg 4800  
agacagcgtc tcctctggga gctggggggg cacagcatcc tcagttctgt gcccagccaa 4860  
gggtgagcat ctctgctgag acagtccttt tgctctcgga ggccagggaa gatggtaactt 4920  
agaggcttt cccctatcgc tctgggtgtc taggaatccc accagttgt cttaacagta 4980  
caacagcttc tttgaggacc cagtgggtat ggagtataga cagaacccag gggtgagaac 5040  
agaagggtggg cggcaggatc agagtggaaag cagaggcgtg aggagagggaa agcagggagg 5100  
tctcctgggc tgccaggatca gcctctctgg caaggcttc ttgagccccg cccctttctt 5160  
tccccggagt ccctccaccc cataacaata cctcgaattt cccaaagagg tcaccagat 5220  
cacatgggcc gcaaaacaca cagtcaggct tccagcacat tctccccat ttggaggata 5280  
ctcgaatgtc aggtttttgg ttttatttattt atttcagaac tagctcagcc catctcta 5340  
tataaaacat ggttttgttt ttttttttc cttttttct tgatttaggtc tggaacagct 5400  
ctagaatgaa cacataaaat ttagcaattt aaaatcttc tttactgcaa gtttaaatag 5460  
ttgtacagat agtttataag cacaatattt taagaaaaaa aagtggctgg tctactaggc 5520

agccttgc ccacttcagt gctagaaaat taaagaaaaa aaaactttg tgattataa 5580  
atactatttc tgtgaaataa ttataaaaat atgacccccc taaatcaacc ttatttgat 5640  
gcatctgaac cagcagagct gtgttatatt ttctatctt gctagaactt cgtcattgaa 5700  
ggacaatttc ttcaaagtgg ttacaattca taatgcagca gtttctccaa aaacaaaaac 5760  
aaaacacaca ccacacacac gcgctttcc agtcacacac ccctgatgtt ggaaccaagt 5820  
tttggacct tctgttccaa aacctttgc aggtcaatct ttgtatttga aatgatccaa 5880  
tccaacttga agtcaattga atattaaggc gcttacttc cgtgtgctt cagttttcc 5940  
atcatgagat gaatgagcat tactcttagat aaatttcaag acaggatact acaggtggcc 6000  
tgctgaggct gccccatatt ttagaaaatg taaaaatggt gggttggcca ttaatttgc 6060  
ttccatttga tgataccgca aaattccgtg agtccattcc tttggcatgg cactttccct 6120  
gggcctacag ttggatttac ctctgtgctc agtgcagggc aaaacactag ctcaaaggag 6180  
agtcaaggaa accgctggca gacgataacc agtcgaaact cgtgacttcg gtttggaa 6240  
ctttggcagc cagttggtga gggccagatg ttattccctt tcttaaagat actccaagcc 6300  
acatgccact aaccacaagc aagctggctg caagactaaa gagctgataa catagttat 6360  
ttttacactg tcttattata gagaagtaat agacctatca gaacctgcac tgaccaacaa 6420  
ataaacacat gttgccaaga tgaatcggtc tctatctcta tctgcttatt ttggactga 6480  
aagcaatagt tcctcattca aatcaccacc cactgttctc ccccttggg acatgttagg 6540  
acgaggccct attccatgcc cctcttaat ggtggaccaa atgttaaact gctcatctaa 6600  
agatcatgtt gatattttc caggtttaa gatcaacttt tgttacatac tgtaatttaa 6660  
ataaaactgca tttacatgcc tagttctgt aatattgtgt atacaaaacc caaatctctc 6720  
aaaatgtaaa ttatgtatac ctgccaagat acctttcca ggggtctgc gcacattta 6780  
agttaattca cataatataa aaattactca atgtgactgt tgatttgctg aactttacat 6840  
atcacaatgtt gaatttttg tgatacttta gttaataaaa tggtaaattt ttttctcagt 6900  
tattgaacaa gcaagcatta tccagttgat ctggcaatga cttttgtgt gtggccaca 6960  
atattgatt tcccattaac aattttttt tggtaaattt atactaatat gtttcacact 7020  
atagttgtg taacaacacg tggtcgatt atctatgtt ctgttacttt tggtaaattt 7080  
ttcttttag actttataaa aaaaaaaaaa agctccgtta atttgactt tctcccaatc 7140  
cttaaatctc ttgtatggca accaaaatataa ctgtaaaaaa ataaatatac tattgcacta 7200

aggttgtggt tctgattgca aacaaacagt gaacactgtc tgaattaaac aaaaagctgc	7260
ccgacttgca atctaattgt a gattatctca ggcattgtgg ccagctctgc ctctctaaaa	7320
ctgaccagaa aaatctctct catcgagtaa acaggctcct gtcactgagc taatctgcct	7380
tggttccatt tccttattct caatttatca atggatacgt gcatgttatt tcagaattat	7440
gcaaaacgtc aaaatctgct tctgtgaccg ctgctataagg cgtggagctg aggctcggct	7500
ttcccttttgg ttctgggtgg aagcagcggt gccgcggagg gccagccaga tccggaccct	7560
tcccttaggg tccagtc tcc acacacccca gcagggtgtc ttctagccat aaggccaagg	7620
gagtggcaga actggccgc ctctctgggtt gacaagcaaa ccacatgcta aggcttggag	7680
caagagagaa tttgtgtcta ttggcaaaga actaagccag gaagacatgg gccatccc tcc	7740
cgctttaggg aagcatat taaacctaaa cgttgaacctt ctctttggc ctcaccagtg	7800
aaaacttggtt gtcttagtt cctaaagttt cttctacttt ggcacattcc ccagttgagc	7860
agcagcctct atgcttccac gttcaggaaa aattccagtc ctcataatctt ttgttagttca	7920
ccctcaagct ctcccgcttc accatccaat agtttctccc aaaccttggc acccccctag	7980
actttgcttc caatggtttc ttccagacca ct tttccttag atgaatata ttcgatcac	8040
tactaggaaa attattggaa gat tttttct tttactt gaa attggaggca tttaataac	8100
tggcgaactg gaatgtgttt ctgtat tttgtt agacaaccat gtacccatgc aagttaggtga	8160
acattccaca gtggctgggt gaccacagca gctgc tgc a gacaggactg cccgtgctt	8220
gtggaaatc agagaatttca a aacttggttt tctcagactt ccgcagatct catca tttg	8280
atttcta atc catgctgtat tgg tggat tttatcg tttatcg tttatcg tttatcg	8340
ccacagtctt taccgtttta tg tcaaaaat tacaacaatc cctgtccatt gattccactc	8400
tggaaactctt tg tcaatgcc aat tttgaaa tttaataacg agc ttc aaaa taaacacaga	8460
aaagaaaaaaa aaaaaaaaaa aaaaaaaaaa	8488

<210> 165  
 <211> 1254  
 <212> PRT  
 <213> human organism

<400> 165

Met	Met	Met	Asn	Val	Pro	Gly	Gly	Gly	Ala	Ala	Ala	Val	Met	Met	Thr
1				5					10				15		

Gly Tyr Asn Asn Gly Arg Cys Pro Arg Asn Ser Leu, Tyr Ser Asp Cys

20

25

30

Ile Ile Glu Glu Lys Thr Val Val Leu Gln Lys Lys Asp Asn Glu Gly  
35 40 45

Phe Gly Phe Val Leu Arg Gly Ala Lys Ala Asp Thr Pro Ile Glu Glu  
50 55 60

Phe Thr Pro Thr Pro Ala Phe Pro Ala Leu Gln Tyr Leu Glu Ser Val  
65 70 75 80

Asp Glu Gly Gly Val Ala Trp Gln Ala Gly Leu Arg Thr Gly Asp Phe  
85 90 95

Leu Ile Glu Val Asn Asn Glu Asn Val Val Lys Val Gly His Arg Gln  
100 105 110

Val Val Asn Met Ile Arg Gln Gly Gly Asn His Leu Val Leu Lys Val  
115 120 125

Val Thr Val Thr Arg Asn Leu Asp Pro Asp Asp Thr Ala Arg Lys Lys  
130 135 140

Ala Pro Pro Pro Pro Lys Arg Ala Pro Thr Thr Ala Leu Thr Leu Arg  
145 150 155 160

Ser Lys Ser Met Thr Ser Glu Leu Glu Leu Val Asp Lys Asp Lys  
165 170 175

Pro Glu Glu Ile Val Pro Ala Ser Lys Pro Ser Arg Ala Ala Glu Asn  
180 185 190

Met Ala Val Glu Pro Arg Val Ala Thr Ile Lys Gln Arg Pro Ser Ser  
195 200 205

Arg Cys Phe Pro Ala Gly Ser Asp Met Asn Ser Val Tyr Glu Arg Gln  
210 215 220

Gly Ile Ala Val Met Thr Pro Thr Val Pro Gly Ser Pro Lys Ala Pro  
225 230 235 240

Phe Leu Gly Ile Pro Arg Gly Thr Met Arg Arg Gln Lys Ser Ile Asp  
245 250 255

Ser Arg Ile Phe Leu Ser Gly Ile Thr Glu Glu Glu Arg Gln Phe Leu  
260 265 270

Ala Pro Pro Met Leu Lys Phe Thr Arg Ser Leu Ser Met Pro Asp Thr  
275 280 285

Ser Glu Asp Ile Pro Pro Pro Gln Ser Val Pro Pro Ser Pro Pro  
290 295 300

Pro Pro Ser Pro Thr Thr Tyr Asn Cys Pro Lys Ser Pro Thr Pro Arg  
305 310 315 320

Val Tyr Gly Thr Ile Lys Pro Ala Phe Asn Gln Asn Ser Ala Ala Lys  
325 330 335

Val Ser Pro Ala Thr Arg Ser Asp Thr Val Ala Thr Met Met Arg Glu  
340 345 350

Lys Gly Met Tyr Phe Arg Arg Glu Leu Asp Arg Tyr Ser Leu Asp Ser  
355 360 365

Glu Asp Leu Tyr Ser Arg Asn Ala Gly Pro Gln Ala Asn Phe Arg Asn  
370 375 380

Lys Arg Gly Gln Met Pro Glu Asn Pro Tyr Ser Glu Val Gly Lys Ile  
385 390 395 400

Ala Ser Lys Ala Val Tyr Val Pro Ala Lys Pro Ala Arg Arg Lys Gly  
405 410 415

Met Leu Val Lys Gln Ser Asn Val Glu Asp Ser Pro Glu Lys Thr Cys  
420 425 430

Ser Ile Pro Ile Pro Thr Ile Ile Val Lys Glu Pro Ser Thr Ser Ser  
435 440 445

Ser Gly Lys Ser Ser Gln Gly Ser Ser Met Glu Ile Asp Pro Gln Ala  
450 455 460

Pro Glu Pro Pro Ser Gln Leu Arg Pro Asp Glu Ser Leu Thr Val Ser  
465 470 475 480

Ser Pro Phe Ala Ala Ala Ile Ala Gly Ala Val Arg Asp Arg Glu Lys  
485 490 495

Arg Leu Glu Ala Arg Arg Asn Ser Pro Ala Phe Leu Ser Thr Asp Leu  
500 505 510

Gly Asp Glu Asp Val Gly Leu Gly Pro Pro Ala Pro Arg Thr Arg Pro  
515 520 525

Ser Met Phe Pro Glu Glu Gly Asp Phe Ala Asp Glu Asp Ser Ala Glu  
530 535 540

Gln Leu Ser Ser Pro Met Pro Ser Ala Thr Pro Arg Glu Pro Glu Asn  
545 550 555 560

His Phe Val Gly Gly Ala Glu Ala Ser Ala Pro Gly Glu Ala Gly Arg  
565 570 575

Pro Leu Asn Ser Thr Ser Lys Ala Gln Gly Pro Glu Ser Ser Pro Ala  
580 585 590

Val Pro Ser Ala Ser Ser Gly Thr Ala Gly Pro Gly Asn Tyr Val His  
595 600 605

Pro Leu Thr Gly Arg Leu Leu Asp Pro Ser Ser Pro Leu Ala Leu Ala  
610 615 620

Leu Ser Ala Arg Asp Arg Ala Met Lys Glu Ser Gln Gln Gly Pro Lys  
625 630 635 640

Gly Glu Ala Pro Lys Ala Asp Leu Asn Lys Pro Leu Tyr Ile Asp Thr  
645 650 655

Lys Met Arg Pro Ser Leu Asp Ala Gly Phe Pro Thr Val Thr Arg Gln  
660 665 670

Asn Thr Arg Gly Pro Leu Arg Arg Gln Glu Thr Glu Asn Lys Tyr Glu  
675 680 685

Thr Asp Leu Gly Arg Asp Arg Lys Gly Asp Asp Lys Lys Asn Met Leu  
690 695 700

Ile Asp Ile Met Asp Thr Ser Gln Gln Lys Ser Ala Gly Leu Leu Met  
705 710 715 720

Val His Thr Val Asp Ala Thr Lys Leu Asp Asn Ala Leu Gln Glu Glu  
725 730 735

Asp Glu Lys Ala Glu Val Glu Met Lys Pro Asp Ser Ser Pro Ser Glu  
740 745 750

Val Pro Glu Gly Val Ser Glu Thr Glu Gly Ala Leu Gln Ile Ser Ala  
755 760 765

Ala Pro Glu Pro Thr Thr Val Pro Gly Arg Thr Ile Val Ala Val Gly  
770 775 780

Ser Met Glu Glu Ala Val Ile Leu Pro Phe Arg Ile Pro Pro Pro Pro  
785 790 795 800

Leu Ala Ser Val Asp Leu Asp Glu Asp Phe Ile Phe Thr Glu Pro Leu  
805 810 815

Pro Pro Pro Leu Glu Phe Ala Asn Ser Phe Asp Ile Pro Asp Asp Arg  
820 825 830

Ala Ala Ser Val Pro Ala Leu Ser Asp Leu Val Lys Gln Lys Lys Ser  
835 840 845

Asp Thr Pro Gln Ser Pro Ser Leu Asn Ser Ser Gln Pro Thr Asn Ser  
850 855 860

Ala Asp Ser Lys Lys Pro Ala Ser Leu Ser Asn Cys Leu Pro Ala Ser  
865 870 875 880

Phe Leu Pro Pro Pro Glu Ser Phe Asp Ala Val Ala Asp Ser Gly Ile  
885 890 895

Glu Glu Val Asp Ser Arg Ser Ser Asp His His Leu Glu Thr Thr  
900 905 910

Ser Thr Ile Ser Thr Val Ser Ser Ile Ser Thr Leu Ser Ser Glu Gly  
915 920 925

Gly Glu Asn Val Asp Thr Cys Thr Val Tyr Ala Asp Gly Gln Ala Phe

Met Val Asp Lys Pro Pro Val Pro Pro Lys Pro Lys Met Lys Pro Ile	935	940
	945	950
		955
		960
Ile His Lys Ser Asn Ala Leu Tyr Gln Asp Ala Leu Val Glu Glu Asp	965	970
		975
Val Asp Ser Phe Val Ile Pro Pro Pro Ala Pro Pro Pro Pro Gly	980	985
		990
Ser Ala Gln Pro Gly Met Ala Lys Val Leu Gln Pro Arg Thr Ser Lys	995	1000
		1005
Leu Trp Gly Asp Val Thr Glu Ile Lys Ser Pro Ile Leu Ser Gly	1010	1015
		1020
Pro Lys Ala Asn Val Ile Ser Glu Leu Asn Ser Ile Leu Gln Gln	1025	1030
		1035
Met Asn Arg Glu Lys Leu Ala Lys Pro Gly Glu Gly Leu Asp Ser	1040	1045
		1050
Pro Met Gly Ala Lys Ser Ala Ser Leu Ala Pro Arg Ser Pro Glu	1055	1060
		1065
Ile Met Ser Thr Ile Ser Gly Thr Arg Ser Thr Thr Val Thr Phe	1070	1075
		1080
Thr Val Arg Pro Gly Thr Ser Gln Pro Ile Thr Leu Gln Ser Arg	1085	1090
		1095
Pro Pro Asp Tyr Glu Ser Arg Thr Ser Gly Thr Arg Arg Ala Pro	1100	1105
		1110
Ser Pro Val Val Ser Pro Thr Glu Met Asn Lys Glu Thr Leu Pro	1115	1120
		1125
Ala Pro Leu Ser Ala Ala Thr Ala Ser Pro Ser Pro Ala Leu Ser	1130	1135
		1140
Asp Val Phe Ser Leu Pro Ser Gln Pro Pro Ser Gly Asp Leu Phe	1145	1150
		1155

Gly Leu Asn Pro Ala Gly Arg Ser Arg Ser Pro Ser Pro Ser Ile  
1160 1165 1170

Leu Gln Gln Pro Ile Ser Asn Lys Pro Phe Thr Thr Lys Pro Val  
1175 1180 1185

His Leu Trp Thr Lys Pro Asp Val Ala Asp Trp Leu Glu Ser Leu  
1190 1195 1200

Asn Leu Gly Glu His Lys Glu Ala Phe Met Asp Asn Glu Ile Asp  
1205 1210 1215

Gly Ser His Leu Pro Asn Leu Gln Lys Glu Asp Leu Ile Asp Leu  
1220 1225 1230

Gly Val Thr Arg Val Gly His Arg Met Asn Ile Glu Arg Ala Leu  
1235 1240 1245

Lys Gln Leu Leu Asp Arg  
1250

<210> 166  
<211> 2015  
<212> DNA  
<213> human organism

<400> 166  
actgcgaagc ggcttcttca gagcacgggc tggaaactggc aggcaccgcg agccccttagc 60  
acccgacaag ctgagtggtgc aggacgagtc cccaccacac ccacaccaca gccgctgaat 120  
gaggcttcca ggcgtccgct cgccggccgc agagccccgc cgtgggtccg cccgctgagg 180  
cgcccccagc cagtgcgttt acctgccaga ctgcgcgcct tggggcaacc cgggaacggc 240  
agcgccttct tgctggcacc caatagaagc catgcgcgg accacgacgt cacgcagcaa 300  
agggacgagg tgtgggtggt gggcatggc atcgtcatgt ctctcatgt cctggccatc 360  
gtgtttggca atgtgctggt catcacagcc attgccaagt tcgagcgtct gcagacggc 420  
accaactact tcatcacttc actggcctgt gctgatctgg tcatgggcct ggcagtggc 480  
ccctttgggg ccgccccatat tcttatgaaa atgtggactt ttggcaactt ctgggtgcgag 540  
ttttggactt ccattgatgt gctgtgcgtc acggccagca ttgagaccct gtgcgtgatc 600  
gcagtggtac gctactttgc cattacttca cctttcaagt accagagcct gctgaccaag 660

aataaggccc	gggtgatcat	tctgatggtg	tggatttgt	caggcttac	ctccttcttg	720
cccattcaga	tgcactggta	ccgggccacc	caccaggaag	ccatcaactg	ctatgccaat	780
gagacctgct	gtgacttctt	cacgaaccaa	gcctatgcca	ttgcctcttc	catcggtcc	840
ttctacgttc	ccctggtgat	catggtcttc	gtctactcca	gggtctttca	ggaggccaaa	900
aggcagctcc	agaagattga	caaatctgag	ggccgcttcc	atgtccagaa	ccttagccag	960
gtggagcagg	atgggcccac	ggggcatgga	ctccgcagat	cttccaagtt	ctgcttgaag	1020
gagcacaaag	ccctcaagac	gttaggcattc	atcatggca	ctttcaccct	ctgctggctg	1080
cccttcttca	tcgttaacat	tgtcatgtg	atccaggata	acctcatccg	taaggaagtt	1140
tacatcctcc	taaattggat	aggctatgtc	aattctggtt	tcaatcccct	tatctactgc	1200
cggagccccag	atttcaggat	tgccttccag	gagcttctgt	gcctgcgcag	gtcttcttg	1260
aaggcctatg	ggaatggcta	ctccagcaac	ggcaacacag	gggagcagag	tggatatcac	1320
tggaacagg	agaaagaaaa	taaactgctg	tgtgaagacc	tcccaggcac	ggaagacttt	1380
tgggccatc	aaggtactgt	gcctagcgat	aacattgatt	cacaagggag	gaattgtagt	1440
acaatgact	cactgctgta	aagcagttt	tctacttta	aagacccccc	cccccccaac	1500
agaacactaa	acagactatt	taacttgagg	gtaataaact	tagaataaaa	ttgtaaaaat	1560
tgtatagaga	tatgcagaag	gaagggcattc	cttctgcctt	ttttatTTT	ttaagctgta	1620
aaaagagaga	aaacttattt	gagtgattat	ttgttatttg	tacagttcag	ttccttttg	1680
catggaattt	gtaagtttat	gtctaaagag	ctttagtcct	agaggacctg	agtctgctat	1740
attttcatga	ctttccatg	tatctacctc	actattcaag	tattaggggt	aatatattgc	1800
tgctggtaat	ttgtatctga	aggagatttt	cttcctaca	cccttggact	tgaggatttt	1860
gagtatctcg	gaccttcag	ctgtgaacat	ggactcttcc	cccactcctc	ttatTTgctc	1920
acacggggta	ttttaggcag	ggatttgagg	agcagcttca	gttgtttcc	cgagcaaagg	1980
tctaaagttt	acagtaaaata	aaatgtttga	ccatg			2015

<210> 167  
 <211> 413  
 <212> PRT  
 <213> human organism

<400> 167

Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg  
 1 5 10 15

Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp  
20 25 30

Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val  
35 40 45

Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu  
50 55 60

Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu  
65 70 75 80

Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met  
85 90 95

Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile  
100 105 110

Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala  
115 120 125

Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu  
130 135 140

Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val  
145 150 155 160

Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala  
165 170 175

Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp  
180 185 190

Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe  
195 200 205

Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln  
210 215 220

Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe  
225 230 235 240

His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His  
245 250 255

Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu  
260 265 270

Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro  
275 280 285

Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg  
290 295 300

Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly  
305 310 315 320

Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe  
325 330 335

Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn  
340 345 350

Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val  
355 360 365

Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr  
370 375 380

Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp  
385 390 395 400

Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu  
405 410

<210> 168

<211> 3741

<212> DNA

<213> human organism

<400> 168

gaattcgttg ttggaaagga ctgggaaac agctgtaaca tttgccaccc tcagaagctg 60

ctggtcctgt gtcacaccac cttagcctct tgatcgagga agattctgc tgaagtctgt 120

taattctact tttttagtac ttatgaataa ccacgtgtct tcaaaaaccat ctaccatgaa 180

gctaaaacat accatcaaacc ctattctttt atatttata cattttctaa tatkacttta 240  
tactattta acatacattc cgttttatTT tttctccgag tcaagacaag aaaaatcaaa 300  
ccgaattaaa gcaaaggctg taaattcaaa acctgattct gcatacagat ctgttaatag 360  
tttggatggT ttggcttcag tattataccc tggatgtgat actttagata aagttttac 420  
atatgcaaaa aacaaattta agaacaaaag actcttgga acacgtgaag ttttaatga 480  
ggaagatgaa gtacaaccaa atggaaaaat tttaaaaag gttattctg gacagtataa 540  
ttggcttcc tatgaagatg tcttgcTTcg agccttaat tttggaaatg gattacagat 600  
gttgggtcag aaaccaaaga ccaacatcgc catctctgt gagaccaggG ccgagtggat 660  
gatagctgca caggcgtgtt ttatgtataa tttcagctt gttacattat atgccactct 720  
aggaggtcca gccattgttc atgcattaaa tgaaacagag gtgaccaaca tcattactag 780  
taaagaactc ttacaaacaa agttgaagga tatagtttct ttggcccac gcctgcggca 840  
catcatcaCT gttgatggaa agccaccgac ctggTccgac ttccccagg gcatcattgt 900  
gcataccatg gctgcagtgg aggccctggg agccaaggcc agcatggaaa accaacctca 960  
tagcaaacca ttgcctcag atattgcagt aatcatgtac acaagtggat ccacaggact 1020  
tccaaaggga gtcatgatct cacatagtaa cattattgct ggtataactg ggatggcaga 1080  
aaggattcca gaactaggag aggaagatgt ctacattgga tatttgcctc tggccatgt 1140  
tctagaatta agtgctgagC ttgtctgtct ttctcacggA tgccgcattt gttactcttc 1200  
accacagact ttagcagatC agtcttcaaa aattaaaaaa ggaagcaaaag gggatacatc 1260  
catgttggaaa ccaacactga tggcagcagt tccggaaatc atggatcgga tctacaaaaaa 1320  
tgtcatgaat aaagtcaCgt aatgagtag tttcaacgt aatctgtttt ttctggccta 1380  
taattacaaa atggaacaga tttcaaaagg acgtaataact ccactgtgcg acagcttgc 1440  
tttccggaaa gttcgaagct tgctaggggg aaatattcgt ctccTgttgc ttggTggcgc 1500  
tccactttct gcaaccacgc agcgattcat gaacatctgt ttctgctgC ctgttggtca 1560  
gggatacggg ctcactgaat ctgctggggc tggaacaatt tccgaagtgt gggactacaa 1620  
tactggcaga gtgggagcac cattagttt ctgtgaaatc aaattaaaaa actgggagga 1680  
aggtggatac tttaataactg ataagccaca ccccagggtt gaaattcttA ttggggccca 1740  
aagtgtgaca atgggtact acaaaaatga agcaaaaaca aaagctgatt tctctgaaga 1800  
tgaaaatgga caaaggTggc tctgtactgg ggatattgga gagttgaac ccgatggatg 1860  
cttaaagatt attgatcgta aaaaggacct tgtaaaacta caggcaggGG aatatgttcc 1920

tcttggaaa gtagaggcag ctttgaagaa tcttccacta gtagataaca tttgtgcata 1980  
tgcaaacagt tatkattctt atgtcattgg atttgttgtg ccaaataaaa aggaactaac 2040  
tgaacttagct cgaaagaaaag gacttaaagg gacttggag gagctgtgtacagttgtga 2100  
aatggaaaat gaggtactta aagtgcatttc cgaagctgct attcagcaaa gtctggaaaa 2160  
gtttgaaatt ccagtaaaaa ttctgtttag tcctgaaccg tgacccctg aaactggct 2220  
ggtgacagat gccttcaagc tgaaacgcaa agagcttaaa acacattacc aggcggacat 2280  
tgagcgaatg tatggaagaa aataattatt ctcttctggc atcagttgc tacagtggc 2340  
tcacatcaaa taggaaaata ctgaaatgc atgtctcaag ctgcaaggca aactccattc 2400  
ctcatattaa actattactt ctcatgacgt caccatTTT aactgacagg attagtaaaa 2460  
catthaagaca gcaaacttgt gtctgtctct tctttcattt tccccgccac caacttactt 2520  
taccacatat gactgtactt gtcagttatga gaattttctt gaatcatatt ggggaaggcag 2580  
tgatTTTaaa acctcaagtt ttAAACATG atttatatgt tctgtataat gttcagttt 2640  
taacttttaa aaagtttggg tgtatagagg gataaatagg aaatataaga attggttatt 2700  
tgggggcttt ttacttact gtatTTAAA atacaagggt attgatatga aattatgtaa 2760  
atttcaatg cttatgaatc aaatcattgt tgaacaaaag atttggct gtgtattat 2820  
tgtcttgtat gcatttgaga gaaataaata tacccatact tatgtttaa gaagttgaga 2880  
tcttgtgaat atatgcctgt cagtgtcttc ttatatatatt tatttttat tagaaaaat 2940  
gaagtttggg tggtgatgca tgaaacaaaa tagcaagaga gggttatagt ttaatagtaa 3000  
gggagataac acagcatgtg tagcaccagt tgataattgg tctctagtag cttactgtca 3060  
aaatgttcaa tgaagtcttc tgttcatctg ttgaaacttag gaaaataccc aaacttaaat 3120  
ggaagaattc tgaaagagag gatagaattt aaagaacaag agtatataaa gttattctt 3180  
gaatatttcg ttgactatat gtacatttag ttatctatat ttgtaaacaa attagtcattg 3240  
gaaaattatt ctattccaaa gtctcctttt agtctagata atcattattt cattttaaa 3300  
ttatgtttt tcatagtttgcactgatgctg tgtatggatg tgtgtgagtc agtggtagct 3360  
tatTTAAAAA gcacccatc ctttctccca taacccctgt acactaaaaa atgaaagaat 3420  
ttagaatgtt tttgatgata gcattctcac taagacacat gagaatttaa ctttataacc 3480  
gcgtgagttt agattaatt catagttttt gatgtcattt ttgtaaatttttca 3540  
gaaaccttgc ttgtgtgata catagtaagt ctcttcattt attactgctt gcctgttgc 3600

atatctggat tatcaaaagc aatagtgcac caattaagat gtgctcaa at caggacttaa 3660  
atcataggca ccacatttt catgtcagac tagttacttt gttgattctc agttactgta 3720  
ggcatcaaaa ggcaaaaatc a 3741

<210> 169  
<211> 720  
<212> PRT  
<213> human organism

<400> 169

Met Asn Asn His Val Ser Ser Lys Pro Ser Thr Met Lys Leu Lys His  
1 5 10 15

Thr Ile Asn Pro Ile Leu Leu Tyr Phe Ile His Phe Leu Ile Ser Leu  
20 25 30

Tyr Thr Ile Leu Thr Tyr Ile Pro Phe Tyr Phe Phe Ser Glu Ser Arg  
35 40 45

Gln Glu Lys Ser Asn Arg Ile Lys Ala Lys Pro Val Asn Ser Lys Pro  
50 55 60

Asp Ser Ala Tyr Arg Ser Val Asn Ser Leu Asp Gly Leu Ala Ser Val  
65 70 75 80

Leu Tyr Pro Gly Cys Asp Thr Leu Asp Lys Val Phe Thr Tyr Ala Lys  
85 90 95

Asn Lys Phe Lys Asn Lys Arg Leu Leu Gly Thr Arg Glu Val Leu Asn  
100 105 110

Glu Glu Asp Glu Val Gln Pro Asn Gly Lys Ile Phe Lys Lys Val Ile  
115 120 125

Leu Gly Gln Tyr Asn Trp Leu Ser Tyr Glu Asp Val Phe Val Arg Ala  
130 135 140

Phe Asn Phe Gly Asn Gly Leu Gln Met Leu Gly Gln Lys Pro Lys Thr  
145 150 155 160

Asn Ile Ala Ile Phe Cys Glu Thr Arg Ala Glu Trp Met Ile Ala Ala  
165 170 175

Gln Ala Cys Phe Met Tyr Asn Phe Gln Leu Val Thr Leu Tyr Ala Thr  
180 185 190

Leu Gly Gly Pro Ala Ile Val His Ala Leu Asn Glu Thr Glu Val Thr  
195 200 205

Asn Ile Ile Thr Ser Lys Glu Leu Leu Gln Thr Lys Leu Lys Asp Ile  
210 215 220

Val Ser Leu Val Pro Arg Leu Arg His Ile Ile Thr Val Asp Gly Lys  
225 230 235 240

Pro Pro Thr Trp Ser Asp Phe Pro Lys Gly Ile Ile Val His Thr Met  
245 250 255

Ala Ala Val Glu Ala Leu Gly Ala Lys Ala Ser Met Glu Asn Gln Pro  
260 265 270

His Ser Lys Pro Leu Pro Ser Asp Ile Ala Val Ile Met Tyr Thr Ser  
275 280 285

Gly Ser Thr Gly Leu Pro Lys Gly Val Met Ile Ser His Ser Asn Ile  
290 295 300

Ile Ala Gly Ile Thr Gly Met Ala Glu Arg Ile Pro Glu Leu Gly Glu  
305 310 315 320

Glu Asp Val Tyr Ile Gly Tyr Leu Pro Leu Ala His Val Leu Glu Leu  
325 330 335

Ser Ala Glu Leu Val Cys Leu Ser His Gly Cys Arg Ile Gly Tyr Ser  
340 345 350

Ser Pro Gln Thr Leu Ala Asp Gln Ser Ser Lys Ile Lys Lys Gly Ser  
355 360 365

Lys Gly Asp Thr Ser Met Leu Lys Pro Thr Leu Met Ala Ala Val Pro  
370 375 380

Glu Ile Met Asp Arg Ile Tyr Lys Asn Val Met Asn Lys Val Ser Glu  
385 390 395 400

Met Ser Ser Phe Gln Arg Asn Leu Phe Ile Leu Ala Tyr Asn Tyr Lys  
405 410 415

Met Glu Gln Ile Ser Lys Gly Arg Asn Thr Pro Leu Cys Asp Ser Phe  
420 425 430

Val Phe Arg Lys Val Arg Ser Leu Leu Gly Gly Asn Ile Arg Leu Leu  
435 440 445

Leu Cys Gly Gly Ala Pro Leu Ser Ala Thr Thr Gln Arg Phe Met Asn  
450 455 460

Ile Cys Phe Cys Cys Pro Val Gly Gln Gly Tyr Gly Leu Thr Glu Ser  
465 470 475 480

Ala Gly Ala Gly Thr Ile Ser Glu Val Trp Asp Tyr Asn Thr Gly Arg  
485 490 495

Val Gly Ala Pro Leu Val Cys Cys Glu Ile Lys Leu Lys Asn Trp Glu  
500 505 510

Glu Gly Gly Tyr Phe Asn Thr Asp Lys Pro His Pro Arg Gly Glu Ile  
515 520 525

Leu Ile Gly Gly Gln Ser Val Thr Met Gly Tyr Tyr Lys Asn Glu Ala  
530 535 540

Lys Thr Lys Ala Asp Phe Ser Glu Asp Glu Asn Gly Gln Arg Trp Leu  
545 550 555 560

Cys Thr Gly Asp Ile Gly Glu Phe Glu Pro Asp Gly Cys Leu Lys Ile  
565 570 575

Ile Asp Arg Lys Lys Asp Leu Val Lys Leu Gln Ala Gly Glu Tyr Val  
580 585 590

Ser Leu Gly Lys Val Glu Ala Ala Leu Lys Asn Leu Pro Leu Val Asp  
595 600 605

Asn Ile Cys Ala Tyr Ala Asn Ser Tyr His Ser Tyr Val Ile Gly Phe  
610 615 620

Val Val Pro Asn Gln Lys Glu Leu Thr Glu Leu Ala Arg Lys Lys Gly

625 630 635 640

Leu Lys Gly Thr Trp Glu Glu Leu Cys Asn Ser Cys Glu Met Glu Asn  
645 650 655

Glu Val Leu Lys Val Leu Ser Glu Ala Ala Ile Ser Ala Ser Leu Glu  
660 665 670

Lys Phe Glu Ile Pro Val Lys Ile Arg Leu Ser Pro Glu Pro Trp Thr  
675 680 685

Pro Glu Thr Gly Leu Val Thr Asp Ala Phe Lys Leu Lys Arg Lys Glu  
690 695 700

Leu Lys Thr His Tyr Gln Ala Asp Ile Glu Arg Met Tyr Gly Arg Lys  
705 710 715 720

<210> 170  
<211> 4121  
<212> DNA  
<213> human organism

<400> 170  
agcaacgacg ccgggcagcg ggagcggcgg ccgcgccatg tggctgctgg ggccgctgtg 60  
cctgctgctg agcagcggccg cggagagcca gctgctcccc gggacaact tcaccaatga 120  
gtgcaacata ccaggcaact tcatgtgcag caatggacgg tgcatcccg ggcctggca 180  
gtgtgacggg ctgcctgact gcttcgacaa gagtgatgag aaggagtgcc ccaaggctaa 240  
gtcgaaatgt ggcacacct tcttcccctg tgccagcggc atccattgca tcattggtcg 300  
cttccggtgc aatgggttg aggactgtcc cgatggcagc gatgaagaga actgcacagc 360  
aaaccctctg ctttgctcca ccccccgtta ccactgcaag aacggcctct gtattgacaa 420  
gagcttcatc tgcgatggac agaataactg tcaagacaac agtgatgagg aaagctgtga 480  
aagttctcaa gaacccggca gtgggcaggt gtttgtact tcagagaacc aacttgtta 540  
ttacccctcagc atcacctatg ccatcatcg cagctccgtc attttgtgc tgggtggc 600  
cctgctggca ctggcttgc accaccagcg gaagcggAAC aacctcatga cgctgcccgt 660  
gcacccggctg cagcacccctg tgctgctgtc ccgcctgggtg gtcctggacc accccacca 720  
ctgcaacgtc acctacaacg tcaataatgg catccagtat gtggccagcc aggccggagca 780  
gaatgcgtcg gaagttaggct ccccacccctc ctactccgag gccttgctgg accagaggcc 840

tcgtggat gacccctc caccgccta ctcttctgac acggaatctc tgaaccaagc 900  
cgacctgccc ccctaccgct cccggccgg gagtgccaac agtgcagct cccaggcagc 960  
cagcagcctc ctgagcgtgg aagacaccag ccacagcccg gggcagcctg gccccagga 1020  
gggcactgct gagcccaggg actctgagcc cagccaggc actgaagaag tataagtccc 1080  
agttattcca aagtccatat gggtaatct gctctgactt gttgccattc taacaatttg 1140  
tgctcatggg aagctctta agcacctgta aggtgtctc aagttacagt ttggatatt 1200  
aactatctct gcattccct cctccccag acttcagaga tgttttctg gcgtctcagt 1260  
tgacatgate tgggtgcgt ctgttgcgt aggtcactct tccttggga cccgagatca 1320  
caccctcatt ttccacatta ttctgttct gttggagaga cagcatataa aacagtattg 1380  
aaataggctg ggagagagca atgtttctgt gctatattgg atgctcagaa gtgcaggaga 1440  
cgctggaccc aattctctct gctggtagt taccttatag catttggga tttgggttag 1500  
atgatctaac caggaggcca tcactggatg gtcacccccc caaaaaatt ccatttggc 1560  
atcaaaaacct gctttgcaca atcctatttgc atgccccag ttcagcagag tcagtgcc 1620  
aagaaaaactt tggacgtgag taacaccctt cagcagtcgc aacgttattt tggttttgt 1680  
aaggactctg aaaccatcta ccctgtataa attctggctt tagaaatttg cccaaatgt 1740  
ctcattctga gagcttcct cagcagcata tatcatcagc ctcatcctaa aataggcagg 1800  
gagccctcc catgagttt tccaagttct cagtcctaa aatgcaggct gccaagaccc 1860  
tacacctgac ctggctctac agccacttac ctggttctg gactgtcacc ctccagctg 1920  
acctggccgt agccaaggaa tgaggaccta acttgagttg gcccaaagtc tgacctggct 1980  
gtatgtccct gtggcccaca cccagcctgt ctgtcatt catgcagcct caacactggc 2040  
ctccaaagtt cccttaacac ttgcaaagtc ctgttacct gtgcatttgg acttgaggac 2100  
actggttct atcacaggtg agagccatgt tcaatacctc cagcaagtc tcctggctcc 2160  
ctgcactgtg cacgctcctc ttcccaaggt cccaatacca gcaccccttag ttagagttag 2220  
ggtcagggtc aggcctctcc caacatccca gtagttctc ctctgagaca catgggcaag 2280  
agacaatttg gagtcaagat ttccatttgc gatctattt aaatctttt gaaatgcatt 2340  
tgaaacagtg tgtttgggtt ttcccttcta gttaaaggac tatttatatg tgtataggaa 2400  
agctgtctct tttttgttt ttccctttaac aaggtccaaa gaaagatgca aaaggagatc 2460  
acacccttgc cccgctgagc cccgtgataa caagtcactc cagactaacc tgtgtgccag 2520  
acatttgcatttgcac ttggaggta ttatattatca agtttttgc ggaaggcagaa 2580

agagggactc	ctctctccct	ccgtgtata	g tctctatgtt	tgtgctagtt	tttcttttt	2640	
ttctctgtgt	ccagtcagcc	acagggcccg	cctccctgca	ggaataaggg	gtaaaacgtt	2700	
aggtgttgtt	tggcaagaaa	ccacactgac	t gatgagggg	taaaatggaa	ccaggttagag	2760	
ccactccggg	cagctgtcac	ccattcagaa	cttcttccg	cagctgaaga	aatgttcagt	2820	
aacctgtttg	acgctaatta	aaacagagcc	tgcaggaagt	ggggctaaag	tggcattcag	2880	
tgatcctgtt	ctgttagactt	ttctttcttt	tttaaccaa	atccaaagga	tgttacagaa	2940	
aagctagcca	ctggtat	ttttgttta	aaaaaaaaaa	gaaagaaaaga	aagaaagaaa	3000	
aacggaaagg	aacctagctg	cctgtatctt	tcattttaa	aatagcactt	gagttat	3060	
ctgagtaatc	caataaaagaa	ctttgatga	cagccagaat	gtgttagaac	tctggctgaa	3120	
catttcatct	cctgtgagtc	agaagggctt	tatttccc	tttgatgggg	ccccttctc	3180	
tttctgggc	tctggaagtt	gttagagga	aagaattcta	attttaatta	attgcgcagt	3240	
gagttaatct	cactcgctt	tctgctcca	ggcatcttag	aaaaaaca	aa tggttttagt	3300	
agataaggga	tgcctactaa	tgcttttta	aaacaacag	ggacat	ttt attatagatt	3360	
tgat	ttttttt	aatgaatgtt	tttaaaaata	tataaata	agg acaccaagc	3420	
ttttgggg	gagggggtt	gtttccaac	tcaagatggc	acattagtgg	ccagcaat	3480	
tttttaactc	attccaacca	ggaagctt	ttatacattg	cctaaatcta	cgc accag	3540	
aaaatagtct	catctttt	tttctcaa	at gagatccgt	ttttat	ttta gcattaaatt	3600	
agttacactg	t gatgactgg	cctattac	ct gactc	cctctac	ttt gaaattgaca	3660	
tttttaaaaa	atgcaactaa	gtggtaata	gtgtgtgac	ctcaaagtta	atgtaaactg	3720	
gaaagg	ttgtgtgc	ttttgtgtt	ttggtaggc	ttggttt	tttttaattt	3780	
ttatactt	taataaattt	gcagttcat	tcttctgtt	tgtgcaaawg	gw mctamarm	3840	
aammm	aaac awywt	ttgggg	ggc ttgggc	ctcgaaaaaa	gttttaaca	ccacttcggg	3900
tggggcggc	ggcccacgt	agg tacggcg	accacg	ccccacggg	accc cagaag	3960	
gaaacc	ctgg ccaagaaaaa	gg tggcgaga	attctccaca	ccagaaaaaa	acgc gcccggg	4020	
ggaaacc	cgca	gag tggc	taaaccacac	ccgaagagag	aactcagaag	cacacaagcg	4080
ggactcaacc	aggaggaccc	aagggaaccc	gatagagtac	g		4121	

<210> 171

<211> 345

<212> PRT

<213> human organism

<400> 171

Met Trp Leu Leu Gly Pro Leu Cys Leu Leu Leu Ser Ser Ala Ala Glu  
1 5 10 15

Ser Gln Leu Leu Pro Gly Asn Asn Phe Thr Asn Glu Cys Asn Ile Pro  
20 25 30

Gly Asn Phe Met Cys Ser Asn Gly Arg Cys Ile Pro Gly Ala Trp Gln  
35 40 45

Cys Asp Gly Leu Pro Asp Cys Phe Asp Lys Ser Asp Glu Lys Glu Cys  
50 55 60

Pro Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser  
65 70 75 80

Gly Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp  
85 90 95

Cys Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu  
100 105 110

Cys Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys  
115 120 125

Ser Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu  
130 135 140

Glu Ser Cys Glu Ser Ser Gln Glu Pro Gly Ser Gly Gln Val Phe Val  
145 150 155 160

Thr Ser Glu Asn Gln Leu Val Tyr Tyr Pro Ser Ile Thr Tyr Ala Ile  
165 170 175

Ile Gly Ser Ser Val Ile Phe Val Leu Val Val Ala Leu Leu Ala Leu  
180 185 190

Val Leu His His Gln Arg Lys Arg Asn Asn Leu Met Thr Leu Pro Val  
195 200 205

His Arg Leu Gln His Pro Val Leu Leu Ser Arg Leu Val Val Leu Asp

210	215	220
His Pro His His Cys Asn Val Thr Tyr Asn Val Asn Asn Gly Ile Gln		
225	230	235
Tyr Val Ala Ser Gln Ala Glu Gln Asn Ala Ser Glu Val Gly Ser Pro		
245	250	255
Pro Ser Tyr Ser Glu Ala Leu Leu Asp Gln Arg Pro Ala Trp Tyr Asp		
260	265	270
Leu Pro Pro Pro Tyr Ser Ser Asp Thr Glu Ser Leu Asn Gln Ala		
275	280	285
Asp Leu Pro Pro Tyr Arg Ser Arg Ser Gly Ser Ala Asn Ser Ala Ser		
290	295	300
Ser Gln Ala Ala Ser Ser Leu Leu Ser Val Glu Asp Thr Ser His Ser		
305	310	315
Pro Gly Gln Pro Gly Pro Gln Glu Gly Thr Ala Glu Pro Arg Asp Ser		
325	330	335
Glu Pro Ser Gln Gly Thr Glu Glu Val		
340	345	

<210> 172  
 <211> 2479  
 <212> DNA  
 <213> human organism

<400> 172	60
gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg	
ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat ggataccaac	120
cggaaaaccc ctatcccgca cagccccactg tggccccac tgtctacgag gtgcacccgg	180
ctcagtacta cccgtccccc gtgccccagt acgccccgag ggtcctgacg caggcttcca	240
accccgtcgt ctgcacgcag cccaaatccc catccggac agtgtgcacc tcaaagacta	300
agaaaagcact gtgcacccacc ttgaccctgg ggacccctt cgtggagct gcgctggccg	360
ctggcctact ctggaagttc atgggcagca agtgctccaa ctctggata gagtgcgact	420
cctcaggtac ctgcaccaac ccctctaact ggtgtatgg cgtgtcacac tgcccccggcg	480

gggaggacga gaatcggtgt gttcgccctc acggaccaaa cttcatcctt cagatgtact 540  
catctcagag gaagtcctgg caccctgtgt gccaaagacga ctggAACGAG aactacgggc 600  
ggcgccctg cagggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg 660  
atgacagcgg atccaccaggc tttatgaaac tgaacacaag tgccggcaat gtcgatatct 720  
ataaaaaact gtaccacagt gatgcctgtt cttcaaaagc agtggtttct ttacgctgtt 780  
tagcctgcgg ggtcaacttg aactcaagcc gccagagcag gatcgtggc ggtgagagcg 840  
cgctccccggg ggcctggccc tggcaggtca gcctgcacgt ccagaacgtc cacgtgtgcg 900  
gaggctccat catcaccccc gagtgatcg tgacagccgc ccactgcgtg gaaaaacctc 960  
ttaacaatcc atggcattgg acggcatttgc cggggatttt gagacaatct ttcatgttct 1020  
atggagccgg ataccaagta caaaaagtga tttctcatcc aaattatgac tccaagacca 1080  
agaacaatga cattgcgtg atgaagctgc agaaggctct gactttcaac gacctagtga 1140  
aaccagtgtg tctgccaaac ccaggcatga tgctgcagcc agaacagctc tgctggattt 1200  
ccgggtgggg ggccaccgag gagaaaggga agacctcaga agtgctgaac gctgccaagg 1260  
tgcttctcat tgagacacag agatgcaaca gcagatatgt ctatgacaac ctgatcacac 1320  
cagccatgat ctgtgcggc ttccctgcagg ggaacgtcga ttcttgccag ggtgacagt 1380  
gagggcctct ggtcaactcg aacaacaata tctggggct gataggggat acaagctgg 1440  
gttctggctg tgccaaagct tacagaccag gagtgatcg gaatgtgatg gtattcacgg 1500  
actggattta tcgacaaatg aaggcaaacg gctaattccac atggcttcg tccttgacgt 1560  
cgttttacaa gaaaacaatg gggctggtt tgctccccg tgcatgattt actcttagag 1620  
atgattcaga ggtcaactca ttttattaa acagtaact tgtctggctt tggcactctc 1680  
tgccatactg tgcaggctgc agtggctccc ctgcccagcc tgctctccct aacccttgt 1740  
ccgcaagggg tgatggccgg ctgggtgtgg gcactggcgg tcaattgtgg aaggaagagg 1800  
gttggaggct gccccattg agatcttcct gctgagtcct ttccaggggc caattttgga 1860  
tgagcatgga gctgtcactt ctcagctgct ggatgacttg agatgaaaaa ggagagacat 1920  
ggaaaggagg acagccaggt ggcacctgca gcggctgccc tctggggcca cttggtagtg 1980  
tccccagcct acttcacaag gggattttgc tgatgggttc ttagagcctt agcagccctg 2040  
gatggtggcc agaaataaag ggaccagccc ttcatgggtg gtgacgtggt agtcacttgt 2100  
aaggggaaca gaaacatttt tgttcttatg gggtgagaat atagacagtg cccttggc 2160  
gagggaaagca attgaaaagg aacttgcctt gagcactcctt ggtgcaggc tccacctgca 2220

cattgggtgg ggctcctggg agggagactc agccttcctc ctcatcctcc ctgaccctgc 2280  
tccttagcacc ctggagagtg aatccccctt ggtccctggc agggcgccaa gtttggcacc 2340  
atgtcggcct cttcaggcct gatagtcatt ggaaattgag gtccatgggg gaaatcaagg 2400  
atgctcagtt taaggtacac tgtttccatg ttatgtttct acacattgtat ggtggtgacc 2460  
ctgagttcaa agccatctt 2479

<210> 173  
<211> 492  
<212> PRT  
<213> human organism

<400> 173

Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu  
1 5 10 15

Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val  
20 25 30

Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro  
35 40 45

Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val  
50 55 60

Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys  
65 70 75 80

Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val  
85 90 95

Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys  
100 105 110

Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn  
115 120 125

Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp  
130 135 140

Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met  
145 150 155 160

Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp  
165 170 175

Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn  
180 185 190

Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser  
195 200 205

Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys  
210 215 220

Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg  
225 230 235 240

Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile  
245 250 255

Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser  
260 265 270

Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro  
275 280 285

Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn  
290 295 300

Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met  
305 310 315 320

Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn  
325 330 335

Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln  
340 345 350

Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn  
355 360 365

Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp  
370 375 380

Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala  
385                   390                   395                   400

Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr  
405                   410                   415

Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly  
420                   425                   430

Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser  
435                   440                   445

Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly  
450                   455                   460

Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe  
465                   470                   475                   480

Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly  
485                   490

<210> 174  
<211> 3104  
<212> DNA  
<213> human organism

<220>  
<221> misc\_feature  
<222> (2539)..(2539)  
<223> n is a, c, g, or t

<220>  
<221> misc\_feature  
<222> (2967)..(2967)  
<223> n is a, c, g, or t

<220>  
<221> misc\_feature  
<222> (2979)..(2979)  
<223> n is a, c, g, or t

<220>  
<221> misc\_feature  
<222> (2989)..(2990)  
<223> n is a, c, g, or t

<220>  
<221> misc\_feature

```

<222>  (2993)..(2994)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (3006)..(3007)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (3015)..(3015)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (3027)..(3029)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (3040)..(3041)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (3054)..(3054)
<223>  n is a, c, g, or t

<400>  174
cagagaggct gtatttcagt gcagcctgcc agacctttc tggaggaaga ctggacaaag      60
ggggtcacac attccttcca tacgggttag cctctacctg cctggtgctg gtcacagttc
agcttcttca tggatggtaga tcccaatggc aatgaatcca gtgctacata cttcatccta      120
ataggcctcc ctgggttaga agaggcttag ttctgggtgg ccttcccatt gtgctccctc
taccttatttgc ctgtgttagg taacttgaca atcatctaca ttgtgcggac tgagcacagc      180
ctgcgtgagc ccatgtatat atttctttgc atgcttcag gcattgacat cctcatctcc      240
acctcatcca tgccccaaaat gctggccatc ttctgggtca attccactac catccagtt      300
gatgcttgtc tgctacagat gtttgccatc cactccttat ctggcatgga atccacagtg      360
ctgctggcca tggctttga ccgctatgtg gccatctgtc acccaactgctg ccatgccaca      420
gtacttacgt tgcctcgtgt cacaaaaatt ggtgtggctg ctgtggtgctg gggggctgca      480
ctgatggcac cccttcctgt cttcatcaag cagctgcctt tctggcgctc caatatcctt      540
tcccattcct actgcctaca ccaagatgtc atgaagctgg cctgtgatga tatccgggtc      600
aatgtcgatc atggccttat cgtcatcata tccggcattt gcctggactc acttctcatc      660
tccttctcat atctgcttat tcttaagact gtgttggct tgacacgtga agcccaggcc      720
                                         780
                                         840

```

aaggcatttgcgt gcacttgcgt ctctcatgtg tgtgctgtgt tcataattcta tgtaccatttc 900  
atggatttgt ccatggtgca tcgccttagc aagcggcgtg actctccact gcccgtcatc 960  
ttggccaata tctatctgct ggcccttcct gtgctcaacc caattgtcta tggagtgaag 1020  
acaaggaga ttgcacagcg catccttcga ctccatg tggccacaca cgcttcagag 1080  
ccctagggtgt cagtgtacaa acttctttc cattcagagt cctctgattc agatttaat 1140  
gttaacattt tggaagacag tattcagaaa aaaaattcc ttaataaaaaa tacaactcag 1200  
atcctcaaa tatgaaactg gttgggaat ctccatttt tcaatattat tttcttctt 1260  
gtttcttgc tacatataat tattaatacc ctgacttagt tgtggttgga gggttattac 1320  
tttcatttt accatgcagt ccaaatactaa actgcttcta ctgatggttt acagcattct 1380  
gagataagaa tggtacatct agagaacatt tgccaaaggc ctaagcacag caaaggaaaa 1440  
taaacacaga atataataaa atgagataat ctatctaaa actataactt cctcttcaga 1500  
actccccacc acattggatc tcagaaaaat actgtcttca aaatgacttc tacagagaag 1560  
aaataatttt tcctctggac actagcactt aaggggaaga ttggaagtaa agccttgaaa 1620  
agagtacatt tacctacgtt aatgaaagtt gacacactgt tctgagagtt ttcacagcat 1680  
atggaccctg ttttccttat ttaattttct tatcaaccct ttaatttaggc aaagatatta 1740  
ttgtaccctt cattgttagcc atggaaaaat tgatgttcag tggggatcag tgaattaaat 1800  
gggtcatac aagtataaaa attaaaaaaaaa aaagacttca tgcccaatct catatgtgt 1860  
ggaagaactg taaaagagac caacagggtt gtgggttaga gattccaga gtcttacatt 1920  
ttcttaragga ggtatttaat ttcttcac tcatttcgtt ttgtattttag gaatttcctg 1980  
gcaacagaac tcattggctt aatccccacta gctattgtt attgtcctgg tccaaattgcc 2040  
aattacctgt gtcttggaaag aagtgtttc taggttcacc attatggaaat attcttattc 2100  
agaaagtctg catagggctt atagcaagtt atttattttt aaaagttcca taggtgtttc 2160  
tgataggcag tgaggttagg gagccaccag ttatgtggg aagtatggaa tggcaggtgt 2220  
tgaagataac attggcctt tgagtgtgac tcgttagctgg aaagtgggg aatcttcagg 2280  
accatgcttt atttggggct ttgtgcgtt tgaaacaggc actttgagac cgggaaagca 2340  
atctgactta ggcattggaa tcaggcattt ttgcttcgtt gggcttattt ccaagggtta 2400  
ataggttca tcttcaacag gatatgacaa cagtcttac acagaaactc aaattacata 2460  
tactaaaaca tgtgatcata tatgtggtaa gtttcatttt cttttcaat cctcaggttc 2520  
cctgatatgg attcctatna catgcttca tcccccttttgaatggatat catatttgaa 2580

aatgcctatt taatacttgt atttgctgct ggactgttaag cccatgaggg cactgtttat	2640
tattgaatgt catctctgtt catcattgac tgctcttgc tcatttcattga atcccccagc	2700
aaagtgccta gaacataata gtgcttatgc ttgacaccgg ttattttca tcaaacctga	2760
ttccttctgt gctgaacaca tagccaggca atttccagc cttctttgag ttgggtatta	2820
ttaaatttta gccattactt ccaatgtgag tggaaagtgac atgtgcaatt ttatcacctg	2880
gctcataaaaa ccctcccatg tgcagccttt catgttgaca ttaaatgtga ctggggaaagc	2940
tatgtgttac acagagttaa ttaaccngaa aggccctggna atttttgnn aannaaactg	3000
tggccnnngag gcccncaacc cttttnnna atttggcaan ntcccacttt gtanttttgt	3060
aaggaaqqcca qttggataag tgaaaaataa agtactattg tgtc	3104

<210> 175  
<211> 317  
<212> PRT  
<213> human organism

<400> 175

Met	Val	Asp	Pro	Asn	Gly	Asn	Glu	Ser	Ser	Ala	Thr	Tyr	Phe	Ile	Leu
1				5					10					15	

Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe Pro  
20 25 30

Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile Ile  
35 40 45

Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile Phe  
50 55 60

Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser Met  
65 70 75 80

Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe  
85 90 95

Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly Met  
           100           105           110

Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
                   115                  120                  125

Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val Thr  
130 135 140

Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala Pro  
145 150 155 160

Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu  
165 170 175

Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Asp  
180 185 190

Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser Ala  
195 200 205

Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile Leu  
210 215 220

Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe Gly  
225 230 235 240

Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro Phe  
245 250 255

Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser Pro  
260 265 270

Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val Leu  
275 280 285

Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg Ile  
290 295 300

Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro  
305 310 315

<210> 176

<211> 2834

<212> DNA

<213> human organism

<400> 176

tcggagcctg cggagggtgg tggtggtggt ggtggtgcc ctcgcccccc tcactcatgc

60

ctcctcctcc tctgctctcg ctcaggcgcc tcgggtggcg ttgggtcgccg gttacgcggc 120  
tggtggtcgcc ggcggccggg gctcgctctc ggggaggccg gggcgatct cgccggcgag 180  
gcggcgccgg ccgaggtggg gtcgcgcggc ggaggcggtcg agagcttcgt gctgcgcgt 240  
cgctcttggg ctccctcgctg caggaggagt gtgactatgt gcagatgatc gaggtgcagc 300  
acaaggcagtgc cctggaggag gcccagctgg agaatgagac aataggctgc agcaagatgt 360  
gggacaacct cacctgctgg ccagccaccc ctggggcca ggtagttgtc ttggcctgtc 420  
ccctcatctt caagctcttc tcctccattc aaggccgcaa tgtaagccgc agctgcaccg 480  
acgaaggctg gacgcacctg gagcctggcc cgtacccat tgcctgtggg ttggatgaca 540  
aggcagcgag tttggatgag cagcagacca ttttctacgg ttctgtgaag accggctaca 600  
ccattggcta cggcctgtcc ctgcaccc ttctggtcgc cacagctatc ctgaggctgt 660  
tcaggaagct ccactgcacg cgaaactaca tccacatgca cctcttcata tccttcattc 720  
tgagggctgc cgctgtcttc atcaaagact tggccctttt cgacagcggg gagtcggacc 780  
agtgctccga gggctcggtg ggctgttaagg cagccatggg cttttccaa tattgtgtca 840  
tggtctaactt cttctggctg ctgggtggagg gcctctacccgtt acaccctg ctggcgtct 900  
ccttcttctc tgagcggaaag tacttctggg ggtacataact catcggtgg ggggtaccca 960  
gcacattcac catgggtgg accatcgcca ggtacccatt tgaggattat ggtctgtca 1020  
ggtgctggga caccatcaac tcctcactgt ggtggatcat aaaggcccccc atcctcacct 1080  
ccatcttgggaaacttcatc ctgttttattt gcatcatccg aatcctgctt cagaaactgc 1140  
ggccccccaga tatcaggaag agtgcacagca gtccatactc aaggctagcc aggtccacac 1200  
tcctgctgat cccccctgttt ggagttacact acatcatgtt cgccttcttt ccggacaatt 1260  
ttaaggctga agtgaagatg gtctttgagc tcgtcggtgg gtctttccag ggttttgtgg 1320  
tggctatcct ctactgcttc ctcaatggtg aggtgcaggc ggagctgagg cggaagtggc 1380  
ggcgctggca cctgcaggcgtc gtcctgggtcg ggaacccaa ataccggcac ccgtcgggag 1440  
gcagcaacgg cgccacgtgc agcacgcagg tttccatgtc gacccgcgtc agcccagggtg 1500  
cccgccgcgtc ctccagcttc caagccgaag tctccctggt ctgaccacca ggatcccagc 1560  
ccaagcggcc cctcccgcccc cttcccaactc gcagcagacg ccggggacag aggccctggcc 1620  
gggcgcggcca gccccggcccc tgggctcgga ggctggccccc ggccccctgg tctctggtcc 1680  
ggacactcct agagaacgca gcccttagagc ctgcctggag cgtttctagc aagtgagaga 1740

gatggagct ccttcctgg aggatgcagg tggaactcag tcattagact cctcctccaa	1800
aggcccccta cgccaatcaa gggcaaaaag tctacatact ttcatcctga ctctgcccc	1860
tgctggctct tctgccaat tggagggaaag caaccggtgg atcctcaaac aacactggtg	1920
tgacctgagg gcagaaaaggt tctgcccggg aaggtcacca gcaccaacac cacggtagtg	1980
cctgaaaattt caccattgct gtcaagttcc ttgggttaa gcattaccac tcaggcattt	2040
gactgaagat gcagctcaact accctattct ctcttacgc ttagttatca gctttttaaa	2100
gtgggttatt ctggagtttt tgtttgaga gcacacctat cttagtggtt ccccaccgaa	2160
gtggactggc ccctgggtca gtctggtggg aggacggtgc aacccaagga ctgaggggact	2220
ctgaaggcctc tggaaatga gaaggcagcc accagcgaat gctaggtctc ggactaagcc	2280
tacctgctct ccaagtctca gtggcttcat ctgtcaagtg ggactctgtc acaccagcca	2340
ttcttatctc tctgtgctgt ggaagcaaca ggaatcaaga gactgccctc cttgtccacc	2400
cacctatgtg ccaactgttg taactaggct cagagatgtg cacccatggg ctctgacaga	2460
aagcagatcc tcaccctgct acacatacag gatttgaact cagatctgtc tgataggaat	2520
gtgaaagcac ggactcttac tgctaacttt tgtgtatcgt aaccagccag atcctttgg	2580
ttatTTgttt accacttgta ttattaatgc cattatccct gaattccct tgccacccca	2640
ccctccctgg agtgtggctg aggaggcctc catctcatgt atcatctgga taggagcctg	2700
ctggtcacag cctcctctgt ctgcccctca ccccaagtggc cactcagctt cttacccaca	2760
cctctgccag aagatccccct caggactgca acaggcttgt gcaacaataa atgttggctt	2820
qqaaaaaaaaaaaa	2834

<210> 177  
<211> 495  
<212> PRT  
<213> human organism

<400> 177

Met Pro Pro Pro Pro Leu Leu Ser Leu Arg Arg Leu Gly Gly Gly Trp  
1 5 10 15

Ser Ala Val Thr Arg Leu Val Val Ala Ala Ala Gly Ala Arg Ser Arg  
20 25 . 30

Gly Gly Arg Gly Gly Ser Arg Gly Ala Gly Gly Gly Gly Arg Gly Gly  
35 40 45

Val Ala Arg Arg Arg Leu Glu Leu Arg Ala Ala Arg Ser Leu Leu  
50 55 60

Gly Ser Ser Leu Gln Glu Glu Cys Asp Tyr Val Gln Met Ile Glu Val  
65 70 75 80

Gln His Lys Gln Cys Leu Glu Glu Ala Gln Leu Glu Asn Glu Thr Ile  
85 90 95

Gly Cys Ser Lys Met Trp Asp Asn Leu Thr Cys Trp Pro Ala Thr Pro  
100 105 110

Arg Gly Gln Val Val Val Leu Ala Cys Pro Leu Ile Phe Lys Leu Phe  
115 120 125

Ser Ser Ile Gln Gly Arg Asn Val Ser Arg Ser Cys Thr Asp Glu Gly  
130 135 140

Trp Thr His Leu Glu Pro Gly Pro Tyr Pro Ile Ala Cys Gly Leu Asp  
145 150 155 160

Asp Lys Ala Ala Ser Leu Asp Glu Gln Gln Thr Met Phe Tyr Gly Ser  
165 170 175

Val Lys Thr Gly Tyr Thr Ile Gly Tyr Gly Leu Ser Leu Ala Thr Leu  
180 185 190

Leu Val Ala Thr Ala Ile Leu Ser Leu Phe Arg Lys Leu His Cys Thr  
195 200 205

Arg Asn Tyr Ile His Met His Leu Phe Ile Ser Phe Ile Leu Arg Ala  
210 215 220

Ala Ala Val Phe Ile Lys Asp Leu Ala Leu Phe Asp Ser Gly Glu Ser  
225 230 235 240

Asp Gln Cys Ser Glu Gly Ser Val Gly Cys Lys Ala Ala Met Val Phe  
245 250 255

Phe Gln Tyr Cys Val Met Ala Asn Phe Phe Trp Leu Leu Val Glu Gly  
260 265 270

Leu Tyr Leu Tyr Thr Leu Leu Ala Val Ser Phe Phe Ser Glu Arg Lys  
275 280 285

Tyr Phe Trp Gly Tyr Ile Leu Ile Gly Trp Gly Val Pro Ser Thr Phe  
290 295 300

Thr Met Val Trp Thr Ile Ala Arg Ile His Phe Glu Asp Tyr Gly Leu  
305 310 315 320

Leu Arg Cys Trp Asp Thr Ile Asn Ser Ser Leu Trp Trp Ile Ile Lys  
325 330 335

Gly Pro Ile Leu Thr Ser Ile Leu Val Asn Phe Ile Leu Phe Ile Cys  
340 345 350

Ile Ile Arg Ile Leu Leu Gln Lys Leu Arg Pro Pro Asp Ile Arg Lys  
355 360 365

Ser Asp Ser Ser Pro Tyr Ser Arg Leu Ala Arg Ser Thr Leu Leu Leu  
370 375 380

Ile Pro Leu Phe Gly Val His Tyr Ile Met Phe Ala Phe Phe Pro Asp  
385 390 395 400

Asn Phe Lys Pro Glu Val Lys Met Val Phe Glu Leu Val Val Gly Ser  
405 410 415

Phe Gln Gly Phe Val Val Ala Ile Leu Tyr Cys Phe Leu Asn Gly Glu  
420 425 430

Val Gln Ala Glu Leu Arg Arg Lys Trp Arg Arg Trp His Leu Gln Gly  
435 440 445

Val Leu Gly Trp Asn Pro Lys Tyr Arg His Pro Ser Gly Gly Ser Asn  
450 455 460

Gly Ala Thr Cys Ser Thr Gln Val Ser Met Leu Thr Arg Val Ser Pro  
465 470 475 480

Gly Ala Arg Arg Ser Ser Ser Phe Gln Ala Glu Val Ser Leu Val  
485 490 495

<211> 2070  
 <212> DNA  
 <213> human organism

<400> 178		
atgagcggtg	cgggggtggc ggctggacg cggccccc gctgccgac cccgggctct	60
cggcgccggc	gccagcgccc ctctgtggc gtccagtct tgaggccga gagccgcag	120
ctcaggcaga	gcgaccgcga gaaacggaac ctggacctgg agaaaagcct gcagttcctg	180
cagcagcagc	actcggagat gctggccaag ctccatgagg agatcgagca tctgaagcgg	240
aaaaacaagg	gtgagccggc gcggggccct aggccggccc tgcctcccc ggcacactca	300
acactgccgc	tcccgcagca cagaaacaca gccatcaact ccagcacacg cctgggctca	360
gggggaacac	aggacgggga gcccctccag actgtccttg cccacctggc tgcactggcc	420
cctgtatgcc	aacccagtgg gtacaggttc tgggggacct ggacagatgc cgctacctct	480
agccgtggct	ggacgatgtt atgcagccaa gcacagcacg tgctgctctc gggaaagccca	540
gggcctgagg	tcattgcagg gcggcaggtg gccacagggt gctcccaga cttccctct	600
ccaagtagag	ctgaaatggg aaggaacccc tgggacagcc cttgcctgc tagatcttg	660
cctcagattg	ctgctgtggc caggcccagg atttcagcc ctatggctct gagtcctcac	720
atgctggggg	cccagggat atggacacac tccatccagg gatccctcc tgccatctgg	780
gcagcaacca	tggggacaaa gggaggaagc agagtctgt ttccctgcca cttgtccaag	840
gcacttcccc	atcctgacag cggcccccac ccagcccagg atcctggct gtggctcaa	900
gctcaattcc	cattatctt gggctggg ctgacatcag gaggacatct gactggtgga	960
tggagccagc	ctggaaacat cgcagctgg gcagtgccta gggctctccc ttcccaggga	1020
gacatggaga	agggggttga gggagggccc ttccctagcc gctgtggcaa ctccagttag	1080
ctgttctggg	caaagtgtgg cccaagtcgg cagccccagc cttgcagtgc tggggacgct	1140
gacaggacac	ggaaagaggc catgcttcc ctgggacct gctgttccat gtgtcccaag	1200
ccctcctgct	ttccagatgg cccctcagga aaccacctt ccagggcctc tgctccctg	1260
ggcgctcgct	gggtctgcat caacggagtg tggtagagc cgggaggacc cagccctgcc	1320
aggctgaagg	agggctcctc acggacacac aggccaggag gcaagcgtgg gcgttgcg	1380
ggcggtagcg	ccgacactgt gcgcctcct gcagacagcc tctccatgtc aagcttccag	1440
tctgtcaagt	ccatctctaa ttcaagccaa tctcaaggca aggccaggcc ccagccggc	1500
tccttcaaca	agcaagattc aaaagctgac gtctccaga aggcggaccc ggaagaggag	1560

ccctacttc acaacagcaa gctggacaaa gttcctgggg tacaaggcca ggccagaaag 1620  
gagaaagcag aggcctctaa tgcaggagct gcctgtatgg ggaacagcca gcaccaggc 1680  
aggcagatgg gggcgaaaaa acacccccc atgatcctgc ccctccccct gcgaaagccc 1740  
accacactta ggcagtgcga agtgctcatc cgcgagctgt ggaataccaa ctcctgcag 1800  
acccaagagc tgcggcacct caagtccctc ctggaaggga gccagaggcc ccaggcagcc 1860  
ccggaggaag ctagcttcc cagggaccaa gaagccacgc atttcccaa ggtctccacc 1920  
aagagctct ccaagaaatg cctgagccca cctgtggcgg agcgtgccat cctgcccga 1980  
ctgaagcaga ccccgaaagaa caacttgcc gagaggcaga agaggctgca ggcaatgcag 2040  
aacggcgcc tgcatcgctc agtgcttga 2070

<210> 179

<211> 689

<212> PRT

<213> human organism

<400> 179

Met Ser Gly Ala Gly Val Ala Ala Gly Thr Arg Pro Pro Ser Ser Pro  
1 5 10 15

Thr Pro Gly Ser Arg Arg Arg Gln Arg Pro Ser Val Gly Val Gln  
20 25 30

Ser Leu Arg Pro Gln Ser Pro Gln Leu Arg Gln Ser Asp Pro Gln Lys  
35 40 45

Arg Asn Leu Asp Leu Glu Lys Ser Leu Gln Phe Leu Gln Gln His  
50 55 60

Ser Glu Met Leu Ala Lys Leu His Glu Glu Ile Glu His Leu Lys Arg  
65 70 75 80

Glu Asn Lys Gly Glu Pro Ala Arg Gly Pro Arg Pro Ala Leu Pro Pro  
85 90 95

Gln Ala His Ser Thr Leu Pro Leu Pro Gln His Arg Asn Thr Ala Ile  
100 105 110

Asn Ser Ser Thr Arg Leu Gly Ser Gly Gly Thr Gln Asp Gly Glu Pro  
115 120 125

Leu Gln Thr Val Leu Ala His Leu Ala Ala Leu Ala Pro Val Cys Gln  
130 135 140

Pro Ser Gly Tyr Arg Phe Trp Gly Thr Trp Thr Asp Ala Ala Thr Ser  
145 150 155 160

Ser Arg Gly Trp Thr Met Leu Cys Ser Gln Ala Gln His Val Leu Leu  
165 170 175

Ser Gly Ser Pro Gly Pro Glu Val Ile Ala Gly Arg Gln Val Ala Thr  
180 185 190

Gly Cys Ser Pro Asp Leu Pro Pro Ser Arg Ala Glu Met Gly Arg  
195 200 205

Asn Pro Trp Asp Ser Pro Cys Pro Ala Arg Ser Leu Pro Gln Ile Ala  
210 215 220

Ala Val Ala Arg Pro Arg Ile Ser Ser Pro Met Ala Leu Ser Pro His  
225 230 235 240

Met Leu Gly Ala Gln Gly Ile Trp Thr His Ser Ile Gln Gly Ser Leu  
245 250 255

Pro Ala Ile Trp Ala Ala Thr Met Gly Thr Lys Gly Gly Ser Arg Val  
260 265 270

Leu Phe Pro Cys His Leu Ser Lys Ala Leu Pro His Pro Asp Ser Gly  
275 280 285

Pro His Pro Ala Gln Asp Pro Gly Leu Trp Ser Gln Ala His Phe Pro  
290 295 300

Leu Ser Leu Gly Leu Gly Leu Thr Ser Gly Gly His Leu Thr Gly Gly  
305 310 315 320

Trp Ser Gln Pro Gly Asn Ile Ala Ala Gly Ala Val Pro Arg Ala Leu  
325 330 335

Pro Ser Gln Gly Asp Met Glu Lys Gly Val Glu Gly Gly Pro Phe Pro  
340 345 350

Ser Arg Cys Gly Asn Ser Ser Glu Leu Phe Trp Ala Lys Cys Gly Pro  
355 360 365

Ser Arg Gln Pro Gln Pro Cys Ser Ala Gly Asp Ala Asp Arg Thr Arg  
370 375 380

Glu Glu Ala Met Leu Ser Leu Gly Thr Cys Cys Ser Met Cys Pro Lys  
385 390 395 400

Pro Ser Cys Phe Pro Asp Gly Pro Ser Gly Asn His Leu Ser Arg Ala  
405 410 415

Ser Ala Pro Leu Gly Ala Arg Trp Val Cys Ile Asn Gly Val Trp Val  
420 425 430

Glu Pro Gly Gly Pro Ser Pro Ala Arg Leu Lys Glu Gly Ser Ser Arg  
435 440 445

Thr His Arg Pro Gly Gly Lys Arg Gly Arg Leu Ala Gly Gly Ser Ala  
450 455 460

Asp Thr Val Arg Ser Pro Ala Asp Ser Leu Ser Met Ser Ser Phe Gln  
465 470 475 480

Ser Val Lys Ser Ile Ser Asn Ser Ala Asn Ser Gln Gly Lys Ala Arg  
485 490 495

Pro Gln Pro Gly Ser Phe Asn Lys Gln Asp Ser Lys Ala Asp Val Ser  
500 505 510

Gln Lys Ala Asp Leu Glu Glu Pro Leu Leu His Asn Ser Lys Leu  
515 520 525

Asp Lys Val Pro Gly Val Gln Gly Gln Ala Arg Lys Glu Lys Ala Glu  
530 535 540

Ala Ser Asn Ala Gly Ala Ala Cys Met Gly Asn Ser Gln His Gln Gly  
545 550 555 560

Arg Gln Met Gly Ala Gly Ala His Pro Pro Met Ile Leu Pro Leu Pro  
565 570 575

Leu Arg Lys Pro Thr Thr Leu Arg Gln Cys Glu Val Leu Ile Arg Glu

580

585

590

Leu Trp Asn Thr Asn Leu Leu Gln Thr Gln Glu Leu Arg His Leu Lys  
595 600 605

Ser Leu Leu Glu Gly Ser Gln Arg Pro Gln Ala Ala Pro Glu Glu Ala  
610 615 620

Ser Phe Pro Arg Asp Gln Glu Ala Thr His Phe Pro Lys Val Ser Thr  
625 630 635 640

Lys Ser Leu Ser Lys Lys Cys Leu Ser Pro Pro Val Ala Glu Arg Ala  
645 650 655

Ile Leu Pro Ala Leu Lys Gln Thr Pro Lys Asn Asn Phe Ala Glu Arg  
660 665 670

Gln Lys Arg Leu Gln Ala Met Gln Lys Arg Arg Leu His Arg Ser Val  
675 680 685

Leu

<210> 180  
<211> 3461  
<212> DNA  
<213> human organism

<400> 180  
ctcgtgccga attcggcacg agaccgcgtg ttgcgcctg gtagagattt ctcgaagaca 60  
ccagtgggcc cgtgtggaac caaacctgcg cgctggccg ggccgtggga caacgaggcc 120  
gcggagacga aggcgcaatg gcgaggaagt tatctgtaat ctgtatcctg acctttgcc 180  
tctctgtcac aaatcccctt catgaactaa aagcagctgc tttccccag accactgaga 240  
aaattagtcc gaattggaa tctggcatta atgttgactt ggcaatttcc acacggcaat 300  
atcatctaca acagctttc taccgctatg gagaaaataa ttctttgtca gttgaagggt 360  
tcagaaaatt acttcaaaat ataggcatag ataagattaa aagaatccat atacaccatg 420  
accacgacca tcactcagac cacgagcatc actcagacca tgagcgtcac tcagaccatg 480  
agcatcactc agaccacgag catcactctg accatgatca tcactctcac cataatcatg 540  
ctgcttctgg taaaaataag cgaaaagctc tttgcccaga ccatgactca gatagttcag 600

gtaaaatcc tagaaacacgc cagggaaag gagctcaccg accagaacat gccagtggta 660  
gaaggaatgt caaggacagt gtttagtgcta gtgaagtgac ctcaactgtg tacaacactg 720  
tctctgaagg aactcacttt ctagagacaa tagagactcc aagacctgga aaactcttcc 780  
ccaaagatgt aagcagctcc actccaccca gtgtcacatc aaagagccgg gtgagccggc 840  
tggctggtag gaaaacaaaat gaatctgtga gtgagccccg aaaaggctt atgtattcca 900  
gaaacacaaa tgaaaatcct caggagtgtt tcaatgcata aaagctactg acatctcatg 960  
gcatgggcat ccaggttccg ctgaatgcaa cagagttcaa ctatctctgt ccagccatca 1020  
tcaaccaaat tgatgctaga tcttgtctga ttcatacaag tgaaaagaag gctgaaatcc 1080  
ctccaaagac ctattcatta caaatagcct gggttggtgg ttttatagcc atttccatca 1140  
tcagttcct gtctctgctg ggggttatct tagtgcctct catgaatcgg gtgttttca 1200  
aatttctcct gagtttcctt gtggcactgg ccgttggac tttgagtggt gatgctttt 1260  
tacaccttct tccacattct catgcaagtc accaccatag tcatagccat gaagaaccag 1320  
caatggaaat gaaaagagga ccactttca gtcatctgtc ttctcaaaac atagaagaaa 1380  
gtgcctattt tgattccacg tggaagggtc taacagctct aggaggcctg tatttcatgt 1440  
ttcttgtga acatgtcctc acattgatca aacaattaa agataagaag aaaaagaatc 1500  
agaagaaacc tgaaaatgat gatgatgtgg agattaagaa gcagttgtcc aagtatgaat 1560  
ctcaactttc aacaaatgag gagaaagtag atacagatga tcgaactgaa ggctattac 1620  
gaggcagactc acaagagccc tcccactttt attctcagca gcctgcagtc ttggaagaag 1680  
aagaggtcat gatagctcat gtcatccac aggaagtcta caatgaatat gtacccagag 1740  
ggtgcagaa taaatccat tcacattcc acgataact cggccagtc gacgatctca 1800  
ttcaccacca tcatgactac catcatattc tccatcatca ccaccacaa aaccaccatc 1860  
ctcacagtca cagccagcgc tactctcggtt aggagctgaa agatgccggc gtcggcactt 1920  
tggcctggat ggtgataatg ggtgatggcc tgcacaattt cagcgatggc ctagcaattt 1980  
gtgctgcttt tactgaaggc ttatcaagtg gtttaagtac ttctgttgct gtgttctgtc 2040  
atgagttgcc tcatgaatta ggtgactttt ctgttctact aaaggctggc atgaccgtta 2100  
agcaggctgt cctttataat gcattgtcag ccatgctggc gtatcttggaa atggcaacag 2160  
gaattttcat tggtcattat gctgaaaatg tttctatgtg gatatttgcata cttactgctg 2220  
gcttattcat gtatgttgct ctgggttgcata tggtacactga aatgctgcac aatgatgcta 2280  
gtgaccatgg atgtagccgc tgggggtatt tcttttaca gaatgctggg atgctttgg 2340

gttttggaat tatgttactt attccatat ttgaacataa aatcggttt cgtataaatt	2400
tctagtaag gttaaatgc tagagtagct taaaaagttg tcatagttc agtaggtcat	2460
aggagatga gttgtatgc tgtactatgc agcgtaaaa gttagtggt tttgtgattt	2520
tttgtattgaa tattgctgtc tgttacaaag tcagttaag gtacgtttt atatttaagt	2580
tattctatct tggagataaa atctgtatgt gcaattcacc ggtattacca gtttattatg	2640
taaacaagag atttggcatg acatgttctg tatgttcag ggaaaaatgt cttaatgct	2700
tttcaagaa ctaacacagt tattcctata ctggattttt ggtctctgaa gaactgctgg	2760
tgttaggaa taagaatgtg catgaagcct aaaataccaa gaaagcttat actgaattt	2820
agcaaagaaa taaaggagaa aagagaagaa tctgagaatt gggaggcat agattcttat	2880
aaaaatcaca aaatttggaa taaatttagag gggagaaatt tagaattaag tataaaaagg	2940
cagaattagt atagagtaca ttcattaaac attttgcata ggattatttc ccgtaaaaac	3000
gtagtgagca ctctcatata ctaatttagt tacatttaac tttgtataat acagaaatct	3060
aaatatattt aatgaattca agcaatatac acttgaccaa gaaattggaa tttcaaaatg	3120
ttcgtgcggg ttatatacca gatgagtaca gtgagtagtt tatgtatcac cagactgggt	3180
tattgccaag ttatatatca ccaaaagctg tatgactgga tgttctgggt acctggttt	3240
caaaaatttcc agagtagtaa aactttgata tatatgagga tattaaaact acactaagta	3300
tcatttgatt cgattcagaa agtactttga tatctctcag tgcttcagtg ctatcattgt	3360
gagcaattgt ctttatatac ggtactgttag ccatactagg cctgtctgtg gcattctcta	3420
gatgtttctt ttttacacaa taaattcctt atatcagctt g	3461

<210> 181  
 <211> 755  
 <212> PRT  
 <213> human organism

<400> 181

Met Ala Arg Lys Leu Ser Val Ile Leu Ile Leu Thr Phe Ala Leu Ser	
1	5
10	15

Val Thr Asn Pro Leu His Glu Leu Lys Ala Ala Ala Phe Pro Gln Thr	
20	25
30	

Thr Glu Lys Ile Ser Pro Asn Trp Glu Ser Gly Ile Asn Val Asp Leu	
35	40
45	

Ala Ile Ser Thr Arg Gln Tyr His Leu Gln Gln Leu Phe Tyr Arg Tyr  
50 55 60

Gly Glu Asn Asn Ser Leu Ser Val Glu Gly Phe Arg Lys Leu Leu Gln  
65 70 75 80

Asn Ile Gly Ile Asp Lys Ile Lys Arg Ile His Ile His His Asp His  
85 90 95

Asp His His Ser Asp His Glu His His Ser Asp His Glu Arg His Ser  
100 105 110

Asp His Glu His His Ser Asp His Glu His His Ser Asp His Asp His  
115 120 125

His Ser His His Asn His Ala Ala Ser Gly Lys Asn Lys Arg Lys Ala  
130 135 140

Leu Cys Pro Asp His Asp Ser Asp Ser Ser Gly Lys Asp Pro Arg Asn  
145 150 155 160

Ser Gln Gly Lys Gly Ala His Arg Pro Glu His Ala Ser Gly Arg Arg  
165 170 175

Asn Val Lys Asp Ser Val Ser Ala Ser Glu Val Thr Ser Thr Val Tyr  
180 185 190

Asn Thr Val Ser Glu Gly Thr His Phe Leu Glu Thr Ile Glu Thr Pro  
195 200 205

Arg Pro Gly Lys Leu Phe Pro Lys Asp Val Ser Ser Ser Thr Pro Pro  
210 215 220

Ser Val Thr Ser Lys Ser Arg Val Ser Arg Leu Ala Gly Arg Lys Thr  
225 230 235 240

Asn Glu Ser Val Ser Glu Pro Arg Lys Gly Phe Met Tyr Ser Arg Asn  
245 250 255

Thr Asn Glu Asn Pro Gln Glu Cys Phe Asn Ala Ser Lys Leu Leu Thr  
260 265 270

Ser His Gly Met Gly Ile Gln Val Pro Leu Asn Ala Thr Glu Phe Asn  
275 280 285

Tyr Leu Cys Pro Ala Ile Ile Asn Gln Ile Asp Ala Arg Ser Cys Leu  
290 295 300

Ile His Thr Ser Glu Lys Lys Ala Glu Ile Pro Pro Lys Thr Tyr Ser  
305 310 315 320

Leu Gln Ile Ala Trp Val Gly Gly Phe Ile Ala Ile Ser Ile Ile Ser  
325 330 335

Phe Leu Ser Leu Leu Gly Val Ile Leu Val Pro Leu Met Asn Arg Val  
340 345 350

Phe Phe Lys Phe Leu Leu Ser Phe Leu Val Ala Leu Ala Val Gly Thr  
355 360 365

Leu Ser Gly Asp Ala Phe Leu His Leu Leu Pro His Ser His Ala Ser  
370 375 380

His His His Ser His Ser His Glu Glu Pro Ala Met Glu Met Lys Arg  
385 390 395 400

Gly Pro Leu Phe Ser His Leu Ser Ser Gln Asn Ile Glu Glu Ser Ala  
405 410 415

Tyr Phe Asp Ser Thr Trp Lys Gly Leu Thr Ala Leu Gly Gly Leu Tyr  
420 425 430

Phe Met Phe Leu Val Glu His Val Leu Thr Leu Ile Lys Gln Phe Lys  
435 440 445

Asp Lys Lys Lys Lys Asn Gln Lys Lys Pro Glu Asn Asp Asp Asp Val  
450 455 460

Glu Ile Lys Lys Gln Leu Ser Lys Tyr Glu Ser Gln Leu Ser Thr Asn  
465 470 475 480

Glu Glu Lys Val Asp Thr Asp Asp Arg Thr Glu Gly Tyr Leu Arg Ala  
485 490 495

Asp Ser Gln Glu Pro Ser His Phe Asp Ser Gln Gln Pro Ala Val Leu  
500 505 510

Glu Glu Glu Glu Val Met Ile Ala His Ala His Pro Gln Glu Val Tyr  
515 520 525

Asn Glu Tyr Val Pro Arg Gly Cys Lys Asn Lys Cys His Ser His Phe  
530 535 540

His Asp Thr Leu Gly Gln Ser Asp Asp Leu Ile His His His His Asp  
545 550 555 560

Tyr His His Ile Leu His His His His Gln Asn His His Pro His  
565 570 575

Ser His Ser Gln Arg Tyr Ser Arg Glu Glu Leu Lys Asp Ala Gly Val  
580 585 590

Ala Thr Leu Ala Trp Met Val Ile Met Gly Asp Gly Leu His Asn Phe  
595 600 605

Ser Asp Gly Leu Ala Ile Gly Ala Ala Phe Thr Glu Gly Leu Ser Ser  
610 615 620

Gly Leu Ser Thr Ser Val Ala Val Phe Cys His Glu Leu Pro His Glu  
625 630 635 640

Leu Gly Asp Phe Ala Val Leu Leu Lys Ala Gly Met Thr Val Lys Gln  
645 650 655

Ala Val Leu Tyr Asn Ala Leu Ser Ala Met Leu Ala Tyr Leu Gly Met  
660 665 670

Ala Thr Gly Ile Phe Ile Gly His Tyr Ala Glu Asn Val Ser Met Trp  
675 680 685

Ile Phe Ala Leu Thr Ala Gly Leu Phe Met Tyr Val Ala Leu Val Asp  
690 695 700

Met Val Pro Glu Met Leu His Asn Asp Ala Ser Asp His Gly Cys Ser  
705 710 715 720

Arg Trp Gly Tyr Phe Phe Leu Gln Asn Ala Gly Met Leu Leu Gly Phe

725

730

735

Gly Ile Met Leu Leu Ile Ser Ile Phe Glu His Lys Ile Val Phe Arg  
 740 745 750

Ile Asn Phe  
 755

<210> 182  
 <211> 2032  
 <212> DNA  
 <213> human organism

<400> 182		
cgcggggcgc ggagtccggcg gggcctcgcg ggacgcgggc agtgcggaga ccgcggcgct	60	
gaggacgcgg gagccggag cgcacgcgcg gggtgagtt cagcctactc tttcttagat	120	
gtgaaaggaa aggaagatca tttcatgcct tggtataaaa ggttcagact tctgctgatt	180	
cataaccatt tggctctgag ctatgacaag agagggaaaca aaaagttaaa cttacaagcc	240	
tgccataagt gagaagcaaa ctcccttgat aacatgcttt tgcgaagtgc aggaaaatta	300	
aatgtgggca ccaagaaaaga ggttgtgag agtacagccc ccacccccc tccaaaggtc	360	
ttgcgttgta aatgccacca ccattgtcca gaagactcag tcaacaatat ttgcagcaca	420	
gacggatatt gttcacat gatagaagag gatgactctg gttgcctgt ggtcaattct	480	
ggtgccttag gactagaagg ctcagattt cagtgcggg acactcccat tcctcatcaa	540	
agaagatcaa ttgaatgctg cacagaaagg aacgaatgta ataaagacct acaccctaca	600	
ctgcctccat tgaaaaacag agatttgtt gatggaccta tacaccacag ggcttactt	660	
atatctgtga ctgtctgtag tttgctcttg gtccttatca tattatttg ttacttccgg	720	
tataaaagac aagaaaccag acctcgatac agcattgggt tagaacagga tgaaacttac	780	
attcctcctg gagaatccct gagagactta attgagcagt ctcagagctc aggaagtgg	840	
tcaggcctcc ctctgttgt ccaaaggact atagctaagc agattcagat ggtgaaacag	900	
attggaaaag gtcgttatgg ggaagttgg atggaaaagt ggcgtggcga aaaggtagct	960	
tgaaaagtgt tcttaccac agaggaagcc agctggttca gagagacaga aatatatcag	1020	
acagtgttga tgaggcatga aaacattttgg gtttcatttgc ctcagatata caaaggacaa	1080	
gggtcctgga cccagttgtat ctaatcaca gactatcatg aaaatggtc ctttatgtat	1140	
tatctgaagt ccaccaccct agacgctaaa tcaatgctga agttacccata ctcttctgtc	1200	

agtggcttat	gtcatttaca	cacagaaaatc	tttagtactc	aaggcaaacc	agcaattgcc	1260
catcgagatc	tgaaaagtaa	aaacattctg	gtgaagaaaa	atggaacttg	ctgtattgct	1320
gacctgggcc	tggctgttaa	atttattatg	gatacaaatg	aagttgacat	accacctaac	1380
actcgagttg	gcacccaaacg	ctatatgcct	ccagaagtgt	tggacgagag	cttgaacaga	1440
aatcacttcc	agtcttacat	catggctgac	atgtatagtt	ttggcctcat	cctttggag	1500
gttgcttagga	gatgtgtatc	aggaggtata	gtggaagaat	accagctcc	ttatcatgac	1560
ctagtccccca	gtgaccccc	ttatgaggac	atgagggaga	tttgtgtcat	caagaagtta	1620
cgcctctcat	tcccaaaccg	gtggagcagt	gatgagtgtc	taaggcagat	gggaaaactc	1680
atgacagaat	gctgggctca	caatcctgca	tcaaggctga	cagccctgcg	ggttaagaaa	1740
acacttgcca	aatgtcaga	gtcccaggac	attaaactct	gataggagag	gaaaagtaag	1800
catctctgca	gaaagccaac	aggtactctt	ctgtttgtgg	gcagagcaaa	agacatcaaa	1860
taagcatcca	cagtacaagc	cttgaacatc	gtcctgcttc	ccagtgggtt	cagacctcac	1920
cttcagggaa	gcgacctggg	caaagacaga	gaagctccc	gaaggagaga	ttgatccgtg	1980
tctgtttgtta	ggcggagaaa	ccgttgggtta	acttgttcaa	gatatgatgc	at	2032

<210> 183

<211> 502

<212> PRT

<213> human organism

<400> 183

Met	Leu	Leu	Arg	Ser	Ala	Gly	Lys	Leu	Asn	Val	Gly	Thr	Lys	Lys	Glu
1					5				10				15		

Asp	Gly	Glu	Ser	Thr	Ala	Pro	Thr	Pro	Arg	Pro	Lys	Val	Leu	Arg	Cys
					20			25				30			

Lys	Cys	His	His	Cys	Pro	Glu	Asp	Ser	Val	Asn	Asn	Ile	Cys	Ser
					35			40				45		

Thr	Asp	Gly	Tyr	Cys	Phe	Thr	Met	Ile	Glu	Glu	Asp	Asp	Ser	Gly	Leu
					50			55			60				

Pro	Val	Val	Thr	Ser	Gly	Cys	Leu	Gly	Leu	Glu	Gly	Ser	Asp	Phe	Gln
					65			70		75		80			

Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys

85

90

95

Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro  
100 105 110

Leu Lys Asn Arg Asp Phe Val Asp Gly Pro Ile His His Arg Ala Leu  
115 120 125

Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu  
130 135 140

Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Thr Arg Pro Arg Tyr Ser  
145 150 155 160

Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu  
165 170 175

Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu  
180 185 190

Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys  
195 200 205

Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg  
210 215 220

Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser  
225 230 235 240

Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu  
245 250 255

Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp  
260 265 270

Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr  
275 280 285

Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu  
290 295 300

Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe  
305 310 315 320

Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys  
 325 330 335

Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly  
340 345 350

Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro  
355 360 365

Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp  
370 375 380

Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met  
385 390 395 400

Tyr Ser Phe Gly Leu Ile Leu Trp Glu Val Ala Arg Arg Cys Val Ser  
405 410 415

Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro  
 420 425 430

Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Ile Lys Lys  
435 440 445

Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg  
450 455 460

Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala His Asn Pro Ala Ser  
465 470 475 480

Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu  
485 486 487 488 489 490 491 492 493 494 495 496 497 498

Ser Gln Asp Ile Lys Leu  
500

<210> 184  
<211> 3375  
<212> DNA  
<213> human organism

<400> 184  
gacagtgttc gcggtctgcac cqctcqqaqq ctqqqtqacc cgcataqaag tqaagtactt

ttttatggc agacctggc cgatgccgt ttaaaaaacg cgaggggctc tatgcaccc 120  
cctggcggtt gttccctccga cctcagccgg gtcgggtcgt gccgcctct cccaggagag 180  
acaaacaggt gtcccacgtg gcagccgcgc cccgggcgcc cctcctgtga tcccgttagcg 240  
ccccctggcc cgagccgcgc ccgggtctgt gagtagagcc gcccgccac cgagcgctgg 300  
tcgcccgtct cttccgtta tatcaacatg cccctttcc tggattgttggaa ggccgtctgt 360  
gtttccgtt tttccagagt gcccccatct ctccctctcc aggaagtcca tgtaagcaaa 420  
gaaaccatcg ggaagatttc agctgccagc aaaatgtatgt ggtgctcgcc tgcagtggac 480  
atcatgtttc tgtagatgg gtctaacagc gtcggaaag ggagctttga aagggtccaag 540  
cactttgcca tcacagtctg tgacggtctg gacatcagcc ccgagagggt cagagtggga 600  
gcattccagt tcagttcac tcctcatctg gaattccct tggattcatt ttcaacccaa 660  
caggaagtga aggcaagaat caagaggatg gtttcaaag gagggcgcac ggagacggaa 720  
cttgctctga aataccttct gcacagaggg ttgcctggag gcagaaatgc ttctgtgccc 780  
cagatcctca tcatcgac tcatggaaag tcccaggggg atgtggact gccatccaag 840  
cagctgaagg aaaggggtgt cactgtgtt gctgtgggg tcaggtttcc caggtggag 900  
gagctgcattg cactggccag cgagcctaga gggcagcacf tgctgttggc tgagcaggtg 960  
gaggatgcca ccaacggcct cttcagcacc ctcagcagct cggccatctg ctccagcgcc 1020  
acgccagact gcagggtcga ggctcacccc tgtgagcaca ggacgctggaa gatggtccgg 1080  
gagttcgctg gcaatgcccc atgctggaga ggatcgccgc ggacccttgc ggtgctggct 1140  
gcacactgtc cttctacag ctgaaagaga gtgttctaa cccaccctgc cacctgctac 1200  
aggaccacct gcccaggccc ctgtgactcg cagccctgcc agaatggagg cacatgttt 1260  
ccagaaggac tggacggcta ccagtgcctc tgcccgctgg ctttggagg ggaggctaac 1320  
tgtgcctga agctgagcct ggaatgcagg gtcgacccctc tttccctgtt ggacagctct 1380  
gggggcacca ctctggacgg cttcctgcgg gccaaggatct tcgtgaagcg gtttgcgg 1440  
gccgtgctga gcgaggactc tcgggcccga gtgggtgtgg ccacatacag cagggagctg 1500  
ctgggtggcg ggcattccct tccgtgggtgg cccaccctg acgggcagtg cttgcggca ggcggcagag 1560  
cgtggctcg ggagcgccac caggacaggc caggaccggc cacgttagagt ggtggtttg 1620  
ctcaactgagt cacactccga ggatgaggtt gcgggcccag cgcgtcacgc aagggcgcga 1680  
1740

gagctgctcc tgctgggtgt aggcagttag gcccgtgcggg cagagctgga ggagatcaca 1800  
ggcagccaa agcatgtat ggtctactcg gatcctcagg atctgttcaa ccaaattccct 1860  
gagctgcagg ggaagctgtg cagccggcag cggcagggt gccggacaca agccctggac 1920  
ctcgcttc a tttggacac ctctgcctca gttagggcccg agaattttgc tcagatgcag 1980  
agctttgtga gaagctgtgc cctccagtt gaggtgaacc ctgacgtgac acaggtcggc 2040  
ctgggttgtt atggcagcca ggtgcagact gccttcggc tggacaccaa acccaccgg 2100  
gctgcgtatgc tgcggccat tagccaggcc ccctacctag gtgggggtggg ctcagccggc 2160  
accggccctgc tgcacatcta tgacaaaatg atgaccgtcc agaggggtgc cccggctgg 2220  
gtccccaaag ctgtgggtgt gtcacagggc gggagaggcg cagaggatgc agccgttcct 2280  
gcccagaagc tgaggaacaa tggcatctct gtcttggtcg tggcgtggg gcctgtccta 2340  
agtgggtc tgcggaggct tgcagggtccc cgggattccc tgatccacgt ggcagcttac 2400  
gccgacctgc ggtaccacca ggacgtgctc attgagtggc tgtgtggaga agccaaagcag 2460  
ccagtcacc tctgcaaacc cagccgtgc atgaatgagg gcagctgcgt cctgcagaat 2520  
gggagctacc gctgcaagtg tcgggatggc tggaggggcc cccactgcga gaaccgtgag 2580  
tggagctctt gctctgtatg tgtgagccag ggtggatttc ttgagacgcc cctgaggcac 2640  
atggctcccg tgcaggaggg cagcagccgt accccctccca gcaactacag agaaggcctg 2700  
ggcactgaaa tggtgccctac cttctggaat gtctgtccc caggtcctta gaatgtctgc 2760  
ttcccgccgt ggccaggacc actattctca ctgagggagg aggatgtccc aactgcagcc 2820  
atgctgctta gagacaagaa agcagctgat gtcacccaca aacgatgttg ttgaaaagtt 2880  
ttgatgtgta agtaataacc cacttctgt acctgctgtg cttgtttag gctatgtcat 2940  
ctgccacctt tcccttgagg ataaacaagg ggtcctgaag acttaaattt agcggcctga 3000  
cgttcctttg cacacaatca atgctgcca gaatgttggt gacacagtaa tgcccagcag 3060  
aggcctttac tagagcatcc tttggacggc gaaggccacg gccttcaag atggaaagca 3120  
gcagcttttc cacttccccca gagacattct ggtgcattt gcatttagtc tgaaaggggg 3180  
cttgagggac gtttgtgact tcttggcgac tgcctttgt gtgtggaaaga gacttggaaa 3240  
ggtctcagac tgaatgtgac caattaacca gcttgggtga tcatggggga ggggctgagt 3300  
tgtgcattggg cccaggtctg gagggccacg taaaatcggt ctgagtcgtg agcagtgcc 3360  
accttgaagg tcttc 3375

<210> 185  
<211> 807  
<212> PRT  
<213> human organism

<400> 185

Met Pro Pro Phe Leu Leu Leu Glu Ala Val Cys Val Phe Leu Phe Ser  
1 5 10 15

Arg Val Pro Pro Ser Leu Pro Leu Gln Glu Val His Val Ser Lys Glu  
20 25 30

Thr Ile Gly Lys Ile Ser Ala Ala Ser Lys Met Met Trp Cys Ser Ala  
35 40 45

Ala Val Asp Ile Met Phe Leu Leu Asp Gly Ser Asn Ser Val Gly Lys  
50 55 60

Gly Ser Phe Glu Arg Ser Lys His Phe Ala Ile Thr Val Cys Asp Gly  
65 70 75 80

Leu Asp Ile Ser Pro Glu Arg Val Arg Val Gly Ala Phe Gln Phe Ser  
85 90 95

Ser Thr Pro His Leu Glu Phe Pro Leu Asp Ser Phe Ser Thr Gln Gln  
100 105 110

Glu Val Lys Ala Arg Ile Lys Arg Met Val Phe Lys Gly Gly Arg Thr  
115 120 125

Glu Thr Glu Leu Ala Leu Lys Tyr Leu Leu His Arg Gly Leu Pro Gly  
130 135 140

Gly Arg Asn Ala Ser Val Pro Gln Ile Leu Ile Ile Val Thr Asp Gly  
145 150 155 160

Lys Ser Gln Gly Asp Val Ala Leu Pro Ser Lys Gln Leu Lys Glu Arg  
165 170 175

Gly Val Thr Val Phe Ala Val Gly Val Arg Phe Pro Arg Trp Glu Glu  
180 185 190

Leu His Ala Leu Ala Ser Glu Pro Arg Gly Gln His Val Leu Leu Ala  
195 200 205

Glu Gln Val Glu Asp Ala Thr Asn Gly Leu Phe Ser Thr Leu Ser Ser  
210 215 220

Ser Ala Ile Cys Ser Ser Ala Thr Pro Asp Cys Arg Val Glu Ala His  
225 230 235 240

Pro Cys Glu His Arg Thr Leu Glu Met Val Arg Glu Phe Ala Gly Asn  
245 250 255

Ala Pro Cys Trp Arg Gly Ser Arg Arg Thr Leu Ala Val Leu Ala Ala  
260 265 270

His Cys Pro Phe Tyr Ser Trp Lys Arg Val Phe Leu Thr His Pro Ala  
275 280 285

Thr Cys Tyr Arg Thr Thr Cys Pro Gly Pro Cys Asp Ser Gln Pro Cys  
290 295 300

Gln Asn Gly Gly Thr Cys Val Pro Glu Gly Leu Asp Gly Tyr Gln Cys  
305 310 315 320

Leu Cys Pro Leu Ala Phe Gly Gly Glu Ala Asn Cys Ala Leu Lys Leu  
325 330 335

Ser Leu Glu Cys Arg Val Asp Leu Leu Phe Leu Leu Asp Ser Ser Ala  
340 345 350

Gly Thr Thr Leu Asp Gly Phe Leu Arg Ala Lys Val Phe Val Lys Arg  
355 360 365

Phe Val Arg Ala Val Leu Ser Glu Asp Ser Arg Ala Arg Val Gly Val  
370 375 380

Ala Thr Tyr Ser Arg Glu Leu Leu Val Ala Val Pro Val Gly Glu Tyr  
385 390 395 400

Gln Asp Val Pro Asp Leu Val Trp Ser Leu Asp Gly Ile Pro Phe Arg  
405 410 415

Gly Gly Pro Thr Leu Thr Gly Ser Ala Leu Arg Gln Ala Ala Glu Arg  
420 425 430

Gly Phe Gly Ser Ala Thr Arg Thr Gly Gln Asp Arg Pro Arg Arg Val  
435 440 445

Val Val Leu Leu Thr Glu Ser His Ser Glu Asp Glu Val Ala Gly Pro  
450 455 460

Ala Arg His Ala Arg Ala Arg Glu Leu Leu Leu Leu Gly Val Gly Ser  
465 470 475 480

Glu Ala Val Arg Ala Glu Leu Glu Glu Ile Thr Gly Ser Pro Lys His  
485 490 495

Val Met Val Tyr Ser Asp Pro Gln Asp Leu Phe Asn Gln Ile Pro Glu  
500 505 510

Leu Gln Gly Lys Leu Cys Ser Arg Gln Arg Pro Gly Cys Arg Thr Gln  
515 520 525

Ala Leu Asp Leu Val Phe Met Leu Asp Thr Ser Ala Ser Val Gly Pro  
530 535 540

Glu Asn Phe Ala Gln Met Gln Ser Phe Val Arg Ser Cys Ala Leu Gln  
545 550 555 560

Phe Glu Val Asn Pro Asp Val Thr Gln Val Gly Leu Val Val Tyr Gly  
565 570 575

Ser Gln Val Gln Thr Ala Phe Gly Leu Asp Thr Lys Pro Thr Arg Ala  
580 585 590

Ala Met Leu Arg Ala Ile Ser Gln Ala Pro Tyr Leu Gly Gly Val Gly  
595 600 605

Ser Ala Gly Thr Ala Leu Leu His Ile Tyr Asp Lys Val Met Thr Val  
610 615 620

Gln Arg Gly Ala Arg Pro Gly Val Pro Lys Ala Val Val Val Leu Thr  
625 630 635 640

Gly Gly Arg Gly Ala Glu Asp Ala Ala Val Pro Ala Gln Lys Leu Arg  
645 650 655

Asn	Asn	Gly	Ile	Ser	Val	Leu	Val	Val	Gly	Val	Gly	Pro	Val	Leu	Ser
660					665							670			
Glu	Gly	Leu	Arg	Arg	Leu	Ala	Gly	Pro	Arg	Asp	Ser	Leu	Ile	His	Val
675					680							685			
Ala	Ala	Tyr	Ala	Asp	Leu	Arg	Tyr	His	Gln	Asp	Val	Leu	Ile	Glu	Trp
690					695						700				
Leu	Cys	Gly	Glu	Ala	Lys	Gln	Pro	Val	Asn	Leu	Cys	Lys	Pro	Ser	Pro
705					710						715				720
Cys	Met	Asn	Glu	Gly	Ser	Cys	Val	Leu	Gln	Asn	Gly	Ser	Tyr	Arg	Cys
725					730							735			
Lys	Cys	Arg	Asp	Gly	Trp	Glu	Gly	Pro	His	Cys	Glu	Asn	Arg	Glu	Trp
740					745						750				
Ser	Ser	Cys	Ser	Val	Cys	Val	Ser	Gln	Gly	Trp	Ile	Leu	Glu	Thr	Pro
755					760						765				
Leu	Arg	His	Met	Ala	Pro	Val	Gln	Glu	Gly	Ser	Ser	Arg	Thr	Pro	Pro
770					775						780				
Ser	Asn	Tyr	Arg	Glu	Gly	Leu	Gly	Thr	Glu	Met	Val	Pro	Thr	Phe	Trp
785					790						795				800
Asn	Val	Cys	Ala	Pro	Gly	Pro									
					805										

<210>	186					
<211>	1723					
<212>	DNA					
<213>	human organism					
<400>	186					
tgctacccgc	gccccggcctt	ctgggggttt	cccccaaccac	ggcccagccc	tgcacacaccc	60
cccgcccccg	gcctccgcag	ctcggcatgg	gcgcgggggt	gctcgctctg	ggcgccctccg	120
agcccggtaa	cctgtcgtcg	gccgcaccgc	tcccccacgg	cgcggccacc	gcggcgccgc	180
tgctggtgcc	cgcgtcgccg	cccgccctcg	tgctgcctcc	cgccagcgaa	agccccgagc	240
cgctgtctca	gcagtggaca	gcgggcatgg	gtctgctgat	ggcgctcatc	gtgctgctca	300
tcgtggcgaa	caatgtgctg	gtgatcgtgg	ccatcgccaa	gacgcccgg	ctgcagacgc	360

tcaccaacct	cttcatcatg	tccctggcca	gcgccgaccc	ggtcatgggg	ctgctgggtgg	420
tgccgttcgg	ggccaccatc	gtggtgtggg	gccgctggga	gtacggctcc	ttcttctgcg	480
agctgtggac	ctcagtggac	gtgctgtgcg	tgacggccag	catcgagacc	ctgtgtgtca	540
ttgccctgga	ccgctaccc	gccatcaccc	cgccttccg	ctaccagagc	ctgctgacgc	600
gcgcgcccc	gcggggcctc	gtgtgcaccg	tgtggccat	ctcgccctcg	gtgtccttcc	660
tgcccatcct	catgcactgg	tggcgccgg	agagcgacga	ggcgcccccgc	tgctacaacg	720
accccaagtg	ctgcgacttc	gtcaccaacc	gggcctacgc	catcgccctcg	tccgtagtct	780
ccttctacgt	gccccctgtgc	atcatggcct	tcgtgtaccc	gcgggtgttc	cgcgaggccc	840
agaagcaggt	gaagaagatc	gacagctgcg	agcgccgtt	cctcgccggc	ccagcgccgc	900
cgcctcgcc	ctcgccctcg	cccgcccccg	cgcggccgc	gccgccccgg	cccccgccgc	960
ccgcccgcgc	cgcgcacc	gccccgctgg	ccaacggcg	tgcgggtaag	cggcggccct	1020
cgcgcctcg	gcccctacgc	gagcagaagg	cgctcaagac	gctgggcattc	atcatggcg	1080
tcttcacgct	ctgctggctg	cccttcttcc	tggccaacgt	ggtaaggcc	ttccaccgcg	1140
agctggtgcc	cgaccgcctc	ttcgtcttct	tcaactggct	ggctacgccc	aactcgccct	1200
tcaacccat	catctactgc	cgcagcccc	acttccgcaa	ggccttccag	ggactgctct	1260
gctgcgcgc	cagggctgcc	cgcggccgc	acgcgaccca	cggagaccgg	ccgcgcgcct	1320
cgggctgtct	ggcccgcccc	ggaccccccgc	catcgcccc	ggccgcctcg	gacgacgacg	1380
acgacgatgt	cgtcgcccc	acgcccggcc	cgcgcctgct	ggagccctgg	gccggctgca	1440
acggcgcccc	ggcggccggac	agcgactcga	gcctggacga	gccgtgccgc	cccggttcg	1500
cctcggaatc	caaggtgtag	ggcccgccgc	ggggcgccga	ctccgggcac	ggcttcccag	1560
ggaaacgagg	agatctgtgt	ttacttaaga	ccgatagcag	gtgaactcga	agcccacaat	1620
cctcgtctga	atcatccgag	gcaaagagaa	aagccacgga	ccgttgcaca	aaaaggaaag	1680
tttggaaagg	gatgggagag	tggcttgctg	atgttcccttg	ttg		1723

<210> 187  
 <211> 477  
 <212> PRT  
 <213> human organism

<400> 187

Met Gly Ala Gly Val Leu Val Leu Gly Ala Ser Glu Pro Gly Asn Leu  
 1 5 10 15

Ser Ser Ala Ala Pro Leu Pro Asp Gly Ala Ala Thr Ala Ala Arg Leu  
20 25 30

Leu Val Pro Ala Ser Pro Pro Ala Ser Leu Leu Pro Pro Ala Ser Glu  
35 40 45

Ser Pro Glu Pro Leu Ser Gln Gln Trp Thr Ala Gly Met Gly Leu Leu  
50 55 60

Met Ala Leu Ile Val Leu Leu Ile Val Ala Gly Asn Val Leu Val Ile  
65 70 75 80

Val Ala Ile Ala Lys Thr Pro Arg Leu Gln Thr Leu Thr Asn Leu Phe  
85 90 95

Ile Met Ser Leu Ala Ser Ala Asp Leu Val Met Gly Leu Leu Val Val  
100 105 110

Pro Phe Gly Ala Thr Ile Val Val Trp Gly Arg Trp Glu Tyr Gly Ser  
115 120 125

Phe Phe Cys Glu Leu Trp Thr Ser Val Asp Val Leu Cys Val Thr Ala  
130 135 140

Ser Ile Glu Thr Leu Cys Val Ile Ala Leu Asp Arg Tyr Leu Ala Ile  
145 150 155 160

Thr Ser Pro Phe Arg Tyr Gln Ser Leu Leu Thr Arg Ala Arg Ala Arg  
165 170 175

Gly Leu Val Cys Thr Val Trp Ala Ile Ser Ala Leu Val Ser Phe Leu  
180 185 190

Pro Ile Leu Met His Trp Trp Arg Ala Glu Ser Asp Glu Ala Arg Arg  
195 200 205

Cys Tyr Asn Asp Pro Lys Cys Cys Asp Phe Val Thr Asn Arg Ala Tyr  
210 215 220

Ala Ile Ala Ser Ser Val Val Ser Phe Tyr Val Pro Leu Cys Ile Met  
225 230 235 240

Ala Phe Val Tyr Leu Arg Val Phe Arg Glu Ala Gln Lys Gln Val Lys  
245 250 255

Lys Ile Asp Ser Cys Glu Arg Arg Phe Leu Gly Gly Pro Ala Arg Pro  
260 265 270

Pro Ser Pro Ser Pro Ser Pro Val Pro Ala Pro Ala Pro Pro Pro Gly  
275 280 285

Pro Pro Arg Pro Ala Ala Ala Ala Ala Thr Ala Pro Leu Ala Asn Gly  
290 295 300

Arg Ala Gly Lys Arg Arg Pro Ser Arg Leu Val Ala Leu Arg Glu Gln  
305 310 315 320

Lys Ala Leu Lys Thr Leu Gly Ile Ile Met Gly Val Phe Thr Leu Cys  
325 330 335

Trp Leu Pro Phe Phe Leu Ala Asn Val Val Lys Ala Phe His Arg Glu  
340 345 350

Leu Val Pro Asp Arg Leu Phe Val Phe Asn Trp Leu Gly Tyr Ala  
355 360 365

Asn Ser Ala Phe Asn Pro Ile Ile Tyr Cys Arg Ser Pro Asp Phe Arg  
370 375 380

Lys Ala Phe Gln Gly Leu Leu Cys Cys Ala Arg Arg Ala Ala Arg Arg  
385 390 395 400

Arg His Ala Thr His Gly Asp Arg Pro Arg Ala Ser Gly Cys Leu Ala  
405 410 415

Arg Pro Gly Pro Pro Ser Pro Gly Ala Ala Ser Asp Asp Asp Asp  
420 425 430

Asp Asp Val Val Gly Ala Thr Pro Pro Ala Arg Leu Leu Glu Pro Trp  
435 440 445

Ala Gly Cys Asn Gly Gly Ala Ala Ala Asp Ser Asp Ser Ser Leu Asp  
450 455 460

Glu Pro Cys Arg Pro Gly Phe Ala Ser Glu Ser Lys Val  
465 470 475

<210> 188  
<211> 3737  
<212> DNA  
<213> human organism

<400> 188  
ggcgtccgcg cacacctccc cgcgcgcgc cggccaccgc ccgcactccg ccgcctctgc 60  
ccgcaaccgc tgagccatcc atgggggtcg cggccgcga ccgtcccgaa gcggcctggg 120  
cggtgctgct gctgctgctg ctgctgccgc cactgctgct gctggcgaaa gccgtcccg 180  
cgggtcgaaa ccgtgcgcg gggccgcagg aggtatgtaa tgagtgtgcc caagggttag 240  
atgactgcca tgccgacgccc ctgtgtcaga acacacccac ctcctacaag tgctcctgca 300  
agcctggcta ccaaggggaa ggcaggcagt gtgaggacat cgatgaatgt ggaaatgagc 360  
tcaatggagg ctgtgtccat gactgtttga atattccagg caattatcgat tgcacttgtt 420  
ttgatggctt catgtggctt catgacggtc ataattgtct tcatgtggac gagtgccctgg 480  
agaacaatgg cggctgccag catacctgtg tcaacgtcat ggggagctat gagtgctgct 540  
gcaaggagg gttttccctg agtgacaatc agcacacccat cattcaccgc tcggaagagg 600  
gcctgagctg catgaataag gatcacggct gtatgtccat ctgcaaggag gccccaaagg 660  
gcagcgtcgc ctgtgagtgc aggccctgggt ttgagctggc caagaaccag agagactgca 720  
tcttgacctg taaccatggg aacgggtgggt gccagcactc ctgtgacgt acagccgatg 780  
gccccagatg cagctgccat ccacagtaca agatgcacac agatggagg agctgccttg 840  
agcgagagga cactgtcctg gaggtgacag agagcaacac cacatcagtg gtggatgggg 900  
ataaacgggt gaaacggcg ctgctcatgg aaacgtgtgc tgtcaacaat ggaggctgtg 960  
accgcacctg taaggatact tcgacaggtg tccactgcag ttgtccctgtt ggattcactc 1020  
tccagttgga tggaaagaca tgtaaagata ttgatgagtg ccagacccgc aatggaggtt 1080  
gtgatcattt ctgaaaaaac atcgtggca gttttgactg cggctgcaag aaaggattta 1140  
aattattaac agatgagaag tcttgccaaat atgtggatga gtgctctttg gataggacat 1200  
gtgaccacag ctgcatcaac caccctggca catttgcgtt tgcttgcac cgagggtaca 1260  
ccctgtatgg cttcacccac tgtggagaca ccaatgagtg cagcatcaac aacggaggct 1320  
gtcagcaggt ctgtgtgaac acagtggca gctatgaatg ccagtgcac cctgggtaca 1380  
agctccactg gaataaaaaaa gactgtgtgg aagtgaaggg gtcctgccc acaagtgtgt 1440

caccccggtgt gtccctgcac tgcggtaaga gtgggtggagg agacgggtgc ttccctcagat 1500  
gtcaactctgg cattcacctc tcttcagatg tcaccaccat caggacaagt gtaacctta 1560  
agctaaatga aggcaagtgt agtttgaaaa atgctgagct gtttcccag ggtctgcgac 1620  
cagcactacc agagaagcac agctcagtaa aagagagctt ccgctacgta aaccttacat 1680  
gcagctctgg caagcaagtc ccaggagccc ctggccgacc aagcaccctt aaggaaatgt 1740  
ttatcactgt tgagtttgag cttgaaacta accaaaagga ggtgacagct tcttgcacc 1800  
tgagctgcattgt cgtaaagcga accgagaagc ggctccgtaa agccatccgc acgctcagaa 1860  
aggccgtcca cagggagcag tttcacctcc agctctcagg catgaacccctc gacgtggcta 1920  
aaaagcctcc cagaacatct gaacgccagg cagagtccctg tggagtgggc cagggcatg 1980  
cagaaaacca atgtgtcagt tgcagggctg ggaccttatta tgatggagca cgagaacgct 2040  
gcattttatg tccaaatgga accttccaaa atgaggaagg acaaataact tgtgaaccat 2100  
gcccaagacc aggaaattct gggccctga agaccccaga agcttggaaat atgtctgaat 2160  
gtggaggtct gtgtcaacctt ggtaaatatt ctgcagatgg ctttgcacct tgccagctct 2220  
gtgccctggg cacgttccag cctgaagctg gtcgaacttc ctgtttcccc tgtggaggag 2280  
gccttgccac caaacatcag ggagctactt ctttcagga ctgtgaaacc agagttcaat 2340  
gttcacctgg acatttctac aacaccacca ctcaccgatg tattcggtgc ccagtggaa 2400  
cataccagcc tgaatttgga aaaaataatt gtgttcttg cccaggaaat actacgactg 2460  
actttgatgg ctccacaaac ataacccagt gtaaaaacag aagatgtgga ggggagctgg 2520  
gagatttcac tgggtacatt gaatccccaa actaccagg caattaccca gccaacacccg 2580  
agtgtacgtg gaccatcaac ccacccccc agcgcgcgt cctgatcggt gtccctgaga 2640  
tcttcctgcc catagaggac gactgtgggg actatctggt gatgcggaaa acctttcat 2700  
ccaattctgt gacaacatata gaaacctgccc agacctacga acgccccatc gccttcaccc 2760  
ccaggtcaaa gaagctgtgg attcagttca agtccaatga agggAACAGC gctagagggt 2820  
tccaggtccc atacgtgaca tatgatgagg actaccagg actcattgaa gacatagttc 2880  
gagatggcag gctctatgca tctgagaacc atcaggaaat acttaaggat aagaaactta 2940  
tcaaggctct gtgttgcac ccggccatc cccagaacta tttcaagtac acagcccagg 3000  
agtccccaga gatgtttcca agatcggttca tccgattgct acgttccaaa gtgtccagg 3060  
ttttgagacc ttacaaatga ctcagccac gtgccactca atacaaatgt tctgctatag 3120

ggttggtggg acagagctgt cttccttctg catgtcagca cagtcgggta ttgctgcctc 3180  
ccgtatcagt gactcattag agttcaattt ttatagataa tacagatatt ttggtaaatt 3240  
gaaccttgggtt tttcttccc agcatcgtgg atgttagactg agaatggctt tgagtggcat 3300  
cagcttctca ctgctgtggg cgatgtctt ggatagatca cgggctggct gagctggact 3360  
ttggtcagcc taggtgagac tcacctgtcc ttctggggtc ttactcctcc tcaaggagtc 3420  
tgttagtgaa aggaggccac agaataagct gcttattctg aaacttcagc ttcctctagc 3480  
ccggccctct ctaagggagc cctctgcact cgtgtgcagg ctctgaccag gcagaacagg 3540  
caagagggga gggaggaga cccctgcagg ctccctccac ccaccttgag acctggagg 3600  
actcagttc tccacagcct tctccagcct gtgtgataca agtttgcgtcc caggaacttg 3660  
agttctaagc agtgcgtcg aaaaaaaaaa gcagaaaagaa ttagaaataa ataaaaacta 3720  
agcaattctg gagacat 3737

<210> 189

<211> 999

<212> PRT

<213> human organism

<400> 189

Met Gly Val Ala Gly Arg Asn Arg Pro Gly Ala Ala Trp Ala Val Leu  
1 5 10 15

Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu Ala Gly Ala Val  
20 25 30

Pro Pro Gly Arg Gly Arg Ala Ala Gly Pro Gln Glu Asp Val Asp Glu  
35 40 45

Cys Ala Gln Gly Leu Asp Asp Cys His Ala Asp Ala Leu Cys Gln Asn  
50 55 60

Thr Pro Thr Ser Tyr Lys Cys Ser Cys Lys Pro Gly Tyr Gln Gly Glu  
65 70 75 80

Gly Arg Gln Cys Glu Asp Ile Asp Glu Cys Gly Asn Glu Leu Asn Gly  
85 90 95

Gly Cys Val His Asp Cys Leu Asn Ile Pro Gly Asn Tyr Arg Cys Thr  
100 105 110

Cys Phe Asp Gly Phe Met Leu Ala His Asp Gly His Asn Cys Leu Asp  
115 120 125

Val Asp Glu Cys Leu Glu Asn Asn Gly Gly Cys Gln His Thr Cys Val  
130 135 140

Asn Val Met Gly Ser Tyr Glu Cys Cys Cys Lys Glu Gly Phe Phe Leu  
145 150 155 160

Ser Asp Asn Gln His Thr Cys Ile His Arg Ser Glu Glu Gly Leu Ser  
165 170 175

Cys Met Asn Lys Asp His Gly Cys Ser His Ile Cys Lys Glu Ala Pro  
180 185 190

Arg Gly Ser Val Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Ala Lys  
195 200 205

Asn Gln Arg Asp Cys Ile Leu Thr Cys Asn His Gly Asn Gly Gly Cys  
210 215 220

Gln His Ser Cys Asp Asp Thr Ala Asp Gly Pro Glu Cys Ser Cys His  
225 230 235 240

Pro Gln Tyr Lys Met His Thr Asp Gly Arg Ser Cys Leu Glu Arg Glu  
245 250 255

Asp Thr Val Leu Glu Val Thr Glu Ser Asn Thr Thr Ser Val Val Asp  
260 265 270

Gly Asp Lys Arg Val Lys Arg Arg Leu Leu Met Glu Thr Cys Ala Val  
275 280 285

Asn Asn Gly Gly Cys Asp Arg Thr Cys Lys Asp Thr Ser Thr Gly Val  
290 295 300

His Cys Ser Cys Pro Val Gly Phe Thr Leu Gln Leu Asp Gly Lys Thr  
305 310 315 320

Cys Lys Asp Ile Asp Glu Cys Gln Thr Arg Asn Gly Gly Cys Asp His  
325 330 335

Phe Cys Lys Asn Ile Val Gly Ser Phe Asp Cys Gly Cys Lys Lys Gly  
340 345 350

Phe Lys Leu Leu Thr Asp Glu Lys Ser Cys Gln Asp Val Asp Glu Cys  
355 360 365

Ser Leu Asp Arg Thr Cys Asp His Ser Cys Ile Asn His Pro Gly Thr  
370 375 380

Phe Ala Cys Ala Cys Asn Arg Gly Tyr Thr Leu Tyr Gly Phe Thr His  
385 390 395 400

Cys Gly Asp Thr Asn Glu Cys Ser Ile Asn Asn Gly Gly Cys Gln Gln  
405 410 415

Val Cys Val Asn Thr Val Gly Ser Tyr Glu Cys Gln Cys His Pro Gly  
420 425 430

Tyr Lys Leu His Trp Asn Lys Lys Asp Cys Val Glu Val Lys Gly Leu  
435 440 445

Leu Pro Thr Ser Val Ser Pro Arg Val Ser Leu His Cys Gly Lys Ser  
450 455 460

Gly Gly Gly Asp Gly Cys Phe Leu Arg Cys His Ser Gly Ile His Leu  
465 470 475 480

Ser Ser Asp Val Thr Thr Ile Arg Thr Ser Val Thr Phe Lys Leu Asn  
485 490 495

Glu Gly Lys Cys Ser Leu Lys Asn Ala Glu Leu Phe Pro Glu Gly Leu  
500 505 510

Arg Pro Ala Leu Pro Glu Lys His Ser Ser Val Lys Glu Ser Phe Arg  
515 520 525

Tyr Val Asn Leu Thr Cys Ser Ser Gly Lys Gln Val Pro Gly Ala Pro  
530 535 540

Gly Arg Pro Ser Thr Pro Lys Glu Met Phe Ile Thr Val Glu Phe Glu  
545 550 555 560

Leu Glu Thr Asn Gln Lys Glu Val Thr Ala Ser Cys Asp Leu Ser Cys

565

570

575

Ile Val Lys Arg Thr Glu Lys Arg Leu Arg Lys Ala Ile Arg Thr Leu  
580 585 590

Arg Lys Ala Val His Arg Glu Gln Phe His Leu Gln Leu Ser Gly Met  
595 600 605

Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln Ala  
610 615 620

Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val Ser  
625 630 635 640

Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile Leu  
645 650 655

Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys Glu  
660 665 670

Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu Ala  
675 680 685

Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Gly Glu Tyr Ser  
690 695 700

Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Thr Phe Gln  
705 710 715 720

Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Leu Ala  
725 730 735

Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg Val  
740 745 750

Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr His Arg Cys Ile  
755 760 765

Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn Cys  
770 775 780

Val Ser Cys Pro Gly Asn Thr Thr Asp Phe Asp Gly Ser Thr Asn  
785 790 795 800

Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp Phe  
805 810 815

Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala Asn  
820 825 830

Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile Leu  
835 840 845

Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly Asp  
850 855 860

Tyr Leu Val Met Arg Lys Thr Ser Ser Asn Ser Val Thr Thr Tyr  
865 870 875 880

Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg Ser  
885 890 895

Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg  
900 905 910

Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu  
915 920 925

Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His  
930 935 940

Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val  
945 950 955 960

Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser Arg  
965 970 975

Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser  
980 985 990

Arg Phe Leu Arg Pro Tyr Lys  
995

<210> 190  
<211> 2642  
<212> DNA

<213> human organism

<400> 190	
aaggaggcgg cctccgggaa aagcgaccgc aggactcctg agagcagcct ccatgaggcc	60
ctggaccagt gcatgaccgc cctggaccc tcctcacca accagttctc agaagcactc	120
agctacctca agcccagaac caaggaaagc atgtaccact cactgacata tgccaccatc	180
ctggagatgc aggccatgat gaccttgac cctcaggaca tcctgcttgc cggcaacatg	240
atgaaggagg cacagatgct gtgtcagagg caccggagga agtcttctgt aacagattcc	300
ttcagcagcc tggtaaccg ccccacgctg ggccaattca ctgaagaaga aatccacgct	360
gaggtctgct atgcagagtg cctgctgcag cgagcagccc tgaccttcct gcaggacgag	420
aacatggtga gcttcataa aggccgcattc aaagttcgaa acagctacca gacctacaag	480
gagctggaca gccttggta gtcctcacaa tactgcaagg gtgagaacca cccgcacttt	540
gaaggaggag tgaagcttgg tgttagggcc ttcaacctga cactgtccat gttcctact	600
aggatcctga ggctgttgg a gtttgtggg ttttcaggaa acaaggacta tgggctgctg	660
cagctggagg agggagcgtc agggcacagc ttccgctctg tgctctgtgt catgctcctg	720
ctgtcttacc acacccctt caccctcgta ctcggtaactg ggaacgtcaa catcgaggag	780
gccgagaagc tcttgaagcc ctacctgaac cggtaacccta agggtgccat cttcctgttc	840
tttgcaggga ggattgaagt cattaaaggc aacattgtatg cagccatccg gcgtttcgag	900
gagtgcgttg aggccccagca gcaactgaaag cagtttcacc acatgtgcta ctgggagctg	960
atgtggtgct tcacccataa gggccagtgg aagatgtcct acttctacgc cgacctgctc	1020
agcaaggaga actgctggtc caaggccacc tacatttaca tgaaggccgc ctacccatgc	1080
atgtttggga aggaggacca caagccgttc ggggacgacg aagtggaaatt atttcgagct	1140
gtgccaggcc tgaagctcaa gattgctggg aaatctctac ccacagagaa gtttgcattc	1200
cggaagtccc ggcgctactt ctcctccaaac cctatctcg c tgccagtggc tgctctggaa	1260
atgatgtaca tctggAACGG ctacggcgta attggaaagc agccgaaact cacggatggg	1320
atacttgaga ttatcactaa ggctgaagag atgctggaga aaggcccaga gaacgagttac	1380
tcagtgatgc acgaggatgtt ggtggaaattt ttgaaaggcc tggatctgaa atacccggc	1440
cgtgtccagg agggccgagga gaattttagg agcatctctg ccaatgaaaa gaagattaaa	1500
tatgaccact acttgatccc aaacgcccctg ctggagctgg ccctgctgct tatggagcaa	1560
gacagaaacg aagaggccat caaacttttgg gaatctgcca agcaaaaacta caagaattac	1620

tccatggagt caaggacaca ctttcgaatc caggcagcca cactccaagc caagtcttcc	1680
ctagagaaca gcagcagatc catggtctca tcagtgtcct ttagtcttg tgcagcagtt	1740
ccgggctgga agacagagac agctggacag agctcctgaa aacatttcaa aataccccct	1800
ccccctgccc tgccctgcct ttgggtcca ccggcactcc agttggatgg cacaacatag	1860
tgtatccgtg cagaagccga gctggcattt tcaccagtgt agccaaggc ctggccaaag	1920
ggcagagcag gtggagccct ctgcctgccc tatcacacat acgggtactt gctttcact	1980
gtgatgtta agagaatgta tgaacagttt acatttcct tagaaataca ttgatggat	2040
cacagttggc ttaaaaaacc aacaacaatc aaccacctgt aagtcttgc ctgcacccat	2100
tatcatctgg aggtaaatct ctttatatga tgatgccaaa gggcaaattt ctggccaaat	2160
tcagcaagtt ctcagcttgc gtgacggaag gtccttcaga ggacctgagg aatgcctggg	2220
agaggctaag cctcaggcct caatgcttct ggggttggc atgaggatgt acacagacac	2280
ccactacctt actactcaca cttcatttca ctcctttgt aaatttccaa ttaaaaatc	2340
aagcacgtct ttttagtgag ataaaaatctg agctcttctg tagaaaaatc aatctctacc	2400
agtagaaaaat gccagggcct gatggaagag ctgtgttagcc ctttctatgc caaagccagg	2460
aaatttgggg ggcaggagga gttctcaga atccagtctg tatcttgct gtatgccaaa	2520
ctgaaaccac tggaaataat ttatgaaaca taaaaatctt ctgtacttca ctccaaggta	2580
catttgctta ctgacagcat ttttgtaaa actgttattc ttgaaaaaaaaaaaaaaaaaa	2640
aa	2642

<210> 191  
<211> 550  
<212> PRT  
<213> human organism

<400> 191

Met Thr Ala Leu Asp Leu Phe Leu Thr Asn Gln Phe Ser Glu Ala Leu  
1 5 10 15

Ser Tyr Leu Lys Pro Arg Thr Lys Glu Ser Met Tyr His Ser Leu Thr  
                   20                  25                  30

Tyr Ala Thr Ile Leu Glu Met Gln Ala Met Met Thr Phe Asp Pro Gln  
                  35                 40                 45

Asp Ile Leu Leu Ala Gly Asn Met Met Lys Glu Ala Gln Met Leu Cys

50                    55                    60

Gln Arg His Arg Arg Lys Ser Ser Val Thr Asp Ser Phe Ser Ser Leu  
65                    70                    75                    80

Val Asn Arg Pro Thr Leu Gly Gln Phe Thr Glu Glu Glu Ile His Ala  
85                    90                    95

Glu Val Cys Tyr Ala Glu Cys Leu Leu Gln Arg Ala Ala Leu Thr Phe  
100                    105                    110

Leu Gln Asp Glu Asn Met Val Ser Phe Ile Lys Gly Gly Ile Lys Val  
115                    120                    125

Arg Asn Ser Tyr Gln Thr Tyr Lys Glu Leu Asp Ser Leu Val Gln Ser  
130                    135                    140

Ser Gln Tyr Cys Lys Gly Glu Asn His Pro His Phe Glu Gly Gly Val  
145                    150                    155                    160

Lys Leu Gly Val Gly Ala Phe Asn Leu Thr Leu Ser Met Leu Pro Thr  
165                    170                    175

Arg Ile Leu Arg Leu Leu Glu Phe Val Gly Phe Ser Gly Asn Lys Asp  
180                    185                    190

Tyr Gly Leu Leu Gln Leu Glu Gly Ala Ser Gly His Ser Phe Arg  
195                    200                    205

Ser Val Leu Cys Val Met Leu Leu Leu Cys Tyr His Thr Phe Leu Thr  
210                    215                    220

Phe Val Leu Gly Thr Gly Asn Val Asn Ile Glu Glu Ala Glu Lys Leu  
225                    230                    235                    240

Leu Lys Pro Tyr Leu Asn Arg Tyr Pro Lys Gly Ala Ile Phe Leu Phe  
245                    250                    255

Phe Ala Gly Arg Ile Glu Val Ile Lys Gly Asn Ile Asp Ala Ala Ile  
260                    265                    270

Arg Arg Phe Glu Glu Cys Cys Glu Ala Gln Gln His Trp Lys Gln Phe  
275                    280                    285

His His Met Cys Tyr Trp Glu Leu Met Trp Cys Phe Thr Tyr Lys Gly  
290 295 300

Gln Trp Lys Met Ser Tyr Phe Tyr Ala Asp Leu Leu Ser Lys Glu Asn  
305 310 315 320

Cys Trp Ser Lys Ala Thr Tyr Ile Tyr Met Lys Ala Ala Tyr Leu Ser  
325 330 335

Met Phe Gly Lys Glu Asp His Lys Pro Phe Gly Asp Asp Glu Val Glu  
340 345 350

Leu Phe Arg Ala Val Pro Gly Leu Lys Leu Lys Ile Ala Gly Lys Ser  
355 360 365

Leu Pro Thr Glu Lys Phe Ala Ile Arg Lys Ser Arg Arg Tyr Phe Ser  
370 375 380

Ser Asn Pro Ile Ser Leu Pro Val Pro Ala Leu Glu Met Met Tyr Ile  
385 390 395 400

Trp Asn Gly Tyr Ala Val Ile Gly Lys Gln Pro Lys Leu Thr Asp Gly  
405 410 415

Ile Leu Glu Ile Ile Thr Lys Ala Glu Glu Met Leu Glu Lys Gly Pro  
420 425 430

Glu Asn Glu Tyr Ser Val Asp Asp Glu Cys Leu Val Lys Leu Leu Lys  
435 440 445

Gly Leu Cys Leu Lys Tyr Leu Gly Arg Val Gln Glu Ala Glu Glu Asn  
450 455 460

Phe Arg Ser Ile Ser Ala Asn Glu Lys Lys Ile Lys Tyr Asp His Tyr  
465 470 475 480

Leu Ile Pro Asn Ala Leu Leu Glu Leu Ala Leu Leu Leu Met Glu Gln  
485 490 495

Asp Arg Asn Glu Glu Ala Ile Lys Leu Leu Glu Ser Ala Lys Gln Asn  
500 505 510

Tyr Lys Asn Tyr Ser Met Glu Ser Arg Thr His Phe Arg Ile Gln Ala  
515 520 525

Ala Thr Leu Gln Ala Lys Ser Ser Leu Glu Asn Ser Ser Arg Ser Met  
530 535 540

Val Ser Ser Val Ser Leu  
545 550

<210> 192  
<211> 4427  
<212> DNA  
<213> human organism

<400> 192  
atgacttagga agaggacata ctgggtgcc aactttctg gtggcctcgtaaatcgtggc 60  
atcgacatag gcgcgtacat ggtttcagga cttatttata aaacctatac tctccaagat 120  
ggcccccgtggaa gtcagcaaga gagaaatcct gaggctccag ggagggcagc tgtcccaccg 180  
tgggggaagt atgatgctgc cttgagaacc atgattccct tccgtcccaa gccgaggtt 240  
cctgcccccc agcccccgtggaa caatgctggc ctgttctcct acctcacccgt gtcatggctc 300  
accccgctca tgatccaaag cttacggagt cgcttagatg agaacaccat ccctccactg 360  
tcagtcatg atgcctcaga caaaaatgtc caaaggcttc accgcctttg ggaagaagaa 420  
gtctcaaggc gagggattga aaaagcttca gtgcttctgg tgatgctgag gttccagaga 480  
acaagggttga ttttcgatgc acttctggc atctgcttct gcattgccag tgtactcggg 540  
ccaatattga ttataccaaa gatcctggaa tattcagaag agcagttggg gaatgttgc 600  
catggagtgg gactctgctt tgccctttt ctctccgaat gtgtgaagtc tctgagttc 660  
tcctccagtt ggatcatcaa ccaacgcaca gccatcacgt tccgagcagc tgttccctcc 720  
tttgcccttg agaagctcat ccaatttaag tctgtataac acatcaccctc aggagaggcc 780  
atcagcttct tcaccgggtga tgtaaactac ctgttgaag gggtgtgcta tggaccccta 840  
gtactgatca cctgcgcac tcgttgtcatc tgcagcattt cttctactt cattattgg 900  
tacactgcat ttattgcccatttatgctat ctcctggttt tcccactggc ggtattcatg 960  
acaagaatgg ctgtgaaggc tcagcatcac acatctgagg tcagcgacca ggcacccgt 1020  
gtgaccagtg aagttctcac ttgcattaag ctgataaaaa tgtacacatg ggagaaacca 1080  
tttgcacaaaaa tcattgaagg tatggaaagt ctgactttct gctccaaacc tggtgatggc 1140

atggcttca gcatgctggc ctcccttgaat ctcccttcggc tgtcagtgtt ctttgcct 1200  
attgcagtca aaggctcac gaattccaag tctgcagtga tgaggttcaa gaagttttc 1260  
ctccaggaga gccctgtttt ctatgtccag acattacaag accccagcaa agctctggc 1320  
tttgaggagg ccacccctgtc atggcaacag acctgtcccgg gatcgtaa tggggcactg 1380  
gagctggaga ggaacgggca tgcttcttag gggatgacca ggcttagaga tgccctcggg 1440  
ccagaggaag aagggAACAG cctggggccca gagttgcaca agatcaacct ggtggtgtcc 1500  
aagggatga tgtaggggt ctgcggcaac acggggagtg gtaagagcag cctgttgtca 1560  
gccatcctgg aggagatgca cttgctcgag ggctcggtgg ggggcaggg aagcctggcc 1620  
tatgtcccccc agcaggcctg gatcgtaagc gggAACATCA gggagaacat cctcatggga 1680  
ggcgcatatg acaaggccccg atacccctccag gtgctccact gctgctccct gaatcgggac 1740  
ctggaacttc tgccctttgg agacatgaca gagattggag agcggggcct caacctctct 1800  
ggggggcaga aacagaggat cagcctggcc cgccgcgtct attccgaccg tcagatctac 1860  
ctgctggacg accccctgtc tgctgtggac gcccacgtgg ggaagcacat ttttggaggag 1920  
tgcatTAAGA agacactcag gggaaagacg gtcgtcctgg tgacccacca gctgcagtac 1980  
ttagaatttt gtggccagat cattttgttg gaaaatggga aaatctgtga aaatggaaact 2040  
cacagttagt taatgcagaa aaaggggaaa tatGCCAAC ttatccagaa gatgcacaag 2100  
gaagccactt cggacatgtt gcaggacaca gcaaagatag cagagaagcc aaaggtagaa 2160  
agtcaGGGTC tggccacccctc cctggaaagag tctctcaacg gaaatgctgt gccggagcat 2220  
cagctcacac aggaggagga gatggaaagaa ggctccttga gttggagggt ctaccaccac 2280  
tacatccagg cagctggagg ttacatggtc tcttcataa ttttcttctt cgtggtgctg 2340  
atcgctttct taacgatctt cagcttctgg tggctgagct actgggttggc gcagggctcg 2400  
gggaccaata gcagccgaga gagcaatggc accatggcag acctggcaa cattgcagac 2460  
aatcctcaac tgccttcta ccagctggtg tacgggctca acggccctgt cctcatctgt 2520  
gtgggggtct gtcctcagg gatTTTcacc aaagtcacga ggaaggcatc cacggccctg 2580  
cacaacaAGC tcttcaacaa ggTTTCCGC tgccccatga gtttcttga caccatccca 2640  
ataggccggc ttttgaactg cttcgcaggg gacttggAAC agctggacca gctcttgcgg 2700  
atctttcag agcagttcct ggtcctgtcc ttaatgggtga tcgcccgtct gttgattgtc 2760  
agtgtgctgt ctccatatac cctgttaatg ggagccataa tcatggttat ttgcttcatt 2820  
tattatatga tggcaagaa ggccatcggt gtggcaaga gactggagaa ctatagccgg 2880

tctcctttat tctccacat cctcaattct ctgcaaggcc tgagctccat ccatgtctat	2940
ggaaaaactg aagacttcat cagccagttt aagaggctga ctgatgcgca gaataactac	3000
ctgctgttgt ttctatcttc cacacgatgg atggcattga ggctggagat catgaccaac	3060
cttgcacct tggctgttgc cctgttcgtg gctttggca tttcctccac cccctactcc	3120
tttaaagtca tggctgtcaa catcgctgctg cagctggcgt ccagcttcca ggccactgcc	3180
cggattggct tggagacaga ggcacagttc acggctgttag agaggatact gcagtacatg	3240
aagatgtgtg tctcggaaagc tccttacac atggaaggca caagttgtcc ccaggggtgg	3300
ccacagcatg gggaaatcat attcaggat tatkacatga aatacagaga caacacaccc	3360
accgtgcttc acggcatcaa cctgaccatc cgccggccacg aagtgggtgg catcggtgg	3420
aggacgggct ctgggaagtc ctccctggc atggctctct tccgcctggg ggagccatg	3480
gcaggccgga ttctcattga cggcgtggac atttgcagca tcggcctgga ggacttgcgg	3540
tccaagctct cagtatccc tcaagatcca gtgctgtct caggaaccat cagattcaac	3600
ctagatccct ttgaccgtca cactgaccag cagatctggg atgccttgg gaggacattc	3660
ctgaccaagg ccatctcaaa gttccccaaa aagctgcata cagatgtgg ggaaaacgg	3720
ggaaaacttct ctgtggggg gaggcagctg ctctgcattt ccaggcgtgt gcttcgcaac	3780
tccaagatca tccttatcga tgaagccaca gcctccattt acatggagac agacaccctg	3840
atccagcgca caatccgtga agccttccag ggctgcaccc tgctcgtcat tgcccaccgt	3900
gtcaccactg tgctgaactg tgaccacatc ctggatatgg gcaatggaa ggtggtagaa	3960
tttgatccggc cggaggtact gcggagaag cctgggtcat tgccgcagc cctcatggcc	4020
acagccactt cttcaactgag ataaggagat gtggagactt catggaggt ggcagctgag	4080
ctcagaggtt cacacaggtg cagcttcgag gcccacagtc tgccgaccccttcc ttgtttggag	4140
atgagaactt ctcccttggaaag cagggtaaa tgttaggggg gtggggattt ctggatggaa	4200
acccttggaaat aggctacttg atggctctca agaccttaga accccagaac catctaagac	4260
atgggattca gtgatcatgt ggttctcattt ttaacttaca tgctgaataa ttttataata	4320
aggtaaaagc ttatagttt ctgatctgtg tttagaagtgy tgccaaatgt gtactgactt	4380
tgtaaaatataaaaactaagg aaaactcaaaa aaaaaaaaaa aaaaaaaaaa	4427

<210> 193  
<211> 1347  
<212> PRT

<213> human organism

<400> 193

Met Thr Arg Lys Arg Thr Tyr Trp Val Pro Asn Ser Ser Gly Gly Leu  
1 5 10 15

Val Asn Arg Gly Ile Asp Ile Gly Asp Asp Met Val Ser Gly Leu Ile  
20 25 30

Tyr Lys Thr Tyr Thr Leu Gln Asp Gly Pro Trp Ser Gln Gln Glu Arg  
35 40 45

Asn Pro Glu Ala Pro Gly Arg Ala Ala Val Pro Pro Trp Gly Lys Tyr  
50 55 60

Asp Ala Ala Leu Arg Thr Met Ile Pro Phe Arg Pro Lys Pro Arg Phe  
65 70 75 80

Pro Ala Pro Gln Pro Leu Asp Asn Ala Gly Leu Phe Ser Tyr Leu Thr  
85 90 95

Val Ser Trp Leu Thr Pro Leu Met Ile Gln Ser Leu Arg Ser Arg Leu  
100 105 110

Asp Glu Asn Thr Ile Pro Pro Leu Ser Val His Asp Ala Ser Asp Lys  
115 120 125

Asn Val Gln Arg Leu His Arg Leu Trp Glu Glu Val Ser Arg Arg  
130 135 140

Gly Ile Glu Lys Ala Ser Val Leu Leu Val Met Leu Arg Phe Gln Arg  
145 150 155 160

Thr Arg Leu Ile Phe Asp Ala Leu Leu Gly Ile Cys Phe Cys Ile Ala  
165 170 175

Ser Val Leu Gly Pro Ile Leu Ile Ile Pro Lys Ile Leu Glu Tyr Ser  
180 185 190

Glu Glu Gln Leu Gly Asn Val Val His Gly Val Gly Leu Cys Phe Ala  
195 200 205

Leu Phe Leu Ser Glu Cys Val Lys Ser Leu Ser Phe Ser Ser Ser Trp

210                    215                    220  
Ile Ile Asn Gln Arg Thr Ala Ile Arg Phe Arg Ala Ala Val Ser Ser  
225                    230                    235                    240  
  
Phe Ala Phe Glu Lys Leu Ile Gln Phe Lys Ser Val Ile His Ile Thr  
245                    250                    255  
  
Ser Gly Glu Ala Ile Ser Phe Phe Thr Gly Asp Val Asn Tyr Leu Phe  
260                    265                    270  
  
Glu Gly Val Cys Tyr Gly Pro Leu Val Leu Ile Thr Cys Ala Ser Leu  
275                    280                    285  
  
Val Ile Cys Ser Ile Ser Ser Tyr Phe Ile Ile Gly Tyr Thr Ala Phe  
290                    295                    300  
  
Ile Ala Ile Leu Cys Tyr Leu Leu Val Phe Pro Leu Ala Val Phe Met  
305                    310                    315                    320  
  
Thr Arg Met Ala Val Lys Ala Gln His His Thr Ser Glu Val Ser Asp  
325                    330                    335  
  
Gln Arg Ile Arg Val Thr Ser Glu Val Leu Thr Cys Ile Lys Leu Ile  
340                    345                    350  
  
Lys Met Tyr Thr Trp Glu Lys Pro Phe Ala Lys Ile Ile Glu Gly Met  
355                    360                    365  
  
Glu Ser Leu Thr Phe Cys Ser Lys Pro Gly Asp Gly Met Ala Phe Ser  
370                    375                    380  
  
Met Leu Ala Ser Leu Asn Leu Leu Arg Leu Ser Val Phe Phe Val Pro  
385                    390                    395                    400  
  
Ile Ala Val Lys Gly Leu Thr Asn Ser Lys Ser Ala Val Met Arg Phe  
405                    410                    415  
  
Lys Lys Phe Phe Leu Gln Glu Ser Pro Val Phe Tyr Val Gln Thr Leu  
420                    425                    430  
  
Gln Asp Pro Ser Lys Ala Leu Val Phe Glu Glu Ala Thr Leu Ser Trp  
435                    440                    445

Gln Gln Thr Cys Pro Gly Ile Val Asn Gly Ala Leu Glu Leu Glu Arg  
450 455 460

Asn Gly His Ala Ser Glu Gly Met Thr Arg Pro Arg Asp Ala Leu Gly  
465 470 475 480

Pro Glu Glu Glu Gly Asn Ser Leu Gly Pro Glu Leu His Lys Ile Asn  
485 490 495

Leu Val Val Ser Lys Gly Met Met Leu Gly Val Cys Gly Asn Thr Gly  
500 505 510

Ser Gly Lys Ser Ser Leu Leu Ser Ala Ile Leu Glu Glu Met His Leu  
515 520 525

Leu Glu Gly Ser Val Gly Val Gln Gly Ser Leu Ala Tyr Val Pro Gln  
530 535 540

Gln Ala Trp Ile Val Ser Gly Asn Ile Arg Glu Asn Ile Leu Met Gly  
545 550 555 560

Gly Ala Tyr Asp Lys Ala Arg Tyr Leu Gln Val Leu His Cys Cys Ser  
565 570 575

Leu Asn Arg Asp Leu Glu Leu Leu Pro Phe Gly Asp Met Thr Glu Ile  
580 585 590

Gly Glu Arg Gly Leu Asn Leu Ser Gly Gly Gln Lys Gln Arg Ile Ser  
595 600 605

Leu Ala Arg Ala Val Tyr Ser Asp Arg Gln Ile Tyr Leu Leu Asp Asp  
610 615 620

Pro Leu Ser Ala Val Asp Ala His Val Gly Lys His Ile Phe Glu Glu  
625 630 635 640

Cys Ile Lys Lys Thr Leu Arg Gly Lys Thr Val Val Leu Val Thr His  
645 650 655

Gln Leu Gln Tyr Leu Glu Phe Cys Gly Gln Ile Ile Leu Leu Glu Asn  
660 665 670

Gly Lys Ile Cys Glu Asn Gly Thr His Ser Glu Leu Met Gln Lys Lys  
675 680 685

Gly Lys Tyr Ala Gln Leu Ile Gln Lys Met His Lys Glu Ala Thr Ser  
690 695 700

Asp Met Leu Gln Asp Thr Ala Lys Ile Ala Glu Lys Pro Lys Val Glu  
705 710 715 720

Ser Gln Ala Leu Ala Thr Ser Leu Glu Glu Ser Leu Asn Gly Asn Ala  
725 730 735

Val Pro Glu His Gln Leu Thr Gln Glu Glu Glu Met Glu Glu Gly Ser  
740 745 750

Leu Ser Trp Arg Val Tyr His His Tyr Ile Gln Ala Ala Gly Gly Tyr  
755 760 765

Met Val Ser Cys Ile Ile Phe Phe Val Val Leu Ile Val Phe Leu  
770 775 780

Thr Ile Phe Ser Phe Trp Trp Leu Ser Tyr Trp Leu Glu Gln Gly Ser  
785 790 795 800

Gly Thr Asn Ser Ser Arg Glu Ser Asn Gly Thr Met Ala Asp Leu Gly  
805 810 815

Asn Ile Ala Asp Asn Pro Gln Leu Ser Phe Tyr Gln Leu Val Tyr Gly  
820 825 830

Leu Asn Ala Leu Leu Ile Cys Val Gly Val Cys Ser Ser Gly Ile  
835 840 845

Phe Thr Lys Val Thr Arg Lys Ala Ser Thr Ala Leu His Asn Lys Leu  
850 855 860

Phe Asn Lys Val Phe Arg Cys Pro Met Ser Phe Phe Asp Thr Ile Pro  
865 870 875 880

Ile Gly Arg Leu Leu Asn Cys Phe Ala Gly Asp Leu Glu Gln Leu Asp  
885 890 895

Gln Leu Leu Pro Ile Phe Ser Glu Gln Phe Leu Val Leu Ser Leu Met  
900 905 910

Val Ile Ala Val Leu Leu Ile Val Ser Val Leu Ser Pro Tyr Ile Leu  
915 920 925

Leu Met Gly Ala Ile Ile Met Val Ile Cys Phe Ile Tyr Tyr Met Met  
930 935 940

Phe Lys Lys Ala Ile Gly Val Phe Lys Arg Leu Glu Asn Tyr Ser Arg  
945 950 955 960

Ser Pro Leu Phe Ser His Ile Leu Asn Ser Leu Gln Gly Leu Ser Ser  
965 970 975

Ile His Val Tyr Gly Lys Thr Glu Asp Phe Ile Ser Gln Phe Lys Arg  
980 985 990

Leu Thr Asp Ala Gln Asn Asn Tyr Leu Leu Leu Phe Leu Ser Ser Thr  
995 1000 1005

Arg Trp Met Ala Leu Arg Leu Glu Ile Met Thr Asn Leu Val Thr  
1010 1015 1020

Leu Ala Val Ala Leu Phe Val Ala Phe Gly Ile Ser Ser Thr Pro  
1025 1030 1035

Tyr Ser Phe Lys Val Met Ala Val Asn Ile Val Leu Gln Leu Ala  
1040 1045 1050

Ser Ser Phe Gln Ala Thr Ala Arg Ile Gly Leu Glu Thr Glu Ala  
1055 1060 1065

Gln Phe Thr Ala Val Glu Arg Ile Leu Gln Tyr Met Lys Met Cys  
1070 1075 1080

Val Ser Glu Ala Pro Leu His Met Glu Gly Thr Ser Cys Pro Gln  
1085 1090 1095

Gly Trp Pro Gln His Gly Glu Ile Ile Phe Gln Asp Tyr His Met  
1100 1105 1110

Lys Tyr Arg Asp Asn Thr Pro Thr Val Leu His Gly Ile Asn Leu

1115

1120

1125

Thr Ile Arg Gly His Glu Val Val Gly Ile Val Gly Arg Thr Gly  
1130 1135 1140

Ser Gly Lys Ser Ser Leu Gly Met Ala Leu Phe Arg Leu Val Glu  
1145 1150 1155

Pro Met Ala Gly Arg Ile Leu Ile Asp Gly Val Asp Ile Cys Ser  
1160 1165 1170

Ile Gly Leu Glu Asp Leu Arg Ser Lys Leu Ser Val Ile Pro Gln  
1175 1180 1185

Asp Pro Val Leu Leu Ser Gly Thr Ile Arg Phe Asn Leu Asp Pro  
1190 1195 1200

Phe Asp Arg His Thr Asp Gln Gln Ile Trp Asp Ala Leu Glu Arg  
1205 1210 1215

Thr Phe Leu Thr Lys Ala Ile Ser Lys Phe Pro Lys Lys Leu His  
1220 1225 1230

Thr Asp Val Val Glu Asn Gly Gly Asn Phe Ser Val Gly Glu Arg  
1235 1240 1245

Gln Leu Leu Cys Ile Ala Arg Ala Val Leu Arg Asn Ser Lys Ile  
1250 1255 1260

Ile Leu Ile Asp Glu Ala Thr Ala Ser Ile Asp Met Glu Thr Asp  
1265 1270 1275

Thr Leu Ile Gln Arg Thr Ile Arg Glu Ala Phe Gln Gly Cys Thr  
1280 1285 1290

Val Leu Val Ile Ala His Arg Val Thr Thr Val Leu Asn Cys Asp  
1295 1300 1305

His Ile Leu Val Met Gly Asn Gly Lys Val Val Glu Phe Asp Arg  
1310 1315 1320

Pro Glu Val Leu Arg Lys Lys Pro Gly Ser Leu Phe Ala Ala Leu  
1325 1330 1335

Met Ala Thr Ala Thr Ser Ser Leu Arg  
1340 1345

<210> 194  
<211> 3690  
<212> DNA  
<213> human organism

<400> 194  
atgctgtctg gtttcttgat gagtcccagt acccagcaca gagcacagta cactccggaa 60  
ggaaagaaac ttccgtggga ggcttcattc ggtgcgcaca cttcccgagg gcgaggcagc 120  
gaccgggaga gggagagccg gccggaggct gccgggctcc tggggaccg cgctgcagcc 180  
ggggaggcgg agaagggaa ccggggcgag ccgccccctt ggatccgcgc ccagcagcag 240  
ccgcggccgc cgccagctgg gcaggctccc gggactgcgg ctggggcgc gcaggaccct 300  
cgccctgcgtc ctggacgttc ccgggggagg gtccgggtgc cagtgaard tccagaggct 360  
tccggacgac agccccgggg gccttctgac tgcattccgtt gatttcattc agcgagtgc 420  
actcataagg cagtccctaa ggggaccggg ccaccggctg aggacggggaa tggcttagga 480  
gctcctggac cttagggcccg gcgtcgctgc ctccctggcg tcgcggcaga ggggagtggc 540  
ccgcgcggaa agcgccgcgg gacagtcagt gacgaggccc ggggtcgcc ggggccacga 600  
cttctcgag accgtccctgc gctctctgaa gacgcgtgtt ccgcgccttgc ggtgggtcca 660  
tgtggggcgc tcgcgcgtcg tccgtctcctt catcctggaa cgccgcgttcg ctccatgcagc 720  
tgctgctggc tgcgctgctg gccccgggg cgagggccca gcggcgagta ctgcacggc 780  
tggctggacg cgcaaggcgt ctggcgcatc ggcttccagt gtcccgagcg ctgcacggc 840  
ggcgacgcca ccatctgctg cggcagctgc gcgttgcgt actgctgctc cagcgccgag 900  
gcgcgcctgg accagggcgg ctgcgacaat gaccggcagc agggcgctgg cgagccctggc 960  
cgggcggaca aagacggggcc cgcacggctc ggcagggtt catgtcttag ggttacccaa 1020  
ggagacggcg agggtgcgc cccacccgtg agggcctggc agcgggtgc cccctgaaggc 1080  
tccccgaaag gaaggcagct cctcagggtt ttccccgggc tgctgccccg tgccagacgc 1140  
cgcggttcc catcttctcc acgcggcggc ccctctcccc tgcagcggcc cgccttgc 1200  
atctacgtgc cggttccat tgggtgcgtt gtgttgcgtt ctttatcat cttgggtcc 1260  
ctgggtggcag cctgttgctg cagatgtctc cggcctaagc aggttccca gcagagccga 1320  
gccccagggg gtaaccgctt gatggagacc atccccatga tccccagtc cagcacctcc 1380

cgggggtcg cctcacgcca gtccagcaca gctgccagtt ccagctccag cgccaaactcc 1440  
ggggccccggg cgcccccaac aaggtcacag accaactgtt gcttgcggg agggaccatg 1500  
aacaacgtgt atgtcaacat gcccacgaat ttctctgtgc tgaactgtca gcaggccacc 1560  
cagattgtgc cacatcaagg gcagtatctg catccccat acgtggggta cacggtgac 1620  
cacgactctg tgcccatgac agctgtgcc a ctttcatgg acggcctgca gcctggctac 1680  
aggcagattc agtccccctt ccctcacacc aacagtgaac agaagatgta cccagcggtg 1740  
actgtataac cgagagtcac tgggggttc cttaactgaa gggagacgaa ggcaggggtg 1800  
gattctcgag gtggaaagtcc gcacatgtcg gtggattta tggcacgatt ctttggatg 1860  
gcttcatttg cccccagact gatataaaac atctccgaat tagcatttct ggatatgttt 1920  
catccagggt atcattgatt tatgatggaa aaccggcctc agctggagat gactgtgatg 1980  
ttgctgatgg gtgtataaca aatgctttag tccgaagtgc ctttagata tggttgacga 2040  
aagaatttta taaaactgata aattaaggat ttttattatg ttgttattat tatttctttt 2100  
ttgttgttga ctgcacagga tcaaaatgcc ttttatctcc ctttactgg gactttttt 2160  
ttttttttt tttttttaa tcagacaggg tcttgcctcg ttgcccaggc tggagtgcag 2220  
tggcgatc tcggctcaact gcaacttcag ctcctggat tcaggcaaca ctcctgcctc 2280  
agcctccac gtggctgggta ttagggatgc ctggcccat ggctaatttt ttgttatttt 2340  
tgtagagatg gggtttccacc atgttggctg ggctggctc acttcctga cctcaagcaa 2400  
tctgcctgtc tcagcctccc aaagtgcgtt gattacaggg gtgagccacc gccccagcc 2460  
tgagcctttt ttttttcta atgcattccaa ggttaagggg aagacgcaaa taacaggact 2520  
attctaaaag gaaacctgtt tgaactctgt gagatcagtc atcagtctca gtattccaca 2580  
ggcacacctt aatttcattt gaaaaagata tatatatttt gtcttatttt gtgttttgg 2640  
gggcctattt tgtgcctttt taccttatgt agagatctt ttacaaagtg attttctaca 2700  
ttaaaaagag actgaaataa attgtatagt tacttaacta atgaagacat ttcagaactc 2760  
tggatgatt ttaatcttgc agtagtaggt ggtatagtca taaaaccatt catcccttc 2820  
ttgattgtat cttaattttc tggctttaag gtgacatctg agaggtaatg cattttttt 2880  
tatattgaaa tcataaacta tcacccgctg cttctctgag ttactttaa tttgccttgc 2940  
tggttatggg ttggcgtttc ctctgtttt gtttcagag cccatgtct atatagtcct 3000  
gagtgcaggtaatg aattactata ctgtaaatg aagatcagta tttctgcctt gatctgataa 3060

aaaaattttc ttgtcttagt tataaaaatt caaagaaaatg tggcacaaag atacttagta 3120  
tagtcctca gccataacct gagacttggg atgaaattta aaccagatac gatttacttt 3180  
gcagatcata aggctttta tactcttggt atcaaaatgg cttatTTTC aggcactaag 3240  
gattgttaag agaaaagctt ttcaacgaag gattgcctt cttctcccac actgttcttg 3300  
atTCCTCTC tcttcaggc ctcaacaggc actgtattca ttgccaatgt tccaaattat 3360  
caaattcaag tgaatttatt tgtgtgttct ttacttatat aaaaaaaagat aactttaagg 3420  
atgtgcaagt acatttccaa ctgcttagcac aaccagtatt ttgtaattaa acaaatcgct 3480  
gtatggtagt gtcttctaca catttatgtc tatagatatac tatcgatcat ctttctattc 3540  
tgtttcatga ctgaataatg taaaaccagt gttggcaatt ggtatcatca atgatactca 3600  
tttttaata accaaaggca ggggaaaatc attttactta ttaataaaata ttttatgatg 3660  
tgaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3690

<210> 195

<211> 582

<212> PRT

<213> human organism

<400> 195

Met Leu Ser Gly Phe Leu Met Ser Pro Ser Thr Gln His Arg Ala Gln  
1 5 10 15

Tyr Thr Pro Gly Gly Lys Lys Leu Pro Trp Glu Ala Ser Ile Gly Ala  
20 25 30

His Thr Ser Arg Gly Arg Gly Ser Asp Arg Glu Arg Ser Arg Pro  
35 40 45

Glu Ala Ala Gly Leu Leu Trp Asp Arg Ala Ala Ala Gly Glu Ala Glu  
50 55 60

Lys Gly Asn Arg Gly Glu Pro Pro Ala Trp Ile Arg Ala Gln Gln Gln  
65 70 75 80

Pro Arg Pro Pro Pro Ala Gly Gln Ala Pro Gly Thr Ala Ala Gly Gly  
85 90 95

Ala Gln Asp Pro Arg Leu Arg Pro Gly Arg Ser Arg Gly Arg Val Arg  
100 105 110

Leu Pro Val Lys Pro Pro Glu Ala Ser Gly Arg Gln Pro Arg Gly Pro  
115 120 125

Ser Asp Cys Ile Pro Arg Phe Pro Ser Ala Ser Ala Thr His Lys Ala  
130 135 140

Val Pro Lys Gly Thr Gly Pro Pro Ala Glu Asp Gly Asp Gly Leu Gly  
145 150 155 160

Ala Pro Gly Pro Arg Ala Arg Arg Arg Leu Leu Gly Val Ala Ala  
165 170 175

Glu Gly Ser Gly Pro Arg Gly Lys Arg Arg Gly Thr Val Ser Asp Glu  
180 185 190

Ala Arg Gly Ser Pro Gly Pro Arg Leu Leu Gly Asp Arg Pro Ala Leu  
195 200 205

Ser Gly Asp Ala Leu Ser Ala Pro Arg Val Val Pro Cys Gly Ala Leu  
210 215 220

Ala Ala Arg Pro Ser Pro His Pro Gly Thr Pro Leu Arg Ser Cys Ser  
225 230 235 240

Cys Cys Trp Leu Arg Cys Trp Arg Arg Gly Arg Gly Pro Ser Gly Glu  
245 250 255

Tyr Cys His Gly Trp Leu Asp Ala Gln Gly Val Trp Arg Ile Gly Phe  
260 265 270

Gln Cys Pro Glu Arg Phe Asp Gly Gly Asp Ala Thr Ile Cys Cys Gly  
275 280 285

Ser Cys Ala Leu Arg Tyr Cys Cys Ser Ser Ala Glu Ala Arg Leu Asp  
290 295 300

Gln Gly Gly Cys Asp Asn Asp Arg Gln Gln Gly Ala Gly Glu Pro Gly  
305 310 315 320

Arg Ala Asp Lys Asp Gly Pro Arg Arg Leu Gly Arg Ala Ser Cys Leu  
325 330 335

Arg Gly Thr Gln Gly Asp Gly Glu Gly Ala Pro Pro Pro Val Arg Ala  
340 345 350

Trp Gln Arg Cys Ser Pro Glu Gly Ser Pro Lys Gly Arg Gln Leu Leu  
355 360 365

Arg Ala Phe Pro Gly Leu Leu Pro Arg Ala Arg Arg Gly Phe Pro  
370 375 380

Ser Ser Pro Arg Gly Gly Pro Ser Pro Leu Gln Arg Pro Ala Leu Pro  
385 390 395 400

Ile Tyr Val Pro Phe Leu Ile Val Gly Ser Val Phe Val Ala Phe Ile  
405 410 415

Ile Leu Gly Ser Leu Val Ala Ala Cys Cys Cys Arg Cys Leu Arg Pro  
420 425 430

Lys Gln Asp Pro Gln Gln Ser Arg Ala Pro Gly Gly Asn Arg Leu Met  
435 440 445

Glu Thr Ile Pro Met Ile Pro Ser Ala Ser Thr Ser Arg Gly Ser Ser  
450 455 460

Ser Arg Gln Ser Ser Thr Ala Ala Ser Ser Ser Ser Ala Asn Ser  
465 470 475 480

Gly Ala Arg Ala Pro Pro Thr Arg Ser Gln Thr Asn Cys Cys Leu Pro  
485 490 495

Glu Gly Thr Met Asn Asn Val Tyr Val Asn Met Pro Thr Asn Phe Ser  
500 505 510

Val Leu Asn Cys Gln Gln Ala Thr Gln Ile Val Pro His Gln Gly Gln  
515 520 525

Tyr Leu His Pro Pro Tyr Val Gly Tyr Thr Val Gln His Asp Ser Val  
530 535 540

Pro Met Thr Ala Val Pro Pro Phe Met Asp Gly Leu Gln Pro Gly Tyr  
545 550 555 560

Arg Gln Ile Gln Ser Pro Phe Pro His Thr Asn Ser Glu Gln Lys Met

565

570

575

Tyr Pro Ala Val Thr Val  
580

<210> 196  
<211> 3096  
<212> DNA  
<213> human organism

<400> 196  
gccctggac actgacatgg actgaaggag tagaatggag cacgaggaca ctgacatgga 60  
ctgaagaaaa aggagctgga gcaggagaag gaggtgctgc tgcagggttt ggagatgatg  
gcgcggggcc gcgactggta ccagcagcag ctgcaacgag tgcaggagcg ccagcgcgc 120  
ctggccaga gcagagccag cggcacttt gggctgcag ggagcccccg cccactgggg 180  
cggctactgc ccaaggtaa agaggtggcc cggtgccctgg gggagctgct ggctgcagcc 240  
tgtgccagcc gggccctgcc cccgtcctcc tccgggcccc cctgccctgc cctgacgtcc 300  
accccacccc cggtctggca gcagcagacc atcctcatgc tgaaggagca gaaccgactc 360  
ctcacccagg aggtgaccga gaagagttag cgcatcacgc agctggagca ggagaagtcg 420  
gcgcattatta agcagctgtt tgaggccccgc gccctgagcc agcaggacgg gggacctctg 480  
gattccacct tcatctagtc cttgtgggcc gcgtgggccc ccagggccag cctggcactc 540  
agcccttcga gggtgggcgc cccatcgac ccaccctctc tggctggaga ccccccggcag 600  
gcccaggcac agtcccgag tgggcgcctt cctgcgcgcc ttgccagatg ggctccccag 660  
gcctgcccccc ggctggtccc cgcacccgagc gtttactcc gttkggctc ctggttgytg 720  
acatgggctg gggctctct tgagtccgca tagtccgcag ctactactgg ccgctgtcag 780  
tggacagtgg ggtacccctc catgagttag cgtccccccg tttccagcgg tgccgcctg 840  
ggtcccatct tcagggaaag gcaactgcccc caaggcaggctg cacttccaac aacgggcagc 900  
agagggcgcg gggcggtcc gacgcgggtc caagggcagc ttcccgtca accagggcac 960  
caggacgagg tggctgttagc tcggacggac ggaagtagat ggagggggtg gggacggcct 1020  
gtaagcgggg ggtgcctgcc tggctgggg gccccaggaa tagcggctgg acttcaggtt 1080  
ctggccaagg ctgagggacc ctggctgcag cggatcggca cggcgggtgg gcgagagctt 1140  
ggcctgcatt tgcctccac agaccctggg gtgatggcct tccccctttt ggccgggacg 1200  
ttgccccacg ttgagtcata cacaacatcc tgtgagcctg gctccccagg agggccccca 1260  
ttgccccacg ttgagtcata cacaacatcc tgtgagcctg gctccccagg agggccccca 1320

gacagctccc aggcacgtca taggcaaagc ctgtttcccc cgactcagga tttccaaggc 1380  
ctggggtcct gctcacccccc ctttgctctc acgcccagcc tgtccccagg tttcagctgg 1440  
gagaggccac ctccctcagc caaggaaaac gagaacccccc agggtacagg aggaggctgg 1500  
ggcaggtccc cttgggtgtc actccctcag cccctgcccc ggcccactcc cgctggtgct 1560  
ggagtacgca ctggtgaaaa ggccctgctc agcccaacct ggagggtccc agtgtcacca 1620  
gaaccagggg cacggcaaca gcatcgatgg gttctgcagc ccagggcccc cgatgcgggg 1680  
tcagtgtgtg tggggcgcag ggccctccat gcggggtcag tgcgtgggg ggcgcaggggc 1740  
cccgatgcgg ggtcagtgcg tggggggcgc agggccccc cgtgtccagg gcactttgg 1800  
acaactgtccc acaaggcacc tgtctcagag gagggccctt ggcaggcagc gtggcaactc 1860  
ccttccggag cccagctcca tgctaaccctg cccacagcaa ccccacagag ccacattccc 1920  
tgctgcacct ggtctgcagg ggtgtccctg gacaggccca agtcagccca gcatcgact 1980  
gccctcctac cctgaagatg ggagtggct ttccagggga cataaggatg tcaggcctgg 2040  
accccttggg cagggaaaggg tgcaggtcct gagggcctgt gccccacagc cccagcaccc 2100  
aggtggactg cagcgcagtg ggtggccag tggcagccag ggagaagccc cccgtcagca 2160  
ggctggggtc tgcccaccag ggccctccccca cgtctgcctt tgagggtgcc tgccatgccc 2220  
tggggatcc tggcatctt actggactgg aagcaggaga cagaacagtg tctgtcccg 2280  
ggtgacttca tcaggagacc gcccacatag agctggaccc cgcaagctgaa gcggaaatgt 2340  
gagacaggct ggcacccctcg gaaaaactgc cttcagctt tgggtttccg tgcaagggtga 2400  
aaagaaaatag gtcctccctcg ttacagctt gaaatcaggc tagtgagtgg ccctggagac 2460  
cacgagggga gaatttaaag gccccggctg gcagggtcta ggtggctggc agaggcacat 2520  
gcagaccctcg cctggagcct gcccttaggac gctggggggg tcagtcctcg tgcaggatgt 2580  
gagcagcgtc cctggctct atccgcgagg tgccagtagc gtgtgcaggt acatacacgt 2640  
gcgtgcacac tgtgtatgaca cccggaaatg tctcaggatg ttgaaatgtg tccttgggg 2700  
cagaagtgtc cccagttgag aatctgcccc agaggaacac acccacacca ggcctcagga 2760  
ttttgtgtt atcaagttcc aaggaaaagg aacatctcag ccgggcgtgg tggttcacgc 2820  
ctggaatccc agcacttgag gccaggagtt ccagagcagc ctgggcaacg cagtgagaga 2880  
ccccatctct acaaraaaaaaaa aaaaagaaaag aaagaaaatg agagatccag gttaaaaat 2940  
tcataaacac cacaaggaaa caatacacta tgagacccag cagaagcaac agattgactc 3000  
tagaccaga tactagaatt atcagagaga atataaagta acagtgttt atatatctaa 3060

agaaaaataaaaa gagatttctg	gaaacatgaa	aaaaaaa	3096			
<210> 197						
<211> 3171						
<212> DNA						
<213> human organism						
<400> 197						
gcggaacacc	ggcccgccgt	cgcggcagct	gcttcacccc	tctctctgca	gccatggggc	60
tccctcgtgg	acctctcgcg	tctctcctcc	ttctccaggt	ttgctggctg	cagtgcgcgg	120
cctccgagcc	gtgccggcg	gtcttcaggg	aggctgaagt	gaccttggag	gcgggaggcg	180
cggagcagga	gcccggccag	gcgcgtgggg	aagtattcat	ggcgtgcct	ggcaagagc	240
cagctctgtt	tagcaactgat	aatgatgact	tcactgtgcg	aatggcgag	acagtccagg	300
aaagaaggtc	actgaaggaa	aggaatccat	tgaagatctt	cccatccaaa	cgtatcttac	360
gaagacacaa	gagagattgg	gtggttgctc	caatatctgt	ccctgaaaat	ggcaagggtc	420
ccttccccca	gagactgaat	cagctcaagt	ctaataaaga	tagagacacc	aagattttct	480
acagcatcac	ggggccgggg	gcagacagcc	cccctgaggg	tgtcttcgct	gtagagaagg	540
agacaggctg	gttggtttg	aataagccac	tggaccggga	ggagattgcc	aagtatgagc	600
tctttggcca	cgctgtgtca	gagaatggtg	cctcagtgg	ggaccccatg	aacatctcca	660
tcatcgac	cgaccagaat	gaccacaagc	ccaagttac	ccaggacacc	ttccgaggga	720
gtgtcttaga	gggagtccta	ccaggtactt	ctgtgatgca	ggtgacagcc	acagatgagg	780
atgatgccat	ctacacctac	aatggggtgg	ttgcttactc	catccatagc	caagaaccaa	840
aggacccaca	cgacctcatg	ttcacaattc	accggagcac	aggcaccatc	agcgtcatct	900
ccagtggcct	ggaccggaa	aaagtccctg	agtacacact	gaccatccag	gccacagaca	960
tggatgggaa	cggtccacc	accacggcag	tggcagtagt	ggagatcctt	gatgccaatg	1020
acaatgctcc	catgttgac	ccccagaagt	acgaggccca	tgtgcctgag	aatgcagtgg	1080
gccatgaggt	gcagaggctg	acggtcactg	atctggacgc	ccccaaactca	ccagcgtggc	1140
gtgccaccta	ccttatcatg	ggcggtgacg	acggggacca	tttaccatc	accacccacc	1200
ctgagagcaa	ccagggcatc	ctgacaacca	ggaagggttt	ggattttgag	gccaaaaacc	1260
agcacaccct	gtacgttcaa	gtgaccaacg	aggcccttt	tgtgctgaag	ctcccaacct	1320
ccacagccac	catagtggtc	cacgtggagg	atgtaatga	ggcacctgtg	tttgtcccac	1380
cctccaaagt	cgttgaggtc	caggagggca	tccccactgg	ggagcctgtg	tgtgtctaca	1440

ctgcagaaga ccctgacaag gagaatcaaa agatcagcta ccgcacccctg agagacccag 1500  
cagggtggct agccatggac ccagacagtg ggcaggtcac agctgtgggc accctcgacc 1560  
gtgaggatga gcagtttgtg aggaacaaca tctatgaagt catggtcttg gccatggaca 1620  
atgaaagccc tcccaccact ggcacggaa cccttcgtct aacactgatt gatgtcaacg 1680  
accatggccc agtccctgag cccgtcaga tcaccatctg caaccaaagc cctgtgcgcc 1740  
acgtgctgaa catcacggac aaggacctgt ctccccacac ctcccctttc caggcccagc 1800  
tcacagatga ctcagacatc tactggacgg cagaggtcaa cgaggaaggt gacacagtgg 1860  
tctgtccct gaagaagttc ctgaagcagg atacatatga cgtgcacctt tctctgtctg 1920  
accatggcaa caaagagcag ctgacggta tcagggccac tgtgtgcgac tgccatggcc 1980  
atgtcgaaac ctgcccggaa ccctggaaag gaggttcat cctccctgtg ctggggctg 2040  
tcctggctct gctgttcctc ctgctggtgc tgctttgtt ggtgagaaag aagcggaaaga 2100  
tcaaggagcc ctcctactc ccagaagatg acaccgtga caacgtcttc tactatggcg 2160  
aagagggggg tggcgaagag gaccaggact atgacatcac ccagctccac cgaggtctgg 2220  
aggccaggcc ggaggtggtt ctccgcaatg acgtggcacc aaccatcatc ccgacaccca 2280  
tgtaccgtcc taggcccagcc aacccagatg aaatcgccaa ctttataatt gagaacctga 2340  
aggcggctaa cacagacccc acagccccgc cctacgacac cctcttggtg ttgcactatg 2400  
agggcagcgg ctccgacgccc gcgtccctga gctccctcac ctccctccgccc tccgaccaag 2460  
accaagatta cgattatctg aacgagtggg gcagccgctt caagaagctg gcagacatgt 2520  
acggtggcgg ggaggacgac taggcggcct gcctgcaggg ctggggacca aacgtcaggc 2580  
cacagagcat ctccaagggg tctcagttcc cccttcagct gaggacttcg gagcttgtca 2640  
ggaagtggcc gtagcaactt ggccggagaca ggctatgagt ctgacgttag agtggttgct 2700  
tccttagcct ttcaggatgg aggaatgtgg gcagttgac ttcagcactg aaaacctctc 2760  
cacctggccc agggttcct cagaggccaa gtttccagaa gcctcttacc tgccgtaaaa 2820  
tgctcaaccc tgtgtcctgg gcctgggcct gctgtgactg acctacagt gactttctct 2880  
ctggaatggc accttccttag gcctcctggt gcaacttaat ttttttttt aatgtatct 2940  
tcaaaaacgtt agagaaagtt cttcaaaagt gcagcccaga gctgctgggc ccactggccg 3000  
tcctgcattt ctggttcca gaccccaatg cctcccatc gatggatct ctgcgttttt 3060  
atactgagtg tgccttaggtt gccccttatt ttttattttc cctgttgcgt tgctatagat 3120

gaagggtgag gacaatcgta tataatgtact agaactttt tattaaagaa a

3171

<210> 198  
<211> 829  
<212> PRT  
<213> human organism

<400> 198

Met Gly Leu Pro Arg Gly Pro Leu Ala Ser Leu Leu Leu Gln Val  
1 5 10 15

Cys Trp Leu Gln Cys Ala Ala Ser Glu Pro Cys Arg Ala Val Phe Arg  
20 25 30

Glu Ala Glu Val Thr Leu Glu Ala Gly Gly Ala Glu Gln Glu Pro Gly  
35 40 45

Gln Ala Leu Gly Lys Val Phe Met Gly Cys Pro Gly Gln Glu Pro Ala  
50 55 60

Leu Phe Ser Thr Asp Asn Asp Asp Phe Thr Val Arg Asn Gly Glu Thr  
65 70 75 80

Val Gln Glu Arg Arg Ser Leu Lys Glu Arg Asn Pro Leu Lys Ile Phe  
85 90 95

Pro Ser Lys Arg Ile Leu Arg Arg His Lys Arg Asp Trp Val Val Ala  
100 105 110

Pro Ile Ser Val Pro Glu Asn Gly Lys Arg Pro Phe Pro Gln Arg Leu  
115 120 125

Asn Gln Leu Lys Ser Asn Lys Asp Arg Asp Thr Lys Ile Phe Tyr Ser  
130 135 140

Ile Thr Gly Pro Gly Ala Asp Ser Pro Pro Glu Gly Val Phe Ala Val  
145 150 155 160

Glu Lys Glu Thr Gly Trp Leu Leu Leu Asn Lys Pro Leu Asp Arg Glu  
165 170 175

Glu Ile Ala Lys Tyr Glu Leu Phe Gly His Ala Val Ser Glu Asn Gly  
180 185 190

Ala Ser Val Glu Asp Pro Met Asn Ile Ser Ile Ile Val Thr Asp Gln  
195 200 205

Asn Asp His Lys Pro Lys Phe Thr Gln Asp Thr Phe Arg Gly Ser Val  
210 215 220

Leu Glu Gly Val Leu Pro Gly Thr Ser Val Met Gln Val Thr Ala Thr  
225 230 235 240

Asp Glu Asp Asp Ala Ile Tyr Thr Tyr Asn Gly Val Val Ala Tyr Ser  
245 250 255

Ile His Ser Gln Glu Pro Lys Asp Pro His Asp Leu Met Phe Thr Ile  
260 265 270

His Arg Ser Thr Gly Thr Ile Ser Val Ile Ser Ser Gly Leu Asp Arg  
275 280 285

Glu Lys Val Pro Glu Tyr Thr Leu Thr Ile Gln Ala Thr Asp Met Asp  
290 295 300

Gly Asp Gly Ser Thr Thr Ala Val Ala Val Val Glu Ile Leu Asp  
305 310 315 320

Ala Asn Asp Asn Ala Pro Met Phe Asp Pro Gln Lys Tyr Glu Ala His  
325 330 335

Val Pro Glu Asn Ala Val Gly His Glu Val Gln Arg Leu Thr Val Thr  
340 345 350

Asp Leu Asp Ala Pro Asn Ser Pro Ala Trp Arg Ala Thr Tyr Leu Ile  
355 360 365

Met Gly Gly Asp Asp Gly Asp His Phe Thr Ile Thr Thr His Pro Glu  
370 375 380

Ser Asn Gln Gly Ile Leu Thr Thr Arg Lys Gly Leu Asp Phe Glu Ala  
385 390 395 400

Lys Asn Gln His Thr Leu Tyr Val Glu Val Thr Asn Glu Ala Pro Phe  
405 410 415

Val Leu Lys Leu Pro Thr Ser Thr Ala Thr Ile Val Val His Val Glu  
420 425 430

Asp Val Asn Glu Ala Pro Val Phe Val Pro Pro Ser Lys Val Val Glu  
435 440 445

Val Gln Glu Gly Ile Pro Thr Gly Glu Pro Val Cys Val Tyr Thr Ala  
450 455 460

Glu Asp Pro Asp Lys Glu Asn Gln Lys Ile Ser Tyr Arg Ile Leu Arg  
465 470 475 480

Asp Pro Ala Gly Trp Leu Ala Met Asp Pro Asp Ser Gly Gln Val Thr  
485 490 495

Ala Val Gly Thr Leu Asp Arg Glu Asp Glu Gln Phe Val Arg Asn Asn  
500 505 510

Ile Tyr Glu Val Met Val Leu Ala Met Asp Asn Gly Ser Pro Pro Thr  
515 520 525

Thr Gly Thr Gly Thr Leu Leu Leu Thr Leu Ile Asp Val Asn Asp His  
530 535 540

Gly Pro Val Pro Glu Pro Arg Gln Ile Thr Ile Cys Asn Gln Ser Pro  
545 550 555 560

Val Arg His Val Leu Asn Ile Thr Asp Lys Asp Leu Ser Pro His Thr  
565 570 575

Ser Pro Phe Gln Ala Gln Leu Thr Asp Asp Ser Asp Ile Tyr Trp Thr  
580 585 590

Ala Glu Val Asn Glu Glu Gly Asp Thr Val Val Leu Ser Leu Lys Lys  
595 600 605

Phe Leu Lys Gln Asp Thr Tyr Asp Val His Leu Ser Leu Ser Asp His  
610 615 620

Gly Asn Lys Glu Gln Leu Thr Val Ile Arg Ala Thr Val Cys Asp Cys  
625 630 635 640

His Gly His Val Glu Thr Cys Pro Gly Pro Trp Lys Gly Gly Phe Ile

645

650

655

Leu Pro Val Leu Gly Ala Val Leu Ala Leu Leu Phe Leu Leu Val  
660 665 670

Leu Leu Leu Val Arg Lys Lys Arg Lys Ile Lys Glu Pro Leu Leu  
675 680 685

Leu Pro Glu Asp Asp Thr Arg Asp Asn Val Phe Tyr Tyr Gly Glu Glu  
690 695 700

Gly Gly Gly Glu Glu Asp Gln Asp Tyr Asp Ile Thr Gln Leu His Arg  
705 710 715 720

Gly Leu Glu Ala Arg Pro Glu Val Val Leu Arg Asn Asp Val Ala Pro  
725 730 735

Thr Ile Ile Pro Thr Pro Met Tyr Arg Pro Arg Pro Ala Asn Pro Asp  
740 745 750

Glu Ile Gly Asn Phe Ile Ile Glu Asn Leu Lys Ala Ala Asn Thr Asp  
755 760 765

Pro Thr Ala Pro Pro Tyr Asp Thr Leu Leu Val Phe Asp Tyr Glu Gly  
770 775 780

Ser Gly Ser Asp Ala Ala Ser Leu Ser Ser Leu Thr Ser Ser Ala Ser  
785 790 795 800

Asp Gln Asp Gln Asp Tyr Asp Tyr Leu Asn Glu Trp Gly Ser Arg Phe  
805 810 815

Lys Lys Leu Ala Asp Met Tyr Gly Gly Glu Asp Asp  
820 825

<210> 199

<211> 1148

<212> DNA

<213> human organism

<400> 199  
cttctttaaa tttctttcta ggatgttcac ttcttctcca caatgaatga gtgtcactat 60

gacaaggaca tggacttttt ttataatagg agcaaacactg atactgtcga tgactggaca 120

ggaacaaagc ttgtgattgt tttgtgtgtt gggacgtttt tctgcctgtt tattttttt	180
tctaattctc tggtcatcgc ggcaagtatc aaaaacagaa aatttcattt ccccttctac	240
tacctgttgg ctaatttagc tgctgccat ttcttcgctg gaattgccta tgtattcctg	300
atgttaaca caggcccagt ttcaaaaact ttgactgtca accgctggtt tctccgtcag	360
gggcttctgg acagtagctt gactgcttcc ctcaccaact tgctggttat cgccgtggag	420
aggcacatgt caatcatgag gatgcgggtc catagcaacc tgacaaaaaa gagggtgaca	480
ctgctcattt tgcttgtctg gcccattcgcc attttatgg gggcggtccc cacactggc	540
tggaattgcc tctgcaacat ctctgcctgc tcttcctgg cccccattt cagcaggagt	600
tacctgttt tctggacagt gtccaacctc atggccttcc tcatacatggt tgtggtgtac	660
ctgcggatct acgtgtacgt caagagggaaa accaacgtct tgtctccgca tacaagtggg	720
tccatcagcc gccggaggac acccatgaag ctaatgaaga cggtgatgac tgtcttaggg	780
gcgtttgtgg tatgctggac cccgggcctg gtggttctgc tcctcgacgg cctgaactgc	840
aggcagtgtg gcgtgcagca tgtgaaaagg tggttcctgc tgctggcgct gctcaactcc	900
gtcgtgaacc ccatcatcta ctccatacaag gacgaggaca tgtatggcac catgaagaag	960
atgatctgct gcttctctca ggagaaccca gagaggcgtc cctctcgcat cccctccaca	1020
gtcctcagca ggagtgacac aggcaagccag tacatagagg atagtattag ccaaggtgca	1080
gtctgcaata aaagcacttc ctaaactctg gatgcctctc gcccaccca ggtgatgact	1140
gtcttagg	1148

<210> 200  
 <211> 353  
 <212> PRT  
 <213> human organism

<400> 200

Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg			
1	5	10	15

Ser Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile		
20	25	30

Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn		
35	40	45

Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro

50

55

60

Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Ala Asp Phe Phe Ala Gly  
65 70 75 80

Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr  
85 90 95

Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser  
100 105 110

Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His  
115 120 125

Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg  
130 135 140

Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly  
145 150 155 160

Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys  
165 170 175

Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr  
180 185 190

Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg  
195 200 205

Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr  
210 215 220

Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr  
225 230 235 240

Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu  
245 250 255

Val Val Leu Leu Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln  
260 265 270

His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val  
275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met  
290 295 300

Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro  
305 310 315 320

Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln  
325 330 335

Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr  
340 345 350

Ser

<210> 201  
<211> 892  
<212> DNA  
<213> human organism

<400> 201  
atgacctaca gttactcatt tttcaggcct gagttgatcg ttaatcatct taattatgtt 60  
cattctgaag ccaacaggag aaccaagacc aaaactttat tgtctctgct ttcatttctt 120  
gatgaaacct ctggactaag cacacatctt ccttggttat ctctctcaaa ggagtgtgga 180  
gtgcattcatc tggacatcca cgaaaaaaag gaagacatga gaatcacccca acagtcttcc 240  
cagctataacc tgtgggacat ggggggatata acaatattta agaacctgtg gatgagcctc 300  
ataccccagag ggaacaaacg cttcccaaaa agagttacag aaaccatcct gagagatccc 360  
aaggcagaagc aaagttcaaa gatccaagag gagagacgaa gagagtctgc aggaccaaacc 420  
ctctcttcat tctgggttgtt gggaaatgct ggaagaggag acaggccccca gattgggca 480  
ggaagtaaac agttttcagg ctgaggccaa tctgagcagg aacattccaa tatttcttca 540  
gctacgttgtt cccagcactt cactggtaa ccttttatgt ccaccatttg tggatttcac 600  
agctacttgtt caatggtaaa tattgatcat catcattatc tactgagctg ctaccatatc 660  
ccagctactc cttgcattttt gttcattttt ttctcaacac tcagcatatt tgcaatatgt 720  
tatgtatatac cacagacaag gaaactgaac gcagaaatgt tttatccat gccaaacatc 780  
acatgaggat gaacaatgaa accgatttga aaccaggatt gtctgattcc aacatctctg 840  
ggtcctttttt cactctgata tgctgcaatt aaaaagccat ttctaaagact gt 892

<210> 202  
<211> 167  
<212> PRT  
<213> human organism

<400> 202

Met Thr Tyr Ser Tyr Ser Phe Phe Arg Pro Glu Leu Ile Val Asn His  
1 5 10 15

Leu Asn Tyr Val His Ser Glu Ala Asn Arg Arg Thr Lys Thr Lys Thr  
20 25 30

Leu Leu Ser Leu Leu Ser Phe Leu Asp Glu Thr Ser Gly Leu Ser Thr  
35 40 45

His Leu Pro Cys Leu Ser Leu Ser Lys Glu Cys Gly Val Leu His Leu  
50 55 60

Asp Ile His Gly Lys Lys Glu Asp Met Arg Ile Thr Gln Gln Ser Ser  
65 70 75 80

Gln Leu Tyr Leu Trp Asp Met Gly Gly Phe Thr Ile Phe Lys Asn Leu  
85 90 95

Trp Met Ser Leu Ile Pro Arg Gly Asn Lys Arg Ser Pro Lys Arg Val  
100 105 110

Thr Glu Thr Ile Leu Arg Asp Phe Lys Gln Lys Gln Ser Ser Lys Ile  
115 120 125

Gln Glu Glu Arg Arg Glu Ser Ala Gly Pro Asn Leu Ser Ser Phe  
130 135 140

Trp Phe Val Gly Asn Ala Gly Arg Gly Asp Arg Pro Gln Ile Trp Ala  
145 150 155 160

Gly Ser Lys Gln Phe Ser Gly  
165

<210> 203  
<211> 2582  
<212> DNA  
<213> human organism

```

<220>
<221> misc_feature
<222> (2553)..(2553)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (2556)..(2556)
<223> n is a, c, g, or t

<400> 203
tcacacgtgc caaggggctg gtcagcgg aaccagcctgc acgcgcgtggc tccgggtgac      60
agccgcgcgc ctcggccagg atctgagtga tgagacgtgt cccccactgag gtgc(cccaca      120
gcagcaggtg ttgagcatgg gctgagaagc tggaccggca ccaaagggt ggcagaaaatg      180
ggcgcctggc tgattcttag gcagttggcg gcagcaagga ggagaggccg cagttctgg      240
agcagagccg agacgaagca gttctggagt gcctgaacgg ccccctgagc cctacccgcc      300
tggcccacta tggtccagag gctgtgggtg agccgcctgc tgccgcaccg gaaagcccag      360
ctcttgctgg tcaacctgct aacctttggc ctggaggtgt gtttggccgc aggcatcacc      420
tatgtgccgc ctctgctgct ggaagtgggg gtagaggaga agttcatgac catggtgctg      480
ggcattggtc cagtgctggg cctggctgtgt gtcccgctcc taggctcagc cagtgaccac      540
tggcgtggac gctatgcccg ccgcgggccc ttcatctggg cactgtcctt gggcatcctg      600
ctgagcctct ttctcatccc aaggggccggc tggctagcag ggctgctgtg cccggatccc      660
aggccccctgg agctggcact gctcatcctg ggcgtggggc tgctggactt ctgtggccag      720
gtgtgcttca ctccactgga ggcctgctc tctgacctct tccgggaccc ggaccactgt      780
cgccaggcct actctgtcta tgccttcatg atcagtctt ggggctgcct gggctacctc      840
ctgcctgcca ttgactggga caccagtgcc ctggccccct acctgggcac ccaggaggag      900
tgcctctttg gcctgctcac cctcatcttc ctcacctgcg tagcagccac actgctggtg      960
gctgaggagg cagcgctggg ccccaccgag ccagcagaag ggctgtcgcc cccctcctt      1020
tcgccccact gctgtccatg cggggcccgc ttggcttcc ggaacctggg cgccctgctt      1080
cccccggctgc accagctgtg ctgcccgcattt ccccgacccc tgccgggctt ctgcgtggct      1140
gagctgtgca gctggatggc actcatgacc ttcacgctgt tttacacggta tttcgtggc      1200
gaggggctgt accagggcgt gcccagagct gagccggca ccgaggcccg gagacactat      1260
gatgaaggcg ttcggatggg cagcctgggg ctgttccctgc agtgcgcacat ctccctggc      1320

```

ttctctctgg tcatggaccg gctgggcag cgattcgca ctcgacagt ctatggcc	1380
agtgtggcag cttccctgt ggctgccggt gccacatgcc tgtcccacag tgtggccgtg	1440
gtgacagctt cagccgcctt caccgggttc accttctcag ccctgcagat cctgcctac	1500
acactggcct ccctctacca cccggagaag caggtgttcc tgcccaaata ccgagggac	1560
actggaggta ctagcagtga ggacagcctg atgaccagct tcctgccagg ccctaagcct	1620
ggagctccct tccctaattgg acacgtgggt gctggaggca gtggcctgct cccacctcca	1680
cccgcgctct gcggggcctc tgccgtgat gtctccgtac gtgtgggtt gggtagcccc	1740
accgaggcca gggtggttcc gggccggggc atctgcctgg acctcgccat cctggatagt	1800
gccttcctgc tgcctccagg gccccatcc ctgttatgg gtcattgtt ccagctcagc	1860
cagtctgtca ctgcctatat ggtgtctgcc gcaggcctgg gtctggtcgc catttacttt	1920
gctacacagg tagtatttga caagagcgac ttggccaaat actcagcgta gaaaacttcc	1980
agcacattgg ggtggagggc ctgcctcaact gggtcccage tccccgtcc tgtagcccc	2040
atggggctgc cgggctggcc gccagttct gttgctgcc aagtaatgtg gtcctctgct	2100
gccaccctgt gctgctgagg tgctgtactg cacagctggg ggctggggcg tccctctcct	2160
ctctccccag tctctaggc tgccctactg gaggcctcc aaggggttt cagtctggac	2220
ttatacaggg aggccagaag ggctccatgc actggaatgc gggactctg caggtggatt	2280
acccaggctc agggtaaca gctagcctcc tagttgagac acacctagag aagggtttt	2340
gggagctgaa taaactcagt cacctggttt cccatctcta agccccttaa cctgcagctt	2400
cgttaatgt agctttgca tggagtttc taggatgaaa cactcctcca tgggatttga	2460
acatatgaaa gttatttga gggaaagagt cctgaggggc aacacacaag aaccagggtcc	2520
cctcagcccc acaggcactg gtctttttt ctnngantcca cccccccctt cttaaccctt	2580
tt	2582

<210> 204  
 <211> 553  
 <212> PRT  
 <213> human organism

<400> 204

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala			
1	5	10	15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu

20

25

30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
65 70 75 80

Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly  
115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
130 135 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
180 185 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
210 215 220

Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
225 230 235 240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
245 250 255

Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
260 265 270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
275 280 285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
290 295 300

Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
305 310 315 320

Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
325 330 335

Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
340 345 350

Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
355 360 365

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
370 375 380

Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
405 410 415

Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
420 425 430

Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
435 440 445

Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser  
450 455 460

Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
465 470 475 480

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
485 490 495

Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
500 505 510

Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
515 520 525

Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
530 535 540

Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
545 550

<210> 205  
<211> 1593  
<212> DNA  
<213> human organism

<400> 205  
atggttcgcc gggggctgct tgcgtggatt tccccgggtgg tggttttgct ggtgctcctc 60  
tgctgtgcta tctctgtcct gtacatgttg gcctgcaccc caaaaaggtga cgaggagcag 120  
ctggcaactgc ccagggccaa cagccccacg gggaggagg ggtaccaggc cgtccttcag 180  
gagtgggagg agcagcacccg caactacgtg agcagcctga agcggcagat cgcacagctc 240  
aaggaggagc tgcaggagag gagtgagcag ctcaggaatg ggcagtacca agccagcgat 300  
gctgctggcc tgggtctgga caggagcccc ccagagaaaa cccaggccga cctcctggcc 360  
ttcctgcact cgcaggtgga caaggcagag gtgaatgctg gcgtcaagct ggccacagag 420  
tatgcagcag tgccttcga tagcttact ctacagaagg tgtaccagct ggagactggc 480  
cttacccgcc acccccagga gaaggctgtg aggaaggaca agcgggatga gttggtgaa 540  
gccattgaat cagccttgga gaccctgaac aatcctgcag agaacagccc caatcaccgt 600  
ccttacacgg cctctgattt catagaaggg atctaccgaa cagaaaggga caaagggaca 660  
ttgtatgagc tcaccttcaa aggggaccac aaacacgaat tcaaacggct catcttattt 720  
cgaccattcg gccccatcat gaaagtgaaa aatgaaaagc tcaacatggc caacacgctt 780  
atcaatgtta tcgtgcctct agcaaaaagg gtggacaagt tccggcagtt catgcagaat 840  
ttcagggaga tgtgcattga gcaggatggg agagtccatc tcactgttgt ttactttggg 900

aaagaagaaa	taaatgaagt	caaaggaata	cttggaaaaca	cttccaaagc	tgccaaacttc	960
aggaacttta	ccttcatcca	gctgaatgga	gaattttctc	ggggaaagggg	acttgatgtt	1020
ggagccccgt	tctggaaagggg	aagcaacgtc	cttctctttt	tctgtgtatgt	ggacatctac	1080
ttcacatctg	aattcctcaa	tacgtgttagg	ctgaatacac	agccaggaa	gaaggatattt	1140
tatccagttc	ttttcagtca	gtacaatcct	ggcataatat	acggccacca	tgatgcagtc	1200
cctcccttgg	aacagcagct	ggtcataaaag	aaggaaactg	gattttggag	agactttgga	1260
tttgggatga	cgtgtcagta	tcggtcagac	ttcatcaata	taggtgggtt	tgatctggac	1320
atcaaaggct	ggggcggaga	ggatgtgcac	ctttatcgca	agtatctcca	cagcaacctc	1380
atagtggtac	ggacgcctgt	gcgaggactc	ttccacctct	ggcatgagaa	gchgctgcatt	1440
gacgagctga	cccccgagca	gtacaagatg	tgcattgcagt	ccaaggccat	gaacgaggca	1500
tcccacggcc	agctggcat	gctggtgttc	aggcacgaga	tagaggctca	ccttcgcaaa	1560
cagaaacaga	agacaagtag	caaaaaaaca	tga			1593

<210> 206

<211> 530

<212> PRT

<213> human organism

<400> 206

Met	Val	Arg	Arg	Gly	Leu	Leu	Ala	Trp	Ile	Ser	Arg	Val	Val	Val	Leu
1					5				10					15	

Leu	Val	Leu	Leu	Cys	Cys	Ala	Ile	Ser	Val	Leu	Tyr	Met	Leu	Ala	Cys
									25				30		

Thr	Pro	Lys	Gly	Asp	Glu	Glu	Gln	Leu	Ala	Leu	Pro	Arg	Ala	Asn	Ser
								35				45			

Pro	Thr	Gly	Lys	Glu	Gly	Tyr	Gln	Ala	Val	Leu	Gln	Glu	Trp	Glu	Glu
								50			55		60		

Gln	His	Arg	Asn	Tyr	Val	Ser	Ser	Leu	Lys	Arg	Gln	Ile	Ala	Gln	Leu
								65			70		75		80

Lys	Glu	Glu	Leu	Gln	Glu	Arg	Ser	Glu	Gln	Leu	Arg	Asn	Gly	Gln	Tyr
								85			90		95		

Gln Ala Ser Asp Ala Ala Gly Leu Gly Leu Asp Arg Ser Pro Pro Glu

100 105 110

Lys Thr Gln Ala Asp Leu Leu Ala Phe Leu His Ser Gln Val Asp Lys  
115 120 125

Ala Glu Val Asn Ala Gly Val Lys Leu Ala Thr Glu Tyr Ala Ala Val  
130 135 140

Pro Phe Asp Ser Phe Thr Leu Gln Lys Val Tyr Gln Leu Glu Thr Gly  
145 150 155 160

Leu Thr Arg His Pro Glu Glu Lys Pro Val Arg Lys Asp Lys Arg Asp  
165 170 175

Glu Leu Val Glu Ala Ile Glu Ser Ala Leu Glu Thr Leu Asn Asn Pro  
180 185 190

Ala Glu Asn Ser Pro Asn His Arg Pro Tyr Thr Ala Ser Asp Phe Ile  
195 200 205

Glu Gly Ile Tyr Arg Thr Glu Arg Asp Lys Gly Thr Leu Tyr Glu Leu  
210 215 220

Thr Phe Lys Gly Asp His Lys His Glu Phe Lys Arg Leu Ile Leu Phe  
225 230 235 240

Arg Pro Phe Gly Pro Ile Met Lys Val Lys Asn Glu Lys Leu Asn Met  
245 250 255

Ala Asn Thr Leu Ile Asn Val Ile Val Pro Leu Ala Lys Arg Val Asp  
260 265 270

Lys Phe Arg Gln Phe Met Gln Asn Phe Arg Glu Met Cys Ile Glu Gln  
275 280 285

Asp Gly Arg Val His Leu Thr Val Val Tyr Phe Gly Lys Glu Glu Ile  
290 295 300

Asn Glu Val Lys Gly Ile Leu Glu Asn Thr Ser Lys Ala Ala Asn Phe  
305 310 315 320

Arg Asn Phe Thr Phe Ile Gln Leu Asn Gly Glu Phe Ser Arg Gly Lys  
325 330 335

Gly Leu Asp Val Gly Ala Arg Phe Trp Lys Gly Ser Asn Val Leu Leu  
340 345 350

Phe Phe Cys Asp Val Asp Ile Tyr Phe Thr Ser Glu Phe Leu Asn Thr  
355 360 365

Cys Arg Leu Asn Thr Gln Pro Gly Lys Lys Val Phe Tyr Pro Val Leu  
370 375 380

Phe Ser Gln Tyr Asn Pro Gly Ile Ile Tyr Gly His His Asp Ala Val  
385 390 395 400

Pro Pro Leu Glu Gln Gln Leu Val Ile Lys Lys Glu Thr Gly Phe Trp  
405 410 415

Arg Asp Phe Gly Phe Gly Met Thr Cys Gln Tyr Arg Ser Asp Phe Ile  
420 425 430

Asn Ile Gly Gly Phe Asp Leu Asp Ile Lys Gly Trp Gly Gly Glu Asp  
435 440 445

Val His Leu Tyr Arg Lys Tyr Leu His Ser Asn Leu Ile Val Val Arg  
450 455 460

Thr Pro Val Arg Gly Leu Phe His Leu Trp His Glu Lys Arg Cys Met  
465 470 475 480

Asp Glu Leu Thr Pro Glu Gln Tyr Lys Met Cys Met Gln Ser Lys Ala  
485 490 495

Met Asn Glu Ala Ser His Gly Gln Leu Gly Met Leu Val Phe Arg His  
500 505 510

Glu Ile Glu Ala His Leu Arg Lys Gln Lys Gln Lys Thr Ser Ser Lys  
515 520 525

Lys Thr  
530

<210> 207  
<211> 2712  
<212> DNA

<213> human organism

<400> 207  
atgattcctg tattgacatc aaaaaaagca agtgaattac cagtcagtga agttgcaagc 60  
attctccaag ctgatcttca gaatggtcta aacaaatgtg aagttagtca taggcgagcc 120  
tttcatggct ggaatgagtt tgatatttagt gaagatgagc cactgtggaa gaagtatatt 180  
tctcagttta aaaatcccct tattatgctg cttctggctt ctgcagtc cat cagttttta 240  
atgcatcagt ttgatgatgc cgtcagttttc actgtggcaa tacttatcgt tgttacagtt 300  
gcctttgttc aggaatatcg ttcagaaaaaa tctcttgaag aatttagttaa acttgtgcc 360  
ccagaatgcc attgtgtgcg tgaaggaaaaa ttggagcata cacttgcccg agacttggtt 420  
ccaggtgata cagtttgcct ttctgttggg gatagagttc ctgctgactt acgcttggtt 480  
gaggctgtgg atctttccat tgatgagtcc agcttgcacag gtgagacaac gccttggtt 540  
aaggtgacag ctccctcagcc agctgcaact aatggagatc ttgcattcgag aagtaacatt 600  
gcctttatgg gaacactggc cagatgtggc aaagcaaagg gtgttgcatt tggaacagga 660  
gaaaattctg aatttgggaa ggtttttaaa atgatgcaag cagaagaggg accaaaaacc 720  
cctctgcaga agagcatgga cctcttagga aaacaacttt cctttactc ctttggata 780  
ataggaatca tcattgttggt tggctggta ctggggaaag atatccttggaa aatgtttact 840  
attagtgtaa gtttggctgt agcagcaatt cctgaaggc tccccattgt ggtcacagtg 900  
acgctagctc ttgggtttat gagaatggtg aagaaaaagg ccattgtgaa aaagctgcct 960  
attgttggaa ctctggcgtg ctgtaatgtg atttggtagt ataaaactgg aacactgacg 1020  
aagaatgaaa tgactgttac tcacatattt acttcagatg gtctgcattc tgaggttact 1080  
ggagttggct ataatcaatt tggggaaagtg attgttgcattt gtgtatgttgcattt 1140  
tataacccag ctgttagcag aattgtttagt gcccggctgtg tgtcaatgtt tgctgttatt 1200  
agaaacaata ctctaattggg gaagccaaca gaagggccct taattgtct tgcaatgtt 1260  
atgggtcttgcattt atggacttca acaagactac atcagaaaag ctgaaatccc ttttagctct 1320  
gagcaaaagt ggatggctgt taagtgtgtt caccgttac acgttggacat accagagatt 1380  
tgtttttatgtt aaggtgttca cgttacatgtt attaagtact gtactacata ccagagcaaa 1440  
gggcagaccc tgcacacttac tcagcagcag agagatgtgtt accaacaaga gaaggcacgc 1500  
atgggtcttgcattt cgggacttca agttttttgtt ttggcttgcattt gtcctgttactt gggacagctg 1560  
acatttttttttgcattt gcttggtggg aatcattgtt caccgttacatgtt agaagctgtt 1620

acaacactca ttgcctcagg agtatcaata aaaatgatta ctggagattc acaggagact	1680
gcagttgcaa tcgccagtcg tctggattt tattccaaaa cttcccagtc agtctcagga	1740
gaagaaatag atgcaatgga tggtcagcag ctttcacaaa tagtaccaaa ggttgcagta	1800
ttttacagag ctagcccaag gcacaagatg aaaatttata agtcgctaca gaagaacggt	1860
tcatgttag ccatgacagg agatggagta aatgatgcag ttgctctgaa ggctgcagac	1920
atggagttg cgatggcca gactggtaca gatgttgca aagaggcagc agacatgatc	1980
cgttgtatg atgatttca aaccataatg tctgcaatcg aagaggtaa agggatttat	2040
aataacatta aaaattcgt tagattccag ctgagcacga gtatagcagc attaacttta	2100
atctcattgg ctacattaat gaactttcct aatcctctca atgccatgca gatTTTGTGG	2160
atcaatatta ttatggatgg acccccagct cagaggctt gatgtggacc agtggataaa	2220
gatgtcattc gtaaacctcc tcgcaactgg aaagacagca ttttactaa aaacttgata	2280
cttaaaatac ttgtttcatc aataatcatt gtttgggaa ctttgggtt cttctggcgt	2340
gagctacgag acaatgtgat tacacctcga gacacaacaa tgaccttcac atgctttgt	2400
tttttgaca ttttcaatgc actaagttcc agatcccaga ccaagtctgt gtttggatt	2460
ggactctgca gtaatagaat gtttgcata gcatggatc gatccatcat gggacaatta	2520
ctagttattt actttccctcc gtttcagaag gttttcaga ctgagagcct aagcatactg	2580
gatctgtgt ttctttggg ttcacactca tcagtgtgca tagtggcaga aattataaag	2640
aagttgaaa ggagcagggaa aaagatccag aagcatgtt aatcgacatc atcatcttt	2700
cttgaagtat ga	2712

<210> 208  
 <211> 903  
 <212> PRT  
 <213> human organism  
  
 <400> 208

Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro Val Ser  
 1               5                           10                           15

Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu Asn Lys  
 20               25                           30

Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp  
 35               40                           45

Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys  
50 55 60

Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu  
65 70 75 80

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile  
85 90 95

Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu  
100 105 110

Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu  
115 120 125

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr  
130 135 140

Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe  
145 150 155 160

Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr  
165 170 175

Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly  
180 185 190

Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg  
195 200 205

Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu  
210 215 220

Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr  
225 230 235 240

Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser Phe Tyr  
245 250 255

Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly  
260 265 270

Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala Val Ala  
275 280 285

Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu Ala Leu  
290 295 300

Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro  
305 310 315 320

Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp Lys Thr  
325 330 335

Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe Thr Ser  
340 345 350

Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln Phe Gly  
355 360 365

Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala  
370 375 380

Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile  
385 390 395 400

Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala  
405 410 415

Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr Ile Arg  
420 425 430

Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys  
435 440 445

Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys  
450 455 460

Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys  
465 470 475 480

Gly Gln Thr Leu Thr Leu Thr Gln Gln Arg Asp Val Tyr Gln Gln  
485 490 495

Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala Leu Ala

500

505

510

Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val Gly Ile  
515 520 525

Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr Leu Ile  
530 535 540

Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln Glu Thr  
545 550 555 560

Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr Ser Gln  
565 570 575

Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln Leu Ser  
580 585 590

Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro Arg His  
595 600 605

Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val Val Ala  
610 615 620

Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp  
625 630 635 640

Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys Glu Ala  
645 650 655

Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met Ser Ala  
660 665 670

Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe Val Arg  
675 680 685

Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser Leu Ala  
690 695 700

Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp  
705 710 715 720

Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu  
725 730 735

Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp  
740 745 750

Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile  
755 760 765

Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu Arg Asp  
770 775 780

Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val  
785 790 795 800

Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser  
805 810 815

Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val  
820 825 830

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu  
835 840 845

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe  
850 855 860

Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys  
865 870 875 880

Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser Ser Thr  
885 890 895

Ser Ser Ser Phe Leu Glu Val  
900

<210> 209

<211> 1284

<212> DNA

<213> human organism

<400> 209

atgggctacc agaggcagga gcctgtcatc ccggccgcaga gaggattgcc ttattcaatg 60

aagcaagctg ggtttccttt gggatatattt cttttattct gggtttcata tgttacagac 120

ttttcccttg ttttattgtt aaaaggaggg gccctctctg gaacagatac ctaccagtct 180

ttggtaata aaacttcgg cttccaggg tatctgtcc tctctgtct tcagtttg	240
tatccttta tagcaatgat aagttacaat ataatagctg gagatactt gagcaaagtt	300
tttcaaagaa tcccaggagt tgatcctgaa aacgttttgc ttggcgcca cttcatttttgc	360
ggactttcca cagttaccc tactctgcct ttatccttgt accgaaatat agcaaagctt	420
ggaaaggctt ccctcatctc tacaggttta acaactctga ttcttggaa tgtaatggca	480
aggcaattt cactgggtcc acacatacca aaaacagaag acgcttgggt atttgcaaag	540
cccaatgcca ttcaagcggt cggggttatg tctttgcatttgc ttatggcca ccataactcc	600
ttcttagttt acagttctct agaagaaccc acagtagcta agtggtcccc ctttatccat	660
atgtccatcg tgatttctgt atttatctgt atatttttgc ttatggcca ccataactcc	720
tttactggct tcacccaagg ggacttattt gaaaattact gcagaaatga tgacctggta	780
acatttggaa gatttgtta tgggtcaact gtcatttgc cataccctat ggaatgctt	840
gtgacaagag aggttaattgc caatgtgtt tttggggaa atcttcatc ggtttccac	900
attgttgtaa cagtgtatggt catcaactgtt gacacgcttgcatttgc gattgattgc	960
ctcggatag ttctagaact caatgggttg ctctgtcaa ctccctcat ttttgcatttgc	1020
ccatcagcct gttatctgaa actgtctgaa gaaccaagga cacactccga taagattatg	1080
tcttgcgtca tgcttccat tgggtctgtt gtgtggttt ttggattcgt catggctatt	1140
acaaatactc aagactgcac ccatgggcag gaaatgttct actgcttcc tgacaatttc	1200
tctctcacaa atacctcaga gtctcatgtt cagcagacaa cacaactttc tactttaaat	1260
attagtatct ttcaactcga gtaa	1284

<210> 210  
<211> 427  
<212> PRT  
<213> human organism

<400> 210

Met	Gly	Tyr	Gln	Arg	Gln	Glu	Pro	Val	Ile	Pro	Pro	Gln	Arg	Gly	Leu
1															
															15

Pro	Tyr	Ser	Met	Lys	Gln	Ala	Gly	Phe	Pro	Leu	Gly	Ile	Leu	Leu	Leu
			20					25							
															30

Phe	Trp	Val	Ser	Tyr	Val	Thr	Asp	Phe	Ser	Leu	Val	Leu	Leu	Ile	Lys
								35							
									40						45

Gly Gly Ala Leu Ser Gly Thr Asp Thr Tyr Gln Ser Leu Val Asn Lys  
50 55 60

Thr Phe Gly Phe Pro Gly Tyr Leu Leu Leu Ser Val Leu Gln Phe Leu  
65 70 75 80

Tyr Pro Phe Ile Ala Met Ile Ser Tyr Asn Ile Ile Ala Gly Asp Thr  
85 90 95

Leu Ser Lys Val Phe Gln Arg Ile Pro Gly Val Asp Pro Glu Asn Val  
100 105 110

Phe Ile Gly Arg His Phe Ile Ile Gly Leu Ser Thr Val Thr Phe Thr  
115 120 125

Leu Pro Leu Ser Leu Tyr Arg Asn Ile Ala Lys Leu Gly Lys Val Ser  
130 135 140

Leu Ile Ser Thr Gly Leu Thr Thr Leu Ile Leu Gly Ile Val Met Ala  
145 150 155 160

Arg Ala Ile Ser Leu Gly Pro His Ile Pro Lys Thr Glu Asp Ala Trp  
165 170 175

Val Phe Ala Lys Pro Asn Ala Ile Gln Ala Val Gly Val Met Ser Phe  
180 185 190

Ala Phe Ile Cys His His Asn Ser Phe Leu Val Tyr Ser Ser Leu Glu  
195 200 205

Glu Pro Thr Val Ala Lys Trp Ser Arg Leu Ile His Met Ser Ile Val  
210 215 220

Ile Ser Val Phe Ile Cys Ile Phe Phe Ala Thr Cys Gly Tyr Leu Thr  
225 230 235 240

Phe Thr Gly Phe Thr Gln Gly Asp Leu Phe Glu Asn Tyr Cys Arg Asn  
245 250 255

Asp Asp Leu Val Thr Phe Gly Arg Phe Cys Tyr Gly Val Thr Val Ile  
260 265 270

Leu Thr Tyr Pro Met Glu Cys Phe Val Thr Arg Glu Val Ile Ala Asn  
275 280 285

Val Phe Phe Gly Gly Asn Leu Ser Ser Val Phe His Ile Val Val Thr  
290 295 300

Val Met Val Ile Thr Val Ala Thr Leu Val Ser Leu Leu Ile Asp Cys  
305 310 315 320

Leu Gly Ile Val Leu Glu Leu Asn Gly Val Leu Cys Ala Thr Pro Leu  
325 330 335

Ile Phe Ile Ile Pro Ser Ala Cys Tyr Leu Lys Leu Ser Glu Glu Pro  
340 345 350

Arg Thr His Ser Asp Lys Ile Met Ser Cys Val Met Leu Pro Ile Gly  
355 360 365

Ala Val Val Met Val Phe Gly Phe Val Met Ala Ile Thr Asn Thr Gln  
370 375 380

Asp Cys Thr His Gly Gln Glu Met Phe Tyr Cys Phe Pro Asp Asn Phe  
385 390 395 400

Ser Leu Thr Asn Thr Ser Glu Ser His Val Gln Gln Thr Thr Gln Leu  
405 410 415

Ser Thr Leu Asn Ile Ser Ile Phe Gln Leu Glu  
420 425

<210> 211  
<211> 1203  
<212> DNA  
<213> human organism

<400> 211  
atgggctacc agaggcagga gcctgtcatc ccggccgcagt tttcccttgt tttattgata 60  
aaaggagggg ccctctctgg aacagataacc taccagtctt tggtcaataaa aactttcgac 120  
tttccagggt atctgctcct ctctgttctt cagtttttgt atccttttat agcaatgata 180  
agttacaata taatagctgg agatactttg agcaaagttt ttcaaagaat cccaggagtt 240  
gatcctgaaa acgtgtttat tggtcgccac ttcattattt gactttccac agttaccc 300

actctgcctt tatccttgta ccgaaatata gcaaagctt gaaaggctc cctcatct	360
acaggtttaa caactctgat tcttggatt gtaatggcaa gggcaatttc actgggtcca	420
cacataccaa aaacagaaga cgcttggta tttgcaaagc ccaatgccat tcaagcggtc	480
ggggttatgt ctttgcatt tatttgcac cataactcct tcttagttt cagttctcta	540
gaagaaccca cagtagctaa gtggtcccgc cttatccata tgtccatcg gatttctgta	600
tttatctgta tattcttgc tacatgtgga tacttgacat ttactggctt caccaaggg	660
gacttatttg aaaattactg cagaaatgat gacctggtaa catttggaaat attttggat	720
ggtgtcactg tcatttgac ataccatatg gaatgcttg tgacaagaga ggtaattgcc	780
aatgtgtttt ttgggtggaa tctttcatcg gttttccaca ttgttgtaac agtcatggc	840
atcaactgttag ccacgcttgc gtcattgctg attgattgcc tcgggatagt tctagaactc	900
aatgggtgac tctgtgcaac tcccctcatt tttatcattt catcagcctg ttatctgaaa	960
ctgtctgaag aaccaaggac acactccgat aagattatgt cttgtgtcat gcttcccatt	1020
ggtgctgtgg tcatgggtttt tggattcgat atggcttta caaatactca agactgcacc	1080
catgggcagg aaatgttcta ctgcttcct gacaatttct ctctcacaaa tacctcagag	1140
tctcatgttc agcagacaac acaactttct actttaaata ttagtatctt tcaactcgag	1200
taa	1203

<210> 212  
 <211> 400  
 <212> PRT  
 <213> human organism

<400> 212

Met Gly Tyr Gln Arg Gln Glu Pro Val Ile Pro Pro Gln Phe Ser Leu  
 1 5 10 15

Val Leu Leu Ile Lys Gly Gly Ala Leu Ser Gly Thr Asp Thr Tyr Gln  
 20 25 30

Ser Leu Val Asn Lys Thr Phe Gly Phe Pro Gly Tyr Leu Leu Leu Ser  
 35 40 45

Val Leu Gln Phe Leu Tyr Pro Phe Ile Ala Met Ile Ser Tyr Asn Ile  
 50 55 60

Ile Ala Gly Asp Thr Leu Ser Lys Val Phe Gln Arg Ile Pro Gly Val

65                   70                   75                   80

Asp Pro Glu Asn Val Phe Ile Gly Arg His Phe Ile Ile Gly Leu Ser  
85   90                                 95

Thr Val Thr Phe Thr Leu Pro Leu Ser Leu Tyr Arg Asn Ile Ala Lys  
100   105                                 110

Leu Gly Lys Val Ser Leu Ile Ser Thr Gly Leu Thr Thr Leu Ile Leu  
115   120                                 125

Gly Ile Val Met Ala Arg Ala Ile Ser Leu Gly Pro His Ile Pro Lys  
130   135                                 140

Thr Glu Asp Ala Trp Val Phe Ala Lys Pro Asn Ala Ile Gln Ala Val  
145   150                                 155                                 160

Gly Val Met Ser Phe Ala Phe Ile Cys His His Asn Ser Phe Leu Val  
165   170   175

Tyr Ser Ser Leu Glu Glu Pro Thr Val Ala Lys Trp Ser Arg Leu Ile  
180   185   190

His Met Ser Ile Val Ile Ser Val Phe Ile Cys Ile Phe Phe Ala Thr  
195   200   205

Cys Gly Tyr Leu Thr Phe Thr Gly Phe Thr Gln Gly Asp Leu Phe Glu  
210   215   220

Asn Tyr Cys Arg Asn Asp Asp Leu Val Thr Phe Gly Arg Phe Cys Tyr  
225   230   235   240

Gly Val Thr Val Ile Leu Thr Tyr Pro Met Glu Cys Phe Val Thr Arg  
245   250   255

Glu Val Ile Ala Asn Val Phe Phe Gly Gly Asn Leu Ser Ser Val Phe  
260   265   270

His Ile Val Val Thr Val Met Val Ile Thr Val Ala Thr Leu Val Ser  
275   280   285

Leu Leu Ile Asp Cys Leu Gly Ile Val Leu Glu Leu Asn Gly Val Leu  
290   295   300

Cys Ala Thr Pro Leu Ile Phe Ile Ile Pro Ser Ala Cys Tyr Leu Lys  
305 310 315 320

Leu Ser Glu Glu Pro Arg Thr His Ser Asp Lys Ile Met Ser Cys Val  
325 330 335

Met Leu Pro Ile Gly Ala Val Val Met Val Phe Gly Phe Val Met Ala  
340 345 350

Ile Thr Asn Thr Gln Asp Cys Thr His Gly Gln Glu Met Phe Tyr Cys  
355 360 365

Phe Pro Asp Asn Phe Ser Leu Thr Asn Thr Ser Glu Ser His Val Gln  
370 375 380

Gln Thr Thr Gln Leu Ser Thr Leu Asn Ile Ser Ile Phe Gln Leu Glu  
385 390 395 400

<210> 213  
<211> 1140  
<212> DNA  
<213> human organism

<400> 213  
atgggctacc agaggcagga gcctgtcatc ccggccgcagg tcaataaaac tttcggcttt 60  
ccagggtatac tgctcccttc tggcttcag tttttgtatc cttttatagc aatgataagt 120  
tacaatataa tagctggaga tacttgagc aaagttttc aaagaatccc aggagttgat 180  
cctgaaaacg tggattttgg tcgccacttc attattggac tttccacagt tacctttact 240  
ctgcctttat ctttgtaccg aaatatagca aagcttgaa aggtctccct catctctaca 300  
ggtttaacaa ctctgattct tggattgtatc atggcaaggg caatttcact gggccacac 360  
ataccaaaaaa cagaagacgc ttgggtatcc gcaaagccca atgccattca agcggtcggg 420  
gttatgtctt ttgcattttat ttgccaccat aactccttct tagttacag ttctctagaa 480  
gaacccacag tagctaagtg gtccgcctt atccatatgt ccatcgtat ttctgtatcc 540  
atctgtatat tctttgtac atgtggatac ttgacattta ctggcttcac ccaaggggac 600  
ttatggaaa attactgcag aaatgatgac ctggtaacat ttggaagatt ttgttatgg 660  
gtcactgtca ttttgacata ccctatggaa tgctttgtga caagagaggt aattgccaat 720  
gtgttttttg gtggaaatct ttcatcggtt ttccacattt tgtaacagt gatggtcattc 780

actgttagcca cgcttgcgtc attgctgatt gattgcctcg ggatagttct agaactcaat 840  
ggtgtgtctt gtgcaactcc cctcattttt atcattccat cagcctgtta tctgaaactg 900  
tctgaagaac caaggacaca ctccgataag attatgtctt gtgtcatgct tcccattgg 960  
gctgtggtga tggttttgg attcgtcatg gctattacaa atactcaaga ctgcacccat 1020  
gggcaggaaa tgttctactg ctttcctgac aatttctctc tcacaaatac ctcagagtct 1080  
catgttcagc agacaacaca actttctact ttaaatatta gatatcttca actcgagtaa 1140

<210> 214  
<211> 379  
<212> PRT  
<213> human organism

<400> 214

Met Gly Tyr Gln Arg Gln Glu Pro Val Ile Pro Pro Gln Val Asn Lys  
1 5 10 15

Thr Phe Gly Phe Pro Gly Tyr Leu Leu Leu Ser Val Leu Gln Phe Leu  
20 25 30

Tyr Pro Phe Ile Ala Met Ile Ser Tyr Asn Ile Ile Ala Gly Asp Thr  
35 40 45

Leu Ser Lys Val Phe Gln Arg Ile Pro Gly Val Asp Pro Glu Asn Val  
50 55 60

Phe Ile Gly Arg His Phe Ile Ile Gly Leu Ser Thr Val Thr Phe Thr  
65 70 75 80

Leu Pro Leu Ser Leu Tyr Arg Asn Ile Ala Lys Leu Gly Lys Val Ser  
85 90 95

Leu Ile Ser Thr Gly Leu Thr Thr Leu Ile Leu Gly Ile Val Met Ala  
100 105 110

Arg Ala Ile Ser Leu Gly Pro His Ile Pro Lys Thr Glu Asp Ala Trp  
115 120 125

Val Phe Ala Lys Pro Asn Ala Ile Gln Ala Val Gly Val Met Ser Phe  
130 135 140

Ala Phe Ile Cys His His Asn Ser Phe Leu Val Tyr Ser Ser Leu Glu  
145 150 155 160

Glu Pro Thr Val Ala Lys Trp Ser Arg Leu Ile His Met Ser Ile Val  
165 170 175

Ile Ser Val Phe Ile Cys Ile Phe Phe Ala Thr Cys Gly Tyr Leu Thr  
180 185 190

Phe Thr Gly Phe Thr Gln Gly Asp Leu Phe Glu Asn Tyr Cys Arg Asn  
195 200 205

Asp Asp Leu Val Thr Phe Gly Arg Phe Cys Tyr Gly Val Thr Val Ile  
210 215 220

Leu Thr Tyr Pro Met Glu Cys Phe Val Thr Arg Glu Val Ile Ala Asn  
225 230 235 240

Val Phe Phe Gly Gly Asn Leu Ser Ser Val Phe His Ile Val Val Thr  
245 250 255

Val Met Val Ile Thr Val Ala Thr Leu Val Ser Leu Leu Ile Asp Cys  
260 265 270

Leu Gly Ile Val Leu Glu Leu Asn Gly Val Leu Cys Ala Thr Pro Leu  
275 280 285

Ile Phe Ile Ile Pro Ser Ala Cys Tyr Leu Lys Leu Ser Glu Glu Pro  
290 295 300

Arg Thr His Ser Asp Lys Ile Met Ser Cys Val Met Leu Pro Ile Gly  
305 310 315 320

Ala Val Val Met Val Phe Gly Phe Val Met Ala Ile Thr Asn Thr Gln  
325 330 335

Asp Cys Thr His Gly Gln Glu Met Phe Tyr Cys Phe Pro Asp Asn Phe  
340 345 350

Ser Leu Thr Asn Thr Ser Glu Ser His Val Gln Gln Thr Thr Gln Leu  
355 360 365

Ser Thr Leu Asn Ile Ser Ile Phe Gln Leu Glu

370

375

<210>	215					
<211>	1389					
<212>	DNA					
<213>	human organism					
<400>	215					
atgggctacc	agaggcagga	gcctgtcatc	ccgcccgcaga	gagatttaga	tgacagagaa	60
acccttgttt	ctgaacatga	gtataaagag	aaaacctgtc	agtctgctgc	tcttttaat	120
gttgtcaact	cgattatagg	atctggtata	ataggattgc	cttattcaat	gaagcaagct	180
gggttcctt	tggaatattt	gcttttattt	tgggttcat	atgttacaga	ctttccctt	240
gttttattga	taaaaggagg	ggccctctct	ggaacagata	cctaccagtc	tttggtcaat	300
aaaactttcg	gctttccagg	gtatctgctc	ctctctgttc	ttcagttttt	gtatccttt	360
atagcaatga	taagttacaa	tataatagct	ggagataactt	tgagcaaagt	ttttcaaaga	420
atcccaggag	ttgatcctga	aaacgtttt	attggtcgcc	acttcattat	tggactttcc	480
acagttacct	ttactctgcc	tttacccctt	taccgaaata	tagcaaagct	tggaaaggc	540
tccctcatct	ctacaggttt	aacaactctg	attcttgaa	ttgtatggc	aaggcaatt	600
tcactgggtc	cacacatacc	aaaaacagaa	gacgcttggg	tatggcaaa	gcccaatgcc	660
attcaagcgg	tcggggttat	gtctttgca	tttatttgc	accataactc	cttcttagtt	720
tacagttctc	tagaagaacc	cacagtagct	aagtggtccc	gccttatcca	tatgtccatc	780
gtgatttctg	tatattctg	tatattctt	gctacatgtg	gatacttgac	atttactggc	840
ttcacccaaag	gggacttatt	tgaaaattac	tgcagaaatg	atgacctgg	aacatttgg	900
agatttgtt	atgggtcac	tgtcatttt	acatacccta	tggaatgctt	tgtgacaaga	960
gaggtaattg	ccaatgtgtt	tttggtggg	aatcttcat	cggtttcca	cattgttga	1020
acagtgtatgg	tcatcactgt	agccacgctt	gtgtcattgc	tgattgattt	cctcggata	1080
gttctagaac	tcaatggtgt	gctctgtgca	actccctca	tttttatcat	tccatcagcc	1140
tgttatctga	aactgtctga	agaaccaagg	acacactccg	ataagattat	gtcttgc	1200
atgcttccca	ttgggtctgt	ggtgatggtt	tttggattcg	tcatggctat	tacaaatact	1260
caagactgca	cccatgggca	ggaaatgttc	tactgcttcc	ctgacaattt	ctctctcaca	1320
aatacctcag	agtctcatgt	tcagcagaca	acacaacttt	ctacttaaa	tattagtatc	1380
tttcaatga						1389

<210> 216  
<211> 462  
<212> PRT  
<213> human organism

<400> 216

Met Gly Tyr Gln Arg Gln Glu Pro Val Ile Pro Pro Gln Arg Asp Leu  
1 5 10 15

Asp Asp Arg Glu Thr Leu Val Ser Glu His Glu Tyr Lys Glu Lys Thr  
20 25 30

Cys Gln Ser Ala Ala Leu Phe Asn Val Val Asn Ser Ile Ile Gly Ser  
35 40 45

Gly Ile Ile Gly Leu Pro Tyr Ser Met Lys Gln Ala Gly Phe Pro Leu  
50 55 60

Gly Ile Leu Leu Leu Phe Trp Val Ser Tyr Val Thr Asp Phe Ser Leu  
65 70 75 80

Val Leu Leu Ile Lys Gly Gly Ala Leu Ser Gly Thr Asp Thr Tyr Gln  
85 90 95

Ser Leu Val Asn Lys Thr Phe Gly Phe Pro Gly Tyr Leu Leu Ser  
100 105 110

Val Leu Gln Phe Leu Tyr Pro Phe Ile Ala Met Ile Ser Tyr Asn Ile  
115 120 125

Ile Ala Gly Asp Thr Leu Ser Lys Val Phe Gln Arg Ile Pro Gly Val  
130 135 140

Asp Pro Glu Asn Val Phe Ile Gly Arg His Phe Ile Ile Gly Leu Ser  
145 150 155 160

Thr Val Thr Phe Thr Leu Pro Leu Ser Leu Tyr Arg Asn Ile Ala Lys  
165 170 175

Leu Gly Lys Val Ser Leu Ile Ser Thr Gly Leu Thr Thr Leu Ile Leu  
180 185 190

Gly Ile Val Met Ala Arg Ala Ile Ser Leu Gly Pro His Ile Pro Lys

195

200

205

Thr Glu Asp Ala Trp Val Phe Ala Lys Pro Asn Ala Ile Gln Ala Val  
210 215 220

Gly Val Met Ser Phe Ala Phe Ile Cys His His Asn Ser Phe Leu Val  
225 230 235 240

Tyr Ser Ser Leu Glu Glu Pro Thr Val Ala Lys Trp Ser Arg Leu Ile  
245 250 255

His Met Ser Ile Val Ile Ser Val Phe Ile Cys Ile Phe Phe Ala Thr  
260 265 270

Cys Gly Tyr Leu Thr Phe Thr Gly Phe Thr Gln Gly Asp Leu Phe Glu  
275 280 285

Asn Tyr Cys Arg Asn Asp Asp Leu Val Thr Phe Gly Arg Phe Cys Tyr  
290 295 300

Gly Val Thr Val Ile Leu Thr Tyr Pro Met Glu Cys Phe Val Thr Arg  
305 310 315 320

Glu Val Ile Ala Asn Val Phe Phe Gly Gly Asn Leu Ser Ser Val Phe  
325 330 335

His Ile Val Val Thr Val Met Val Ile Thr Val Ala Thr Leu Val Ser  
340 345 350

Leu Leu Ile Asp Cys Leu Gly Ile Val Leu Glu Leu Asn Gly Val Leu  
355 360 365

Cys Ala Thr Pro Leu Ile Phe Ile Ile Pro Ser Ala Cys Tyr Leu Lys  
370 375 380

Leu Ser Glu Glu Pro Arg Thr His Ser Asp Lys Ile Met Ser Cys Val  
385 390 395 400

Met Leu Pro Ile Gly Ala Val Val Met Val Phe Gly Phe Val Met Ala  
405 410 415

Ile Thr Asn Thr Gln Asp Cys Thr His Gly Gln Glu Met Phe Tyr Cys  
420 425 430

Phe Pro Asp Asn Phe Ser Leu Thr Asn Thr Ser Glu Ser His Val Gln  
435 440 445

Gln Thr Thr Gln Leu Ser Thr Leu Asn Ile Ser Ile Phe Gln  
450 455 460

<210> 217  
<211> 3501  
<212> DNA  
<213> human organism

<400> 217  
atggaggatg ctttcggggc agccgtggtg accgtgtggg acagcgatgc acacaccacg 60  
gagaagccca ccgatgccta cgagagactg gacttcacgg gggccggccg caagcacagc 120  
aatttcctcc ggctctctga ccgaacggat ccagctgcag ttatagtc ggtcacacgc 180  
acatggggct tccgtgcccc gaacctggtg gtgtcagtgc tggggggatc gggggggccc 240  
gtcctccaga cctggctgca ggacctgctg cgtcgtggc tggcggccg tgcccaagagc 300  
acaggagcct ggattgtcac tgggggtctg cacacggca tcggccggca tgggtgtg 360  
gctgtacggg accatcagat ggccagcaact gggggcacca aggtggtggc catgggtgtg 420  
gccccctggg gtgtggccg gaatagagac accctcatca accccaaggg ctgcgtccct 480  
gcgaggtacc ggtggcgcgg tgacccggag gacggggtcc agtttccct ggactacaac 540  
tactcggcct tcttcctggt ggacgcacggc acacacggct gcctgggggg cgagaaccgc 600  
ttccgcttgc gcctggagtc ctacatctca cagcagaaga cggcgtggg agggactgga 660  
attgacatcc ctgtcctgct ctcctgatt gatggtgatg agaagatgtt gacgcgaata 720  
gagaacgcca cccaggctca gctccatgt ctcctcgtgg ctggctcagg gggagctgcg 780  
gactgcctgg cggagaccct ggaagacact ctggcccccag ggagtggggg agccaggcaa 840  
ggcgaagccc gagatcaat caggcggttc ttcccaaag gggaccttga ggtcctgcag 900  
gcccagggtgg agaggattt gacccgaaag gagctcctga cagtctattc ttctgaggat 960  
gggtctgagg aattcgagac catagtttg aaggcccttg tgaaggcctg tggagctcg 1020  
gaggcctcag ctcacccgttgc tgagctgcgt ttggctgtgg cttggacccg cgtggacatt 1080  
gcccagatgt aactcttcg gggggacatc caatggcggt cttccatct cgaagcttcc 1140  
ctcatggacg ccctgctgaa tgaccggcct gagttcgtgc gtttgcata ttccacggc 1200  
ctcaggctgg gccacttcct gaccccgatg cgcctggccc aactctacag cgcggcggcc 1260

tccaaactcgc tcatccgcaa cctttggac caggcgccc acagcgcagg caccaaagcc 1320  
ccagccctaa aagggggagc tgcggagctc cggccccctg acgtggggca tgtgctgagg 1380  
atgctgctgg ggaagatgtg cgccgcccagg taccctccg ggggcgcctg ggaccctcac 1440  
ccaggccagg gttcgggga gagcatgtat ctgctctcgg acaaggccac ctcgcccgtc 1500  
tcgctggatg ctggcctcgg gcaggcccc tggagcgtacc tgcttcttg ggcactgttg 1560  
ctgaacaggg cacagatggc catgtacttc tggagatgg gttccaatgc agtttctca 1620  
gctcttgggg cctgtttgct gctccgggtg atggcacgcc tggagcctga cgctgaggag 1680  
gcagcacgga ggaaagacct ggcgttcaag tttgagggga tggcggttga cctcttggc 1740  
gagtgtatc gcagcagtga ggtgagggtc gcccgcctcc tccctccgtcg ctgcccgtc 1800  
tggggggatg ccacttgccc ccagctggcc atgcaagctg acgcccgtgc cttcttggc 1860  
cagggatgggg tacagtctct gctgacacag aagtggtggg gagatatggc cagcactaca 1920  
cccatctggg ccctggttct cgcccttctt tgccctccac tcatctacac ccgcctcatc 1980  
accttcagga aatcagaaga ggagcccaca cgggaggagc tagagtttga catggatagt 2040  
gtcattaatg gggaaaggccc tgcgggacg gcggacccag ccgagaagac gccgctgggg 2100  
gtccccggcc agtcggggcg tccgggttgc tgcggggcc gctgcggggg gcccgggtgc 2160  
ctacgcgcgt gttccactt ctggggcgcc ccgggtacca tcttcatggg caacgtggtc 2220  
agctacctgc tttccatgtc gctttctcg cgggtgtgc tcgtggatt ccagccggcg 2280  
ccgccccggct ccctggagct gctgctctat ttctggctt tcaacgtgtc gtgcgaggaa 2340  
ctgcgccagg gcctgagcgg aggccggggc agcctcgcca gcgggggccc cgggctggc 2400  
catgcctcac tggccagcg cctgcgcctc tacctcgccg acagctggaa ccagtgcgac 2460  
ctagtggctc tCACCTGCTT CCTCCTGGGC GTGGGCTGCC GGCTGACCCC GGGTTGTAC 2520  
cacctggcc gcactgtcct ctgcacatcgac ttcatggtt tCACGGTGC GCTGCTTCAC 2580  
atcttcacgg tcaacaaaaca gctggggccc aagatcgta tcgtgagcaa gatgtgaag 2640  
gacgtgttct tcttccttctt ctgcgtggc gtgtggctgg tagcctatgg cgtggccacg 2700  
gaggggctcc tgaggccacg ggacagtgtac ttcccaagta tccctgcgcgg cgtcttctac 2760  
cgtccctacc tgcagatctt cggcagatt cccaggagg acatggacgt gcccctcatg 2820  
gagcacagca actgctcgac ggagcccgac ttctgggcac accctcctgg ggcccaggcg 2880  
ggcacctgcg tctccagta tgccaaactgg ctgggtggtgc tgctcctcgt catcttcctg 2940

ctcgtggcca acatcctgct ggtcaacttg ctcattgcca tggcagttt cacattcgcc	3000
aaagtacagg gcaacagcga tctctactgg aaggcgcagc gttaccgcct catccggaa	3060
ttccactctc ggcccgcgct ggccccgccc tttatcgta tctcccaactt gcgcctcctg	3120
ctcaggcaat tgtgcaggcg accccggagc ccccagccgt cctccccggc cctcgagcat	3180
ttccgggtt acctttctaa ggaagccgag cggaagctgc taacgtggga atcggtgcat	3240
aaggagaact ttctgctggc acgcgctagg gacaagcggg agagcgactc cgagcgtctg	3300
aagcgcacgt cccagaaggt ggacttggca ctgaaacagc tgggacacat ccgcgagtac	3360
gaacagcgcc tgaaaagtgct ggagcgggag gtccagcagt gtagccgcgt cctggggtgg	3420
gtggccgagg ccctgagccg ctctgccttg ctgccccag gtggggccgcc accccctgac	3480
ctgcctgggt ccaaagactg.a	3501

<210> 218  
 <211> 1166  
 <212> PRT  
 <213> human organism

<400> 218

Met Glu Asp Ala Phe Gly Ala Ala Val Val Thr Val Trp Asp Ser Asp	
1	5
	10
	15

Ala His Thr Thr Glu Lys Pro Thr Asp Ala Tyr Gly Glu Leu Asp Phe	
20	25
	30

Thr Gly Ala Gly Arg Lys His Ser Asn Phe Leu Arg Leu Ser Asp Arg	
35	40
	45

Thr Asp Pro Ala Ala Val Tyr Ser Leu Val Thr Arg Thr Trp Gly Phe	
50	55
	60

Arg Ala Pro Asn Leu Val Val Ser Val Leu Gly Gly Ser Gly Gly Pro	
65	70
	75
	80

Val Leu Gln Thr Trp Leu Gln Asp Leu Leu Arg Arg Gly Leu Val Arg	
85	90
	95

Ala Ala Gln Ser Thr Gly Ala Trp Ile Val Thr Gly Gly Leu His Thr	
100	105
	110

Gly Ile Gly Arg His Val Gly Val Ala Val Arg Asp His Gln Met Ala

115                    120                    125

Ser Thr Gly Gly Thr Lys Val Val Ala Met Gly Val Ala Pro Trp Gly  
130                    135                    140

Val Val Arg Asn Arg Asp Thr Leu Ile Asn Pro Lys Gly Ser Phe Pro  
145                    150                    160

Ala Arg Tyr Arg Trp Arg Gly Asp Pro Glu Asp Gly Val Gln Phe Pro  
165                    170                    175

Leu Asp Tyr Asn Tyr Ser Ala Phe Phe Leu Val Asp Asp Gly Thr His  
180                    185                    190

Gly Cys Leu Gly Gly Glu Asn Arg Phe Arg Leu Arg Leu Glu Ser Tyr  
195                    200                    205

Ile Ser Gln Gln Lys Thr Gly Val Gly Gly Thr Gly Ile Asp Ile Pro  
210                    215                    220

Val Leu Leu Leu Ile Asp Gly Asp Glu Lys Met Leu Thr Arg Ile  
225                    230                    240

Glu Asn Ala Thr Gln Ala Gln Leu Pro Cys Leu Leu Val Ala Gly Ser  
245                    250                    255

Gly Gly Ala Ala Asp Cys Leu Ala Glu Thr Leu Glu Asp Thr Leu Ala  
260                    265                    270

Pro Gly Ser Gly Gly Ala Arg Gln Gly Glu Ala Arg Asp Arg Ile Arg  
275                    280                    285

Arg Phe Phe Pro Lys Gly Asp Leu Glu Val Leu Gln Ala Gln Val Glu  
290                    295                    300

Arg Ile Met Thr Arg Lys Glu Leu Leu Thr Val Tyr Ser Ser Glu Asp  
305                    310                    320

Gly Ser Glu Glu Phe Glu Thr Ile Val Leu Lys Ala Leu Val Lys Ala  
325                    330                    335

Cys Gly Ser Ser Glu Ala Ser Ala Tyr Leu Asp Glu Leu Arg Leu Ala  
340                    345                    350



Val Ala Trp Asn Arg Val Asp Ile Ala Gln Ser Glu Leu Phe Arg Gly  
355 360 365

Asp Ile Gln Trp Arg Ser Phe His Leu Glu Ala Ser Leu Met Asp Ala  
370 375 380

Leu Leu Asn Asp Arg Pro Glu Phe Val Arg Leu Leu Ile Ser His Gly  
385 390 395 400

Leu Ser Leu Gly His Phe Leu Thr Pro Met Arg Leu Ala Gln Leu Tyr  
405 410 415

Ser Ala Ala Pro Ser Asn Ser Leu Ile Arg Asn Leu Leu Asp Gln Ala  
420 425 430

Ser His Ser Ala Gly Thr Lys Ala Pro Ala Leu Lys Gly Gly Ala Ala  
435 440 445

Glu Leu Arg Pro Pro Asp Val Gly His Val Leu Arg Met Leu Leu Gly  
450 455 460

Lys Met Cys Ala Pro Arg Tyr Pro Ser Gly Gly Ala Trp Asp Pro His  
465 470 475 480

Pro Gly Gln Gly Phe Gly Glu Ser Met Tyr Leu Leu Ser Asp Lys Ala  
485 490 495

Thr Ser Pro Leu Ser Leu Asp Ala Gly Leu Gly Gln Ala Pro Trp Ser  
500 505 510

Asp Leu Leu Leu Trp Ala Leu Leu Leu Asn Arg Ala Gln Met Ala Met  
515 520 525

Tyr Phe Trp Glu Met Gly Ser Asn Ala Val Ser Ser Ala Leu Gly Ala  
530 535 540

Cys Leu Leu Leu Arg Val Met Ala Arg Leu Glu Pro Asp Ala Glu Glu  
545 550 555 560

Ala Ala Arg Arg Lys Asp Leu Ala Phe Lys Phe Glu Gly Met Gly Val  
565 570 575

Asp Leu Phe Gly Glu Cys Tyr Arg Ser Ser Glu Val Arg Ala Ala Arg  
580 585 590

Leu Leu Leu Arg Arg Cys Pro Leu Trp Gly Asp Ala Thr Cys Leu Gln  
595 600 605

Leu Ala Met Gln Ala Asp Ala Arg Ala Phe Phe Ala Gln Asp Gly Val  
610 615 620

Gln Ser Leu Leu Thr Gln Lys Trp Trp Gly Asp Met Ala Ser Thr Thr  
625 630 635 640

Pro Ile Trp Ala Leu Val Leu Ala Phe Phe Cys Pro Pro Leu Ile Tyr  
645 650 655

Thr Arg Leu Ile Thr Phe Arg Lys Ser Glu Glu Glu Pro Thr Arg Glu  
660 665 670

Glu Leu Glu Phe Asp Met Asp Ser Val Ile Asn Gly Glu Gly Pro Val  
675 680 685

Gly Thr Ala Asp Pro Ala Glu Lys Thr Pro Leu Gly Val Pro Arg Gln  
690 695 700

Ser Gly Arg Pro Gly Cys Cys Gly Gly Arg Cys Gly Gly Arg Arg Cys  
705 710 715 720

Leu Arg Arg Trp Phe His Phe Trp Gly Ala Pro Val Thr Ile Phe Met  
725 730 735

Gly Asn Val Val Ser Tyr Leu Leu Phe Leu Leu Phe Ser Arg Val  
740 745 750

Leu Leu Val Asp Phe Gln Pro Ala Pro Pro Gly Ser Leu Glu Leu Leu  
755 760 765

Leu Tyr Phe Trp Ala Phe Thr Leu Leu Cys Glu Glu Leu Arg Gln Gly  
770 775 780

Leu Ser Gly Gly Gly Ser Leu Ala Ser Gly Gly Pro Gly Pro Gly  
785 790 795 800

His Ala Ser Leu Ser Gln Arg Leu Arg Leu Tyr Leu Ala Asp Ser Trp  
805 810 815

Asn Gln Cys Asp Leu Val Ala Leu Thr Cys Phe Leu Leu Gly Val Gly  
820 825 830

Cys Arg Leu Thr Pro Gly Leu Tyr His Leu Gly Arg Thr Val Leu Cys  
835 840 845

Ile Asp Phe Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val  
850 855 860

Asn Lys Gln Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys  
865 870 875 880

Asp Val Phe Phe Phe Leu Phe Leu Gly Val Trp Leu Val Ala Tyr  
885 890 895

Gly Val Ala Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro  
900 905 910

Ser Ile Leu Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly  
915 920 925

Gln Ile Pro Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn  
930 935 940

Cys Ser Ser Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala  
945 950 955 960

Gly Thr Cys Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu  
965 970 975

Val Ile Phe Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile  
980 985 990

Ala Met Phe Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu  
995 1000 1005

Tyr Trp Lys Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser  
1010 1015 1020

Arg Pro Ala Leu Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg

1025	1030	1035
Leu Leu Leu Arg Gln Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro		
1040	1045	1050
Ser Ser Pro Ala Leu Glu His Phe Arg Val Tyr Leu Ser Lys Glu		
1055	1060	1065
Ala Glu Arg Lys Leu Leu Thr Trp Glu Ser Val His Lys Glu Asn		
1070	1075	1080
Phe Leu Leu Ala Arg Ala Arg Asp Lys Arg Glu Ser Asp Ser Glu		
1085	1090	1095
Arg Leu Lys Arg Thr Ser Gln Lys Val Asp Leu Ala Leu Lys Gln		
1100	1105	1110
Leu Gly His Ile Arg Glu Tyr Glu Gln Arg Leu Lys Val Leu Glu		
1115	1120	1125
Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly Trp Val Ala Glu		
1130	1135	1140
Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly Pro Pro Pro		
1145	1150	1155
Pro Asp Leu Pro Gly Ser Lys Asp		
1160	1165	
<210> 219		
<211> 894		
<212> DNA		
<213> human organism		
<400> 219		
atggagccgc gggcgctcgt cacggcgctc agcctcgccc tcagcctgtg ctccctgggg		60
ctgctcgtca cggccatctt caccgaccac tggtagaca ccgacccccc gcgccacaag		120
gagagctgca agcgcagccg cgccccggcc gaccccccgg accagaagaa ccgcctgatg		180
ccgctgtcgc acctgccgct gcgggactcg ccccccgtgg ggccggggct gctccgggc		240
ggcccggggc gcgccgaccc cgagtcctgg cgctcgctcc tggggctcgg cgggctggac		300
gccgagtgcg gccggccctt ctccgccacc tactcgggcc tctggaggaa gtgctacttc		360

ctgggcatcg accgggacat cgacaccctc atcctgaaag gtattgcgc	420
gcatcaagt accactttc tcagccatc cgcttgcga acattcctt taatttaacc	480
aagaccatac agcaagatga gtggcacctg cttcatttaa gaagaatcac tgctggcttc	540
ctcggcatgg ccgttagccgt cttctctgc ggctgcattg tggccacagt cagttcttc	600
tggaggaga gcttgaccca gcacgtggct ggactcctgt tcctcatgac agggatattt	660
tgcaccattt ccctctgtac ttatgccgcc agtatctcgt atgatttcaa ccggctccca	720
aagctaattt atagcctgcc tgctgatgtg gaacatggtt acagctggtc catctttgc	780
gcctggtgca gtttaggctt tattgtggca gctggaggtc tctgcatcgc ttatccgtt	840
attagccgga ccaagattgc acagctaaag tctggcagag actccacggt atga	894

<210> 220

<211> 297

<212> PRT

<213> human organism

<400> 220

Met Glu Pro Arg Ala Leu Val Thr Ala Leu Ser Leu Gly Leu Ser Leu			
1	5	10	15

Cys Ser Leu Gly Leu Leu Val Thr Ala Ile Phe Thr Asp His Trp Tyr		
20	25	30

Glu Thr Asp Pro Arg Arg His Lys Glu Ser Cys Glu Arg Ser Arg Ala		
35	40	45

Gly Ala Asp Pro Pro Asp Gln Lys Asn Arg Leu Met Pro Leu Ser His		
50	55	60

Leu Pro Leu Arg Asp Ser Pro Pro Leu Gly Arg Arg Leu Leu Pro Gly			
65	70	75	80

Gly Pro Gly Arg Ala Asp Pro Glu Ser Trp Arg Ser Leu Leu Gly Leu		
85	90	95

Gly Gly Leu Asp Ala Glu Cys Gly Arg Pro Leu Phe Ala Thr Tyr Ser		
100	105	110

Gly Leu Trp Arg Lys Cys Tyr Phe Leu Gly Ile Asp Arg Asp Ile Asp		
115	120	125

Thr Leu Ile Leu Lys Gly Ile Ala Gln Arg Cys Thr Ala Ile Lys Tyr  
130 135 140

His Phe Ser Gln Pro Ile Arg Leu Arg Asn Ile Pro Phe Asn Leu Thr  
145 150 155 160

Lys Thr Ile Gln Gln Asp Glu Trp His Leu Leu His Leu Arg Arg Ile  
165 170 175

Thr Ala Gly Phe Leu Gly Met Ala Val Ala Val Leu Leu Cys Gly Cys  
180 185 190

Ile Val Ala Thr Val Ser Phe Phe Trp Glu Glu Ser Leu Thr Gln His  
195 200 205

Val Ala Gly Leu Leu Phe Leu Met Thr Gly Ile Phe Cys Thr Ile Ser  
210 215 220

Leu Cys Thr Tyr Ala Ala Ser Ile Ser Tyr Asp Leu Asn Arg Leu Pro  
225 230 235 240

Lys Leu Ile Tyr Ser Leu Pro Ala Asp Val Glu His Gly Tyr Ser Trp  
245 250 255

Ser Ile Phe Cys Ala Trp Cys Ser Leu Gly Phe Ile Val Ala Ala Gly  
260 265 270

Gly Leu Cys Ile Ala Tyr Pro Phe Ile Ser Arg Thr Lys Ile Ala Gln  
275 280 285

Leu Lys Ser Gly Arg Asp Ser Thr Val  
290 295

<210> 221

<211> 1134

<212> DNA

<213> human organism

<400> 221

atgaggcgac tgaatcgaa aaaaacttta agtttgtaa aagagttgga tgccttcg 60

aaggttcctg agagctatgt agagacttca gccagtggag gtacagtttc tctaatacg 120

tttacaacta tggctttatt aaccataatg gaattctcag tatatcaaga tacatggatg 180

aagtatgaat acgaagtaga caaggatttt tctagcaaat taagaattaa tatagatatt	240
actgttgc当地 tgaagtgtca atatgttggc gcggatgtat tggatttgc agaaacaatg	300
gttgc当地 ctg cagatggtt agtttatgaa ccaacagtat ttgatcttc accacagcag	360
aaagagtggc agaggatgct gcagctgatt cagagtaggc tacaagaaga gcattcactt	420
caagatgtga tatttaaaag tgctttaaa agtacatcaa cagcttcc accaagagaa	480
gatgattcat cacagtctcc aaatgc当地 agaattcatg gccatctata tgtcaataaa	540
gtagcaggga attttcacat aacagtggc aaggcaattc cacatcctcg tggcatgca	600
catttggc当地 gag cacttgc当地 ccatgaatct tacaattttt ctc当地 agatcatttg	660
tctttggag agcttggcc agcaatttattt aatccttttag atggaactga aaaaattgct	720
atagatcaca accagatgtt ccaatattttt attacagttg tgccaacaaa actacataca	780
tataaaat cagcagacac ccatcagttt tctgtgacag aaaggaaacg tatcattaac	840
catgctgc当地 gag cc当地 atatttgc当地 aatatgatct cagttctt	900
atggtgacag ttactgagga gcacatgcca ttctggc当地 ttttgtaag actctgtggt	960
attggtggag gaatctttc aacaacaggc atgttacatg gaattggaaa atttata	1020
gaaataattt gctgtcg当地 cagacttggc tcctataaac ctgtcaattc tgccctt	1080
gaggatggcc acacagacaa ccacttaccc cttttagaaa ataatacaca ttga	1134

<210> 222

<211> 377

<212> PRT

<213> human organism

<400> 222

Met Arg Arg Leu Asn Arg Lys Lys Thr Leu Ser Leu Val Lys Glu Leu			
1	5	10	15

Asp Ala Phe Pro Lys Val Pro Glu Ser Tyr Val Glu Thr Ser Ala Ser		
20	25	30

Gly Gly Thr Val Ser Leu Ile Ala Phe Thr Thr Met Ala Leu Leu Thr		
35	40	45

Ile Met Glu Phe Ser Val Tyr Gln Asp Thr Trp Met Lys Tyr Glu Tyr		
50	55	60

Glu Val Asp Lys Asp Phe Ser Ser Lys Leu Arg Ile Asn Ile Asp Ile

65	70	75	80
Thr Val Ala Met Lys Cys Gln Tyr Val Gly Ala Asp Val Leu Asp Leu			
85	90	95	
Ala Glu Thr Met Val Ala Ser Ala Asp Gly Leu Val Tyr Glu Pro Thr			
100	105	110	
Val Phe Asp Leu Ser Pro Gln Gln Lys Glu Trp Gln Arg Met Leu Gln			
115	120	125	
Leu Ile Gln Ser Arg Leu Gln Glu Glu His Ser Leu Gln Asp Val Ile			
130	135	140	
Phe Lys Ser Ala Phe Lys Ser Thr Ser Thr Ala Leu Pro Pro Arg Glu			
145	150	155	160
Asp Asp Ser Ser Gln Ser Pro Asn Ala Cys Arg Ile His Gly His Leu			
165	170	175	
Tyr Val Asn Lys Val Ala Gly Asn Phe His Ile Thr Val Gly Lys Ala			
180	185	190	
Ile Pro His Pro Arg Gly His Ala His Leu Ala Ala Leu Val Asn His			
195	200	205	
Glu Ser Tyr Asn Phe Ser His Arg Ile Asp His Leu Ser Phe Gly Glu			
210	215	220	
Leu Val Pro Ala Ile Ile Asn Pro Leu Asp Gly Thr Glu Lys Ile Ala			
225	230	235	240
Ile Asp His Asn Gln Met Phe Gln Tyr Phe Ile Thr Val Val Pro Thr			
245	250	255	
Lys Leu His Thr Tyr Lys Ile Ser Ala Asp Thr His Gln Phe Ser Val			
260	265	270	
Thr Glu Arg Glu Arg Ile Ile Asn His Ala Ala Gly Ser His Gly Val			
275	280	285	
Ser Gly Ile Phe Met Lys Tyr Asp Leu Ser Ser Leu Met Val Thr Val			
290	295	300	

Thr Glu Glu His Met Pro Phe Trp Gln Phe Phe Val Arg Leu Cys Gly  
305 310 315 320

Ile Val Gly Gly Ile Phe Ser Thr Thr Gly Met Leu His Gly Ile Gly  
325 330 335

Lys Phe Ile Val Glu Ile Ile Cys Cys Arg Phe Arg Leu Gly Ser Tyr  
340 345 350

Lys Pro Val Asn Ser Val Pro Phe Glu Asp Gly His Thr Asp Asn His  
355 360 365

Leu Pro Leu Leu Glu Asn Asn Thr His  
370 375

<210> 223  
<211> 3407  
<212> DNA  
<213> human organism

<400> 223  
cgcgcggtctc cgccgcccgc gtgacttctg cctgcgtcc ttctctgaac gtcacttcc 60.  
gaggagacgc cgacgatgaa gacaccgtgg aagattcttc tgggactgct gggtgctgct 120  
gcgcttgtca ccatcatcac cgtgcccgtg gttctgctga acaaaggcac agatgatgct 180  
acagctgaca gtcgaaaaac ttacactcta actgattact taaaaataac ttatagactg 240  
aagttatact ccttaagatg gatttcagat catgaatatc tctacaaaca agaaaataat 300  
atcttggtat tcaatgctga atatggaaac agtcagttt tcttggagaa cagtagattt 360  
gatgagtttg gacattctat caatgattat tcaatatctc ctgatggca gtttattctc 420  
ttagaataca actacgtaa gcaatggagg cattcctaca cagttcata tgacattat 480  
gatttaaata aaaggcagct gattacagaa gagaggattc caaacaacac acagtggtc 540  
acatggtcac cagtggtca taaattggca tatgttggc acaatgacat ttatgttaaa 600  
attgaaccaa atttaccaag ttacagaatc acatggacgg ggaaagaaga tataatata 660  
aatgaaataa ctgactgggt ttatgaagag gaagtcttca gtgcctactc tgctctgtgg 720  
tggtctccaa acggcacttt ttttagcatat gcccaattta acgacacaga agtcccactt 780  
attgaatact ctttctactc tgatgagtca ctgcagttacc caaagactgt acgggttcca 840  
tatccaaagg caggagctgt gaatccaact gtaaagttct ttgttgtaaa tacagactct 900

ctcagctcag tcaccaatgc aacttccata caaatcactg ctccctgcttc tatgttgata 960  
gggatcaact acttgtgtga tgtgacatgg gcaacacaag aaagaatttc tttgcagtgg 1020  
ctcaggagga ttccagaacta ttccggcatg gatatttgcg actatgtga atccagtgga 1080  
agatggaact gcttagtggc acggcaacac attgaaatga gtactactgg ctgggttgg 1140  
agatttaggc cttcagaacc tcattttacc cttgatggta atagcttcta caagatcatc 1200  
agcaatgaag aaggttacag acacattgc tatttccaaa tagataaaaaa agactgcaca 1260  
tttattacaa aaggcacctg ggaagtcatc gggatagaag ctctaaccag tgattatcta 1320  
tactacatta gtaatgaata taaaggaatg ccaggaggaa ggaatcttta taaaatccaa 1380  
cttattgact atacaaaagt gacatgcctc agttgtgagc tgaatccgg aaggtgtcag 1440  
tactattctg tgtcattcag taaagaggcg aagtattatc agctgagatg ttccggcct 1500  
ggtctgcccc tctatactct acacagcagc gtgaatgata aagggctgag agtcctggaa 1560  
gacaattcag ctttgataa aatgctgcag aatgtccaga tgccctccaa aaaactggac 1620  
ttcatttattt tgaatgaaac aaaattttgg tatcagatga tcttgccccc tcattttgat 1680  
aaatccaaga aatatcctct actatttagat gtgtatgcag gcccatgtag tcaaaaagca 1740  
gacactgtct tcagactgaa ctgggccact taccttgcaaa gcacagaaaa cattatagta 1800  
gctagctttg atggcagagg aagtggttac caaggagata agatcatgca tgcaatcaac 1860  
agaagactgg gaacatttga agttgaagat caaattgaag cagccagaca attttccaaa 1920  
atgggatttg tggacaacaa acgaattgca atttggggct ggtcatatgg agggtagtca 1980  
acctcaatgg tcctgggatc gggaaagtggc gtgttcaagt gtggaatagc cgtggcgct 2040  
gtatcccggt gggagttacta tgactcagtg tacacagaac gttacatggg tctcccaact 2100  
ccagaagaca accttgacca ttacagaaat tcaacagtca tgagcagagc tgaaaaatttt 2160  
aaacaagttg agtacccct tattcatggc acagcagatg ataacgttca ctttcagcag 2220  
tcagctcaga tctccaaagc cctggcgtat gttggagtgg atttccagggc aatgtggtat 2280  
actgatgaag accatggaat agcttagcagc acagcacacc aacatatata taccacatg 2340  
agccacttca taaaacaatg tttctttta ctttagcacc tcaaaaatacc atgcattta 2400  
aagcttatta aaactcattt ttgttttcat tatctcaaaa ctgcactgtc aagatgtga 2460  
tgatcttaa aatacacact caaatcaaga aacttaaggt tacctttgtt cccaaatttc 2520  
atacctatca tcttaagtag ggacttctgt ctccacaaca gattattacc ttacagaagt 2580

ttgaattatc	cggtcgggtt	ttattgtta	aatcatttc	tgcatacgct	gctgaaacaa	2640
caaataaggaa	ttgttttat	ggaggcttg	catagattcc	ctgagcagga	tttaatctt	2700
tttctaactg	gactggttca	aatgttgttc	tcttctttaa	agggatggca	agatgtggc	2760
agtatgtca	ctagggcagg	gacaggataa	gagggattag	ggagagaaga	tagcagggca	2820
tggctggaa	cccaagtcca	agcataccaa	cacgagcagg	ctactgtcag	ctcccctcgg	2880
agaagagctg	ttcaccacga	gactggcaca	gttttctgag	aaagactatt	caaacagtct	2940
cagaaaatca	aatatcgaaa	gcaactgactt	ctaagtaaac	cacagcagtt	gaaagactcc	3000
aaagaaaatgt	aaggaaact	gccagcaacg	cagccccag	gtgccagtta	tggctatagg	3060
tgctacaaaa	acacagcaag	ggtgatggaa	aagcattgta	aatgtgctt	aaaaaaaaaa	3120
tactgatgtt	cctagtgaaa	gaggcagctt	gaaactgaga	tgtgaacaca	tcagcttgcc	3180
ctgttaaaag	atgaaaatat	ttgtatcaca	aatcttaact	tgaaggagtc	cttgcataaa	3240
tttttcttat	ttcatttctt	tgagtgtctt	aattaaaaga	atatttaac	ttccttggac	3300
tcattttaaa	aatggaaca	taaaatacaa	tgttatgtat	tattattccc	attctacata	3360
ctatggaatt	tctcccagtc	attnataaaa	tgtgccttca	ttttttc		3407

<210> 224

<211> 766

<212> PRT

<213> human organism

<400> 224

Met	Lys	Thr	Pro	Trp	Lys	Ile	Leu	Leu	Gly	Leu	Leu	Gly	Ala	Ala	Ala
1					5			10				15			

Leu	Val	Thr	Ile	Ile	Thr	Val	Pro	Val	Val	Leu	Leu	Asn	Lys	Gly	Thr
					20			25				30			

Asp	Asp	Ala	Thr	Ala	Asp	Ser	Arg	Lys	Thr	Tyr	Thr	Leu	Thr	Asp	Tyr
					35			40				45			

Leu	Lys	Asn	Thr	Tyr	Arg	Leu	Lys	Leu	Tyr	Ser	Leu	Arg	Trp	Ile	Ser
					50			55				60			

Asp	His	Glu	Tyr	Leu	Tyr	Lys	Gln	Glu	Asn	Asn	Ile	Leu	Val	Phe	Asn
						65		70			75			80	

Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu Glu Asn Ser Thr Phe Asp

85

90

95

Glu Phe Gly His Ser Ile Asn Asp Tyr Ser Ile Ser Pro Asp Gly Gln  
100 105 110

Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys Gln Trp Arg His Ser Tyr  
115 120 125

Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn Lys Arg Gln Leu Ile Thr  
130 135 140

Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp Val Thr Trp Ser Pro Val  
145 150 155 160

Gly His Lys Leu Ala Tyr Val Trp Asn Asn Asp Ile Tyr Val Lys Ile  
165 170 175

Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr Trp Thr Gly Lys Glu Asp  
180 185 190

Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val Tyr Glu Glu Val Phe  
195 200 205

Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala  
210 215 220

Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro Leu Ile Glu Tyr Ser Phe  
225 230 235 240

Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys Thr Val Arg Val Pro Tyr  
245 250 255

Pro Lys Ala Gly Ala Val Asn Pro Thr Val Lys Phe Phe Val Val Asn  
260 265 270

Thr Asp Ser Leu Ser Ser Val Thr Asn Ala Thr Ser Ile Gln Ile Thr  
275 280 285

Ala Pro Ala Ser Met Leu Ile Gly Asp His Tyr Leu Cys Asp Val Thr  
290 295 300

Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln Trp Leu Arg Arg Ile Gln  
305 310 315 320

Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr Asp Glu Ser Ser Gly Arg  
325 330 335

Trp Asn Cys Leu Val Ala Arg Gln His Ile Glu Met Ser Thr Thr Gly  
340 345 350

Trp Val Gly Arg Phe Arg Pro Ser Glu Pro His Phe Thr Leu Asp Gly  
355 360 365

Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu Glu Gly Tyr Arg His Ile  
370 375 380

Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys Thr Phe Ile Thr Lys Gly  
385 390 395 400

Thr Trp Glu Val Ile Gly Ile Glu Ala Leu Thr Ser Asp Tyr Leu Tyr  
405 410 415

Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro Gly Gly Arg Asn Leu Tyr  
420 425 430

Lys Ile Gln Leu Ile Asp Tyr Thr Lys Val Thr Cys Leu Ser Cys Glu  
435 440 445

Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser Val Ser Phe Ser Lys Glu  
450 455 460

Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly Pro Gly Leu Pro Leu Tyr  
465 470 475 480

Thr Leu His Ser Ser Val Asn Asp Lys Gly Leu Arg Val Leu Glu Asp  
485 490 495

Asn Ser Ala Leu Asp Lys Met Leu Gln Asn Val Gln Met Pro Ser Lys  
500 505 510

Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr Lys Phe Trp Tyr Gln Met  
515 520 525

Ile Leu Pro Pro His Phe Asp Lys Ser Lys Lys Tyr Pro Leu Leu Leu  
530 535 540

Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys Ala Asp Thr Val Phe Arg  
545 550 555 560

Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala  
565 570 575

Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His  
580 585 590

Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu  
595 600 605

Ala Ala Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asn Lys Arg Ile  
610 615 620

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu  
625 630 635 640

Gly Ser Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val  
645 650 655

Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr Thr Glu Arg Tyr Met Gly  
660 665 670

Leu Pro Thr Pro Glu Asp Asn Leu Asp His Tyr Arg Asn Ser Thr Val  
675 680 685

Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His  
690 695 700

Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Ile Ser  
705 710 715 720

Lys Ala Leu Val Asp Val Gly Val Asp Phe Gln Ala Met Trp Tyr Thr  
725 730 735

Asp Glu Asp His Gly Ile Ala Ser Ser Thr Ala His Gln His Ile Tyr  
740 745 750

Thr His Met Ser His Phe Ile Lys Gln Cys Phe Ser Leu Pro  
755 760 765

<210> 225  
 <211> 261  
 <212> DNA  
 <213> human organism

<400> 225  
 atggctctgg cgaaggtagag ggagccaaac gcaaattgaca atgccccatcag agttgacaac 60  
 agaagtgtga ttaaaggtagcg tgcttaaccag tgttccctgc atgaggcaga aagtgaatcc 120  
 agaaaaccctc aggagctctg gatgggcctg ctcccttga tgggggtcct agaagcatgt 180  
 gtggaaatga ggcctctgtc agtctggtcc ctgagagatg acaaggagca gagcccccac 240  
 cagccccacac tggatgtcta a 261

<210> 226  
 <211> 86  
 <212> PRT  
 <213> human organism

<400> 226  
 Met Ala Leu Ala Lys Val Arg Glu Pro Asn Ala Asn Asp Asn Ala Ile  
 1 5 10 15

Arg Val Asp Asn Arg Ser Val Ile Lys Val Arg Ala Asn Gln Cys Ser  
 20 25 30

Leu His Glu Ala Glu Ser Glu Ser Arg Asn Pro Gln Glu Leu Trp Met  
 35 40 45

Gly Leu Leu Leu Met Gly Val Leu Glu Ala Cys Val Glu Met Arg  
 50 55 60

Pro Leu Ser Val Trp Ser Leu Arg Asp Asp Lys Glu Gln Ser Pro His  
 65 70 75 80

Gln Pro Thr Leu Asp Val  
 85

<210> 227  
 <211> 462  
 <212> DNA  
 <213> human organism

<400> 227  
 atgccaaatg ctgagttaga agcaaagagc cttggaaagca gttaaatgttt aaaaaactgct 60  
 ctcataacttg ctgtatgttg tggatcagca aatatagtca gccctctact tgagcaaat 120

attgatgtat	cttctcaaga	tctggacaga	cggccagaga	gtatgctgtt	tctagtcatc	180
atcatgtgga	ccagtttgt	ggaagacaat	cttccatgg	gctggggaa	gctagaagat	240
tttatggcta	ttgaagaaga	aatgaagaag	cacggaagta	ctcatgtggg	attcccagaa	300
aacctgacta	atggtgcgc	tgctggcaat	ggtgatgatg	gattaattcc	tccaaggaag	360
agcagaacac	ctgaaagcca	gcaatttcct	gacactgaga	atgaagagta	tcacaggaaa	420
gtcaaagatc	agatagttgt	agatatgcgg	cgttatttct	ga		462

<210> 228

<211> 153

<212> PRT

<213> human organism

<400> 228

Met	Pro	Asn	Ala	Glu	Leu	Glu	Ala	Lys	Ser	Leu	Gly	Ser	Ser	Lys	Cys
1				5				10						15	

Leu	Lys	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Asn	Ile
	20					25						30			

Val	Ser	Pro	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	Ser	Gln	Asp	Leu
		35					40					45			

Asp	Arg	Arg	Pro	Glu	Ser	Met	Leu	Phe	Leu	Val	Ile	Ile	Met	Trp	Thr
			50				55				60				

Ser	Phe	Val	Glu	Asp	Asn	Leu	Ser	Met	Gly	Trp	Gly	Lys	Leu	Glu	Asp
	65					70			75			80			

Phe	Met	Ala	Ile	Glu	Glu	Met	Lys	Lys	His	Gly	Ser	Thr	His	Val
			85				90				95			

Gly	Phe	Pro	Glu	Asn	Leu	Thr	Asn	Gly	Ala	Ala	Ala	Gly	Asn	Gly	Asp
			100				105					110			

Asp	Gly	Leu	Ile	Pro	Pro	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Ser	Gln	Gln
			115			120						125			

Phe	Pro	Asp	Thr	Glu	Asn	Glu	Glu	Tyr	His	Arg	Phe	Val	Lys	Asp	Gln
			130			135				140					

Ile Val Val Asp Met Arg Arg Tyr Phe  
145                           150

<210> 229  
<211> 12880  
<212> DNA  
<213> human organism

<400> 229  
gactgcttgc attaaaggac ttccatcc ttttttcatt gaaactgagc ttgcttaatc         60  
agagatggag caaactgact gcaaacccta ccagcctcta ccaaaagtca agcatgaaat         120  
ggatcttagt tacaccagtt ctctgtatga gagtgaagat ggaagaaaac caagacagtc         180  
atacaactcc agggagaccc tgacgagta taaccaggag ctgaggatga attacaatag         240  
ccagagtaga aagagggaaag aagttagaaaa atctactcaa gagatgaaat tctgtgaaac         300  
ctctcacact ctgtgctctg gctaccaaacc acatgcac agcgttctc ggcattggcta         360  
ccagctagag atgggatctg atgtggacac agagacagaa ggtgctgcct cacctgacca         420  
tgcaactaaga atgtggataa gggaaatgaa atcagagcat agttcctgtt tgtccagccg         480  
ggccaactct gcattatcct tgactgacac tgaccatgaa aggaagtctg atggggaaaa         540  
tggtttcaaa ttctctcctg ttttgtgtga catggaggct caagctgggt ctactcaaga         600  
tgtgcagagc agccccacaca accagttcac ctccagaccc ctcccacccg cacctccgccc         660  
tcctcatgcc tgcacccgtg ccaggaagcc accccctgca gcggactctc ttcagaggag         720  
atcaatgact acccgccagcc agccccagccc agctgctcca gctcccccaa ccagcacgca         780  
ggattcagtc catctgcata acagctgggt cctgaacagc aacataaccat tggagaccag         840  
gcattccctg ttcaaacatg gatctggttc ctctgcgtac ttcaagtgcag ccagtcagaa         900  
ctaccctctg acatccaata ccgtgtactc gccccctccc aggccctttc ctcgaagcac         960  
ctttccccga cctgccttta cctttaacaa accttacagg tgctgcaact ggaagtgcac         1020  
agcattgagc gccactgcaa tcacagtgac tttggccttg ttactagcct atgtgattgc         1080  
agtgcatttg ttggcctga ctggcagtt gcaaccagtt gaaggagagc tgtatgcaaa         1140  
tggagtttagc aaagggaaca gggggaccga gtccatggac actacttact ctccaattgg         1200  
aggaaaaagtt tctgataaat cagagaaaaaa agtgtttcag aaggacggg cgatagacac         1260  
tggagaagtt gacattggtg cacaggtcat gcagaccatt ccacccgtt tattctggcg         1320  
tttccagatt actatccacc atccaaatata tctgaagttc aatatttctt tagccaagga         1380  
ctctctgctg ggaatttatg gcagaagaaa cattccaccc acacataactc agtttgattt         1440

tgtaaaacta atggatggca aacagctgg tccaagggt ctgatgatac 1500  
acagcaactcc cctcggaacc tgatcttaac ttgcgttcag gagacagggt tcataagaga 1560  
tatggatcaa ggaccttggt atctggcggt ttacaatgtat ggaaaaaaaaga tggagcaagt 1620  
attcgtgtta actacagcaa ttgaaataat ggatgactgt tcaaccaatt gcaatggaaa 1680  
tggagagtgt atctctggcc attgtcattt tttcccagga ttccttggac ctgactgtgc 1740  
tagagattcc tgccctgtgc tgtgtggtgg gaatggagaa tacgagaaag gacactgtgt 1800  
ctgccggcat ggctggaagg ggcagagtg tgacgttccg gaagaacaat gcattgatcc 1860  
aacatgcttt ggccacggca cctgcattcat gggagtctgc atctgtgtgc caggatacaa 1920  
aggagaaaata tgcgaggaag aggactgcct agacccaatg tttccaacc atggcatctg 1980  
tgtaaaagga gaatgtcaact gttctactgg ctggggagga gttaactgtg aaacaccact 2040  
tcctgtatgt caagagcagt gctcaggaca cgaaactttt cttctggacg ctggagtatg 2100  
cagctgtatgt cccaaatggc caggatctga ctgctcaaca gagctgtgtt ccatggagtg 2160  
tggtagccat ggagtctgct caagaggaat ttgccagtgt gaagaaggct ggtaggacc 2220  
aacatgtgag gaacgctcct gtcattctca ttgtactgag catggccaaat gcaaagatgg 2280  
aaaatgtgag tgttagccctg gatggggaggg cgaccactgc acaattgctc actacttaga 2340  
tgctgtccga gatggctgcc cagggctctg ctttggaaat ggacgtgtt ccctggatca 2400  
aaatgggtgg cactgtgtgt gtcagggtggg ttggagtgaa acaggctgca atgttgcata 2460  
ggaaatgctt tgtggagata acttggacaa tggatggatgt ggtttaaccg actgtgtgg 2520  
tcctgactgt tgtcaacaaa gcaactgtta tataagtccct ctctgccagg gtcaccaga 2580  
tcctcttgac ctcattcagc aaagccaaac tctcttcct cagcacactt caagactttt 2640  
ttatgatcga atcaaattcc tcattggcaa ggacagtact catgtcattc ctcctgaggt 2700  
gtcatttgac agcaggcgtg cctgtgtatgt tcgaggccaa gtggggccaa tagatggaaac 2760  
tcctcttagtg ggagtgaatg tcagtttctt gcaccacagt gattatgggt ttaccatcag 2820  
ccggcaagat ggaagctttg acctcggtggc catcggtggc atctctgtca tcttaatctt 2880  
cgaccgatcc ctttcctgc ctgagaagag aacactctgg ttgccttggaa atcagtttat 2940  
tgtggtagag aaagtcacca tgcagagagt tgtatcagac ccgcacatccct gcgatatctc 3000  
caactttatc agccccaaacc ctattgtgct tccttcaccg ctcacatcat ttggagggtc 3060  
ctgtccagag aggggaacta ttgttcctga gctgcagggtt gtacaggagg aaattcccat 3120

tccctccagc tttgtgaggc tgagttacct gagcagccgc accccctgggt ataaaaccct 3180  
gctacggatc cttctgacac attcaacgat tcccgttaggc atgataaaag tacacctcac 3240  
atgtatgtg gaagggcgac tcacacagaa gtggttccc gccgcaatta atcttgtcta 3300  
cacatttgc tggacaacaaga ccgatatcta tggacagaag gtttggggcc tggcagaggc 3360  
tttggtatct gtgggatatg aatatgaaac gtgcctgac tttattctct gggagcaaag 3420  
gacagtcgtt ttacaagggtt ttgagatgga tgcttctaac ctaggagact ggtcttgaa 3480  
taagcatcac attttgaatc ctcaaaagtgg aatcatacat aaaggaaatg gagaaaatat 3540  
gttcatttcc cagcagcccc cagtcataatc aaccataatg ggtaatggac accaaaggag 3600  
tgtagcctgc accaactgca atggcccgac ccacaacaac aaactctttg ctccctgtcgc 3660  
cttagcttct ggccctgatg gcagtgtgta tggtggcgac ttcaattttg taaggagaat 3720  
atttccctcg ggaaactccg ttagtatttt ggaattaagc acaagtccctg ctcacaaata 3780  
ctatctggct atggaccctg tgtctgaatc actctatcta tcagacacca atactcgcaa 3840  
agtctacaag ttgaaatctc ttgtggagac gaaagatctg tccaagaatt ttgaagtgg 3900  
ggcaggaact ggtgatcagt gccttccctt tgaccagagt cattgtggag atgggtggag 3960  
agcatcgaa gcttcactga atagccctcg aggcatacaca gttgataggc atggatttat 4020  
ttactttgtg gatggacta tgattcgcaa aattgatgag aatgctgtga tcacaactgt 4080  
aatcggctca aatggctga ctccacaca accactgagc tgtgactcag gaatggacat 4140  
cactcaggtg cgatttaggtt ggccaaacaga ctttcagta aatcctatgg acaattcatt 4200  
gtatgtcttgc gataacaaca ttgtgctgca aatttctgag aacaggcggt ttcggatcat 4260  
cgcaggacgc cccatttact gccagggtgcc aggcatcgat catttcctgg tcagcaaggt 4320  
agcaattcac tccactctag agtcagcgag ggccatcagt gtctcccaca gcgggctgt 4380  
cttcatacgat gaaacagacg agaggaaagt aaaccgcatt cagcaagtaa ccaccaatgg 4440  
ggagatctac atcatcgctg gtgcacccac tgactgtgac tgcaaaattt atccaaactg 4500  
tgactgtttt tcaggtgatg gtggctatgc caaagatgca aagatgaaag ccccttcctc 4560  
cttagcagtgc tcgcctgatg gaaccctcta tgtggcagac ctcggaaatg ttcgaattcg 4620  
taccatcagc aggaaccaag cccacctgaa tgacatgaac atttatgaga ttgcttcacc 4680  
cgctgatcag gaactgtacc agttcactgt aaatggaacc cacctacaca ccctgaactt 4740  
gataacaagg gactatgttt ataacttcac ctacaattct gaaggtgact tggggcgat 4800  
taccagcagc aatggcaatt cagtgcacat tcgcccgtatg gcaggcgaa tgccgctatg 4860

gcttgtggc cctggcgac aagtatactg gctgactata agcagcaatg gagtcctgaa 4920  
aagagtgtca gcccaaggct ataatccggc cttaatgacc tatccaggaa acacagggct 4980  
tctggctacc aaaagtaacg aaaatggatg gacaaccgtt tatgagtgatg accccgaggg 5040  
acacctgacc aatgcaacgt ttcccactgg agaggtcagc agttccaca gtgacctgga 5100  
gaagctgaca aaagtggagc tagatacttc caaccgtgaa aatgtcctca tgtcaaccaa 5160  
cttgacggca actagtagcca tatatatattt aaaacaagaa aatactcaaa gtacctatcg 5220  
ggtgaatcca gatggttccc tgcgtgtcac tttgccagc gggatggaga tcggcctcag 5280  
ctcagagccc cacatcctgg cagggcagt caaccctacc ctgggcaaatt gcaacatctc 5340  
attgcccgg a gacacaatg caaacctcat cgagtggcgg cagaggaagg agcaaaacaa 5400  
aggcaatgtt tcggctttt g a a a g g a g g c t g a g g a c c a a a a a c a a a 5460  
agatttgat catataaccc gcacaggaaa gatctatgat gaccatcgaa aattcaccct 5520  
tcgaattctt tatgaccaga ctggcgacc cattctgtgg ttcctgtaa gcagatataa 5580  
tgaagtgaac atcacatatt cacttcggg attggtgacg ttattcaaa gaggaacgtg 5640  
gaatgaaaaa atggaatatg accagagtgg gaaaattatt tcaagaactt gggctgatgg 5700  
gaaaattgg agctataacct acttagaaaa atctgtgatg cttctcctac acagccagcg 5760  
gcgttacatc tttgagtgatg accaattcaga ttgcctgctg tcagttacca tgcctagcat 5820  
ggtgccgac acgttacaaa ccatgcttc agtggctac taccgtata tctacacccc 5880  
accggacagt agcacttctt ttatccaaga ctatagtcga gatggccgat tgctacagac 5940  
cctgcacatcg gggacagggc gcagagtctt atacaagtac accaagcaag caaggcttc 6000  
tgaggttctc tatgataccca ctcaggtcac attaacatata gaagagtctt ctggagtgtat 6060  
taagacaata cacctgatgc atgacggatt catctgcaca atcagataca ggcaaacagg 6120  
acctcttatt ggacgccaga tttcagatt cagtgaagaa ggccttgtga atgcacggtt 6180  
cgactacagc tacaacaatt tccgagtcac aagcatgcaa gctgtatca atgaaacccc 6240  
tttgcctata gatcttacc gatatgttgatgttgttgc agaacagagc agtttgaaa 6300  
attcagtgtatattaaatca ggtcataact actacagtga tgaaacacac 6360  
caaaatcttc agtgccaaatg gacaagtcat tgaagtccaa tatgaaatcc taaaggcaat 6420  
tgcctactgg atgaccattc aatatgataa tgtggccga catgtataa tgtgcataag 6480  
ggttaggagta gatgccaata taacaaggta cttctatgaa tacgtatgctg atggcaact 6540

tcagactgtt tctgtaaaatg acaaaaaccca gtggcggttat agttacgatc tgaatggaga 6600  
catcaacctc ttaagccatg ggaagagtgc tcgtcttact cctctccgat atgacctccg 6660  
agaccgcatac accagattag gagaaattca gtataaaatg gatgaagatg gctttctgag 6720  
gcagagggga aatgatattt ttgaatataa ttctaattggc ctgctgcaga aagcctacaa 6780  
taaggcttct ggctggactg tgcagtatta ctatgatggg cttgggcgac gtgtcgcgag 6840  
taagtccagc ctagggcagc accttcagtt ctttgcgac gcgaccgcga accccataag 6900  
agttactcat ttgtacaacc acacaagctc ggagattaca tctctgtatt atgatctcca 6960  
aggtcacctt attgccatgg agttaagcag tggtaagaa tattatgttag cctgtgataa 7020  
tacaggtacc ccactagctg tggtcagcag ccgaggtcag gtcataaagg agatactata 7080  
cacaccttat ggcgatatact atcatgacac ttaccctgac tttcaggtca taattggtt 7140  
tcatggagga ctctatgatt tccttactaa attagtgcac ctggggcaaa gggattatga 7200  
tggtgtgct ggcagatgga caacggccta tcatcacata tggaaacagt tgaacctcct 7260  
tcctaaacca ttcaacctct actccttga aaataactac ccagttggca aaattcaaga 7320  
tggtgcaaag tataccacag acatcagaag ttgggtggag ctatttggtt tccaattaca 7380  
caatgtacta cctggatttc ccaaaccctga attagaaaat ttagaattaa cttacgagct 7440  
tctacggctt cagacaaaaa ctcaagagtg ggatcctgga aagactatcc tggcattca 7500  
gtgtgaactc cagaaacagc tcaggaattt catttccttg gaccaactac ctatgactcc 7560  
ccgatacaat gatggacggt gccttgaagg agggaaagcaa ccaaggttt ctgctgtccc 7620  
ttctgtttt gggaaaggta taaaatttgc catcaaggat ggcatagtaa cagctgat 7680  
tataggagta gccaatgaag atagcaggcg gcttgcgtcc attctcaata atgcccatta 7740  
cctggaaaac ctacatTTTA ccatagaggg gagggacact cactacttca ttaagcttgg 7800  
gtctctggag gaagacctgg tgctcatcg 1 taacactggg gggaggcgg 1 ttctggagaa 7860  
tggtgtcaat gtcactgtgt cccagatgac ttctctgttg aatggggagga ctagacggtt 7920  
tgcaagatattt cagctccagc atggagccct gtgctcaac atccggat 1 ggacaactgt 7980  
cgaagaggaa aagaatcactg tggggat tgccagacag cgccgagtgg cccaggcctg 8040  
gactaaggaa caaagaaggc tgcaagaggg ggaagagggg attagggcat ggacagaagg 8100  
ggaaaaggcag cagctttga gcactggcg ggtacaagg 1 tacgatgggt attttgg 8160  
gtctgttggag cagtatttag aactttctga cagtgc 1 aatattcact ttatgagaca 8220  
gagcgaaata ggcaggaggt aacaaaaata tctctgcctt tgcgtcacca aagactgcct 8280

gtttttaaaa cataaaatgg tttattgtat tggtttcta gatcagaact ctgtatatgt 8340  
aaatatggag gaaaaacata tccaactgcc tttcaatgtg acggaagatg gtatttaat 8400  
attgtttgtt taaactctt aagaaatgac agagatttt agttcttgc tggcagtatt 8460  
caaaaataaca caagtagaac tcaaacagct aaaaacagtt ttcagaaagc accacttca 8520  
atttgcgag ccatgcata tttccatat ccagaaagaa cccaaaggatc tctatctcta 8580  
tttgtgagaag cagtttcata tttcaactgtt ggcagaactt acgggctatt tgaataggtg 8640  
gtgcaatagt atctgaaact tgccttcga aagactgcc a gcccttgac gtttccaga 8700  
tctgttatag gaaacttaaa aacaggtgt aaatgtctt agccaccatc tcctagatg 8760  
aggaccaat tgcccttcct ttttgattat tcctccttgc ttgttaaagt aatgccata 8820  
ttgttgtgct gtgtttggc gtgtggtgc tgggttctgt ctaccatgtc tccctgtgg 8880  
tgtggtaacc agactgtata gccgctattt gctcggtgt acatgataacc aaagcagctg 8940  
gccagcgtga cctcttcac acgacctgtt ttgactcaat ttttactaa aagttgtca 9000  
gctgtattgg tatcatgtaa acatagctt tattaacctg gtaggaatt tctcatttat 9060  
atataaggatg tggtttggc atagttcac attagtgatt cagtagtcat acactgaccc 9120  
aatggtttg tgcacatgaa cgtaattt cttaaaagta tgattctgg aaaaaacaa 9180  
acaaaggctt tagcaggcat acgtgtctgg gatgccata catacattaa ctactactgc 9240  
agaaattcat aagagccaaa acctaaaaaa aatagacctg gtacttaagt gaaagtacta 9300  
aagggaaagac cagaccaaac atcacagcag ttgctgccac attgtttcag cccacttaga 9360  
tttatcttc aatgtacaa ttctgtattt aacatctccc agccatctt aggaaatcga 9420  
atcaagtaaa tcctttccaa ccgaaaacat ttcaactaac tatagagagg cagactcatt 9480  
tttactaaaa taatttatac agtttagttt ttctgtctc cgtacttacc catttatctt 9540  
tatttaatcg tctctactgc ctagaaaaat aactatttc caggacgggt tatttgttct 9600  
gcgatcattt aaaatttgg aaaaaggatcag gattagtgtt aatatcagct gcaatgttc 9660  
aatctctagg aatcctgcag taaaacaagc cccttggta gctggaaagat ttgtgcccag 9720  
tgacaaaagag atagttgtt aatgtgttgc taattgttgc ttaccacaaa tgaaaataca 9780  
tgacagcaca atgtggccccg tagaaaattc ccctgagcca gcttctgcac tttcatcacc 9840  
gaatctgaac atttgctatg tctgaaggca aatttatgtt ggaatgttag tttggattct 9900  
ttccagatgc tacctaaatg cagtgtgggg tcattgcctt gctttgcgt gacagttct 9960

ttgaaaatat gcaaagtcat aagctcatgt taaggaaaa caagagtctg ctcctacta 10020  
cacaaaggaa agcaaggaa aggaaatgac cctggcaaac agtaggaaag ggtgtattca 10080  
aacatttcat tttcaaaacc ttccgggttag aataccactt acacatgtat tctgagagac 10140  
agaattcatg aggaactcat ctctcttat aactggaaac acaccagctt gatatattgc 10200  
taatccatac taaaatcata ttattgggtt tttctgaat caggcctgta ttaatggta 10260  
agtatttatt cagaatggaa ttctaaaatt actaacaac ttgttggaaa tttgaatacc 10320  
tccacaccaa cctaaaaatg gacctaagt tcctagaacc tctgatgttc tttaaatta 10380  
atgaaaaat aatttgtgaa ctgtatatacg agagtgcatt cataaatgtt attatgtatt 10440  
ttatcacaaa tccaaaatgt caatattaga gtctatttg cttatattt aagcaattat 10500  
acgaaaaatgc aattcattga tgatgtatca tttcaact gctttaata tccattagaa 10560  
acaaatattt gaagcttta cttaatagtg attaccttga actgtgcatt tctagttgt 10620  
aatacgtatt tgggtggttc gtgcctttag tttgtttaag ttacatttgtt attatattca 10680  
ggaaatgcac ttttatttac ttacagctgt ggaaaaataa ctgccttggaa ctattattat 10740  
tcttttaca actcctaaag ctgggggag gaaagaaaaa aaaaacaaaaa ctactaatca 10800  
gtagtaaattc gaagagaaac atttggcat ttcttaagaa gaagatggag atattgagta 10860  
tatcacttcc tattcagctg aatagaaaaga atgccttcat tgacttgcag ttctgcagtt 10920  
taaatttatttgc aaagaacaat tcgaaaatgc ttccctgatga aagtaaaagc attttcaga 10980  
gaaacatatg aatttctcat acccagcaga cagatggctg acactgcaca gccacacacc 11040  
attcgagtaa gttaaagtga gagcatagta gttggactct cctatgaaga acattctggg 11100  
ctggaggcag ggaataactcc atgggtgtt cttttccta cttaaagccca ttttgggtt 11160  
gctttctgt tttgtttgt tttcactctt gcactacagt cttagatcc aatgaactg 11220  
aaaagttcaa agtttaacac atttaaatat gtttactttt agttgtcatt ctaatcgta 11280  
ttgattagaa gcatgactcc tgaaggaaag gggaaataat ctcatttcat actaacttgc 11340  
aacaaaaacac ttttaccata taaaataagta tatgattttt ttttaaccac aaaaatgtat 11400  
aaaataagtg tgtcctttac tgtcaatttgc tcgagaagat ctataatata tagactacat 11460  
atataataata tataacaacat agccaaatgt atgaaaactt gacaatgtat aatttggaaat 11520  
tcacatgcta cctatgtaga caggtatgaa attaagttt aattttcatg agacattttc 11580  
atcactgttgc acacagtttc aaggcattcc atcatgttat tttgactctt tttctttttt 11640  
ttttctttaa aatataattt ttaacttagac caggccccac tataatatac cttaaagagag 11700

tcagggcaaa gttttgcat ttatgaagat gtgttcatgt aagggtgatt gtaatggagt 11760  
tcattggtaa tagaagcaaa agtacagtaa cgaagtattg aaaagaaaaat tttggagaca 11820  
ttggagcata ttatatatag cttgtggaaa gacataaggc tacagatgga atggaacatt 11880  
cctgtttct tgaagaaatt cacatacaca tagctgacct gactagtact tcagctttc 11940  
cacagccttc tataaagggtt ctttcttctg caaagaaaac aaaacaaaac aaaacaaaac 12000  
aaaaaaaaac aaaaaaagcg caaaaaacaa aaaaacaaaaaaaag taaaattaa 12060  
aaatacagaa aacaaacaac aaaaaagaat tcaaccataa atagtgacta ttatttcag 12120  
tgtgtccttc atgtgaaagc tattaaggac caaatatact actgttcata agaagaatt 12180  
actttctaaa cagtaactga aaatacttag agttaaactt gctgtggatt ttgtcttgc 12240  
agttgtcatc ttacattatt tgtcaaagga aatgtgttg gcagttaaaa atcttcctt 12300  
agatttatgt gtggacttta acctcttaaa taaatgttag tatatcagat tgtgtcctt 12360  
aaaaatattt tacttgatg aatcatgaca acgtctaaat cttaacttattt cttctggcaa 12420  
aagcatcagt aagaaagaag gcgaaaaaga gaagtatagc cttagtgc gaaaaacatt 12480  
cttttagct gcttacttcc tcatgaaaag taaagatgtt tacagtgtat gccaagttt 12540  
cagttctgt ataacaacag gtagaggttc taatcatatt gaaaattgtg ttataatggt 12600  
ctgagccatg ttgcttaggaa acaatagggtt ccaattttgtt attcctgctc tcctgtgctg 12660  
aaaagtgact ggatactgta caggttcatg ttctctggct gcagttaaat ggtctttgc 12720  
attttgctct ggcttcagg ccagaagcat gcattttct acaagagcat cacaacaaca 12780  
tgctgtaaat atttaaagtt aaacattatg tggtgatatt tgaaagaaaa gtactttgaa 12840  
tatttcattt ttaaaaaata aaattgccaa tgaaaaaaaaa 12880

<210> 230  
<211> 2725  
<212> PRT  
<213> human organism

<400> 230

Met Glu Gln Thr Asp Cys Lys Pro Tyr Gln Pro Leu Pro Lys Val Lys  
1 5 10 15

His Glu Met Asp Leu Ala Tyr Thr Ser Ser Ser Asp Glu Ser Glu Asp  
20 25 30

Gly Arg Lys Pro Arg Gln Ser Tyr Asn Ser Arg Glu Thr Leu His Glu  
35 40 45

Tyr Asn Gln Glu Leu Arg Met Asn Tyr Asn Ser Gln Ser Arg Lys Arg  
50 55 60

Lys Glu Val Glu Lys Ser Thr Gln Glu Met Glu Phe Cys Glu Thr Ser  
65 70 75 80

His Thr Leu Cys Ser Gly Tyr Gln Thr Asp Met His Ser Val Ser Arg  
85 90 95

His Gly Tyr Gln Leu Glu Met Gly Ser Asp Val Asp Thr Glu Thr Glu  
100 105 110

Gly Ala Ala Ser Pro Asp His Ala Leu Arg Met Trp Ile Arg Gly Met  
115 120 125

Lys Ser Glu His Ser Ser Cys Leu Ser Ser Arg Ala Asn Ser Ala Leu  
130 135 140

Ser Leu Thr Asp Thr Asp His Glu Arg Lys Ser Asp Gly Glu Asn Gly  
145 150 155 160

Phe Lys Phe Ser Pro Val Cys Cys Asp Met Glu Ala Gln Ala Gly Ser  
165 170 175

Thr Gln Asp Val Gln Ser Ser Pro His Asn Gln Phe Thr Phe Arg Pro  
180 185 190

Leu Pro Pro Pro Pro Pro His Ala Cys Thr Cys Ala Arg Lys  
195 200 205

Pro Pro Pro Ala Ala Asp Ser Leu Gln Arg Arg Ser Met Thr Thr Arg  
210 215 220

Ser Gln Pro Ser Pro Ala Ala Pro Pro Thr Ser Thr Gln Asp  
225 230 235 240

Ser Val His Leu His Asn Ser Trp Val Leu Asn Ser Asn Ile Pro Leu  
245 250 255

Glu Thr Arg His Ser Leu Phe Lys His Gly Ser Gly Ser Ser Ala Ile

260

265

270

Phe Ser Ala Ala Ser Gln Asn Tyr Pro Leu Thr Ser Asn Thr Val Tyr  
275 280 285

Ser Pro Pro Pro Arg Pro Leu Pro Arg Ser Thr Phe Ser Arg Pro Ala  
290 295 300

Phe Thr Phe Asn Lys Pro Tyr Arg Cys Cys Asn Trp Lys Cys Thr Ala  
305 310 315 320

Leu Ser Ala Thr Ala Ile Thr Val Thr Leu Ala Leu Leu Ala Tyr  
325 330 335

Val Ile Ala Val His Leu Phe Gly Leu Thr Trp Gln Leu Gln Pro Val  
340 345 350

Glu Gly Glu Leu Tyr Ala Asn Gly Val Ser Lys Gly Asn Arg Gly Thr  
355 360 365

Glu Ser Met Asp Thr Thr Tyr Ser Pro Ile Gly Gly Lys Val Ser Asp  
370 375 380

Lys Ser Glu Lys Lys Val Phe Gln Lys Gly Arg Ala Ile Asp Thr Gly  
385 390 395 400

Glu Val Asp Ile Gly Ala Gln Val Met Gln Thr Ile Pro Pro Gly Leu  
405 410 415

Phe Trp Arg Phe Gln Ile Thr Ile His His Pro Ile Tyr Leu Lys Phe  
420 425 430

Asn Ile Ser Leu Ala Lys Asp Ser Leu Leu Gly Ile Tyr Gly Arg Arg  
435 440 445

Asn Ile Pro Pro Thr His Thr Gln Phe Asp Phe Val Lys Leu Met Asp  
450 455 460

Gly Lys Gln Leu Val Lys Gln Asp Ser Lys Gly Ser Asp Asp Thr Gln  
465 470 475 480

His Ser Pro Arg Asn Leu Ile Leu Thr Ser Leu Gln Glu Thr Gly Phe  
485 490 495

Ile Glu Tyr Met Asp Gln Gly Pro Trp Tyr Leu Ala Phe Tyr Asn Asp  
500 505 510

Gly Lys Lys Met Glu Gln Val Phe Val Leu Thr Thr Ala Ile Glu Ile  
515 520 525

Met Asp Asp Cys Ser Thr Asn Cys Asn Gly Asn Gly Glu Cys Ile Ser  
530 535 540

Gly His Cys His Cys Phe Pro Gly Phe Leu Gly Pro Asp Cys Ala Arg  
545 550 555 560

Asp Ser Cys Pro Val Leu Cys Gly Gly Asn Gly Glu Tyr Glu Lys Gly  
565 570 575

His Cys Val Cys Arg His Gly Trp Lys Gly Pro Glu Cys Asp Val Pro  
580 585 590

Glu Glu Gln Cys Ile Asp Pro Thr Cys Phe Gly His Gly Thr Cys Ile  
595 600 605

Met Gly Val Cys Ile Cys Val Pro Gly Tyr Lys Gly Glu Ile Cys Glu  
610 615 620

Glu Glu Asp Cys Leu Asp Pro Met Cys Ser Asn His Gly Ile Cys Val  
625 630 635 640

Lys Gly Glu Cys His Cys Ser Thr Gly Trp Gly Gly Val Asn Cys Glu  
645 650 655

Thr Pro Leu Pro Val Cys Gln Glu Gln Cys Ser Gly His Gly Thr Phe  
660 665 670

Leu Leu Asp Ala Gly Val Cys Ser Cys Asp Pro Lys Trp Thr Gly Ser  
675 680 685

Asp Cys Ser Thr Glu Leu Cys Thr Met Glu Cys Gly Ser His Gly Val  
690 695 700

Cys Ser Arg Gly Ile Cys Gln Cys Glu Glu Gly Trp Val Gly Pro Thr  
705 710 715 720

Cys Glu Glu Arg Ser Cys His Ser His Cys Thr Glu His Gly Gln Cys  
725 730 735

Lys Asp Gly Lys Cys Glu Cys Ser Pro Gly Trp Glu Gly Asp His Cys  
740 745 750

Thr Ile Ala His Tyr Leu Asp Ala Val Arg Asp Gly Cys Pro Gly Leu  
755 760 765

Cys Phe Gly Asn Gly Arg Cys Thr Leu Asp Gln Asn Gly Trp His Cys  
770 775 780

Val Cys Gln Val Gly Trp Ser Gly Thr Gly Cys Asn Val Val Met Glu  
785 790 795 800

Met Leu Cys Gly Asp Asn Leu Asp Asn Asp Gly Asp Gly Leu Thr Asp  
805 810 815

Cys Val Asp Pro Asp Cys Cys Gln Gln Ser Asn Cys Tyr Ile Ser Pro  
820 825 830

Leu Cys Gln Gly Ser Pro Asp Pro Leu Asp Leu Ile Gln Gln Ser Gln  
835 840 845

Thr Leu Phe Ser Gln His Thr Ser Arg Leu Phe Tyr Asp Arg Ile Lys  
850 855 860

Phe Leu Ile Gly Lys Asp Ser Thr His Val Ile Pro Pro Glu Val Ser  
865 870 875 880

Phe Asp Ser Arg Arg Ala Cys Val Ile Arg Gly Gln Val Val Ala Ile  
885 890 895

Asp Gly Thr Pro Leu Val Gly Val Asn Val Ser Phe Leu His His Ser  
900 905 910

Asp Tyr Gly Phe Thr Ile Ser Arg Gln Asp Gly Ser Phe Asp Leu Val  
915 920 925

Ala Ile Gly Gly Ile Ser Val Ile Leu Ile Phe Asp Arg Ser Pro Phe  
930 935 940

Leu Pro Glu Lys Arg Thr Leu Trp Leu Pro Trp Asn Gln Phe Ile Val  
945 950 955 960

Val Glu Lys Val Thr Met Gln Arg Val Val Ser Asp Pro Pro Ser Cys  
965 970 975

Asp Ile Ser Asn Phe Ile Ser Pro Asn Pro Ile Val Leu Pro Ser Pro  
980 985 990

Leu Thr Ser Phe Gly Gly Ser Cys Pro Glu Arg Gly Thr Ile Val Pro  
995 1000 1005

Glu Leu Gln Val Val Gln Glu Glu Ile Pro Ile Pro Ser Ser Phe  
1010 1015 1020

Val Arg Leu Ser Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Thr  
1025 1030 1035

Leu Leu Arg Ile Leu Leu Thr His Ser Thr Ile Pro Val Gly Met  
1040 1045 1050

Ile Lys Val His Leu Thr Val Ala Val Glu Gly Arg Leu Thr Gln  
1055 1060 1065

Lys Trp Phe Pro Ala Ala Ile Asn Leu Val Tyr Thr Phe Ala Trp  
1070 1075 1080

Asn Lys Thr Asp Ile Tyr Gly Gln Lys Val Trp Gly Leu Ala Glu  
1085 1090 1095

Ala Leu Val Ser Val Gly Tyr Glu Tyr Glu Thr Cys Pro Asp Phe  
1100 1105 1110

Ile Leu Trp Glu Gln Arg Thr Val Val Leu Gln Gly Phe Glu Met  
1115 1120 1125

Asp Ala Ser Asn Leu Gly Asp Trp Ser Leu Asn Lys His His Ile  
1130 1135 1140

Leu Asn Pro Gln Ser Gly Ile Ile His Lys Gly Asn Gly Glu Asn  
1145 1150 1155

Met Phe Ile Ser Gln Gln Pro Pro Val Ile Ser Thr Ile Met Gly

1160

1165

1170

Asn Gly His Gln Arg Ser Val Ala Cys Thr Asn Cys Asn Gly Pro  
1175 1180 1185

Ala His Asn Asn Lys Leu Phe Ala Pro Val Ala Leu Ala Ser Gly  
1190 1195 1200

Pro Asp Gly Ser Val Tyr Val Gly Asp Phe Asn Phe Val Arg Arg  
1205 1210 1215

Ile Phe Pro Ser Gly Asn Ser Val Ser Ile Leu Glu Leu Ser Thr  
1220 1225 1230

Ser Pro Ala His Lys Tyr Tyr Leu Ala Met Asp Pro Val Ser Glu  
1235 1240 1245

Ser Leu Tyr Leu Ser Asp Thr Asn Thr Arg Lys Val Tyr Lys Leu  
1250 1255 1260

Lys Ser Leu Val Glu Thr Lys Asp Leu Ser Lys Asn Phe Glu Val  
1265 1270 1275

Val Ala Gly Thr Gly Asp Gln Cys Leu Pro Phe Asp Gln Ser His  
1280 1285 1290

Cys Gly Asp Gly Gly Arg Ala Ser Glu Ala Ser Leu Asn Ser Pro  
1295 1300 1305

Arg Gly Ile Thr Val Asp Arg His Gly Phe Ile Tyr Phe Val Asp  
1310 1315 1320

Gly Thr Met Ile Arg Lys Ile Asp Glu Asn Ala Val Ile Thr Thr  
1325 1330 1335

Val Ile Gly Ser Asn Gly Leu Thr Ser Thr Gln Pro Leu Ser Cys  
1340 1345 1350

Asp Ser Gly Met Asp Ile Thr Gln Val Arg Leu Glu Trp Pro Thr  
1355 1360 1365

Asp Leu Ala Val Asn Pro Met Asp Asn Ser Leu Tyr Val Leu Asp  
1370 1375 1380

Asn Asn Ile Val Leu Gln Ile Ser Glu Asn Arg Arg Val Arg Ile  
1385 1390 1395

Ile Ala Gly Arg Pro Ile His Cys Gln Val Pro Gly Ile Asp His  
1400 1405 1410

Phe Leu Val Ser Lys Val Ala Ile His Ser Thr Leu Glu Ser Ala  
1415 1420 1425

Arg Ala Ile Ser Val Ser His Ser Gly Leu Leu Phe Ile Ala Glu  
1430 1435 1440

Thr Asp Glu Arg Lys Val Asn Arg Ile Gln Gln Val Thr Thr Asn  
1445 1450 1455

Gly Glu Ile Tyr Ile Ile Ala Gly Ala Pro Thr Asp Cys Asp Cys  
1460 1465 1470

Lys Ile Asp Pro Asn Cys Asp Cys Phe Ser Gly Asp Gly Gly Tyr  
1475 1480 1485

Ala Lys Asp Ala Lys Met Lys Ala Pro Ser Ser Leu Ala Val Ser  
1490 1495 1500

Pro Asp Gly Thr Leu Tyr Val Ala Asp Leu Gly Asn Val Arg Ile  
1505 1510 1515

Arg Thr Ile Ser Arg Asn Gln Ala His Leu Asn Asp Met Asn Ile  
1520 1525 1530

Tyr Glu Ile Ala Ser Pro Ala Asp Gln Glu Leu Tyr Gln Phe Thr  
1535 1540 1545

Val Asn Gly Thr His Leu His Thr Leu Asn Leu Ile Thr Arg Asp  
1550 1555 1560

Tyr Val Tyr Asn Phe Thr Tyr Asn Ser Glu Gly Asp Leu Gly Ala  
1565 1570 1575

Ile Thr Ser Ser Asn Gly Asn Ser Val His Ile Arg Arg Asp Ala  
1580 1585 1590

Gly Gly Met Pro Leu Trp Leu Val Val Pro Gly Gly Gln Val Tyr  
1595 1600 1605

Trp Leu Thr Ile Ser Ser Asn Gly Val Leu Lys Arg Val Ser Ala  
1610 1615 1620

Gln Gly Tyr Asn Pro Ala Leu Met Thr Tyr Pro Gly Asn Thr Gly  
1625 1630 1635

Leu Leu Ala Thr Lys Ser Asn Glu Asn Gly Trp Thr Thr Val Tyr  
1640 1645 1650

Glu Tyr Asp Pro Glu Gly His Leu Thr Asn Ala Thr Phe Pro Thr  
1655 1660 1665

Gly Glu Val Ser Ser Phe His Ser Asp Leu Glu Lys Leu Thr Lys  
1670 1675 1680

Val Glu Leu Asp Thr Ser Asn Arg Glu Asn Val Leu Met Ser Thr  
1685 1690 1695

Asn Leu Thr Ala Thr Ser Thr Ile Tyr Ile Leu Lys Gln Glu Asn  
1700 1705 1710

Thr Gln Ser Thr Tyr Arg Val Asn Pro Asp Gly Ser Leu Arg Val  
1715 1720 1725

Thr Phe Ala Ser Gly Met Glu Ile Gly Leu Ser Ser Glu Pro His  
1730 1735 1740

Ile Leu Ala Gly Ala Val Asn Pro Thr Leu Gly Lys Cys Asn Ile  
1745 1750 1755

Ser Leu Pro Gly Glu His Asn Ala Asn Leu Ile Glu Trp Arg Gln  
1760 1765 1770

Arg Lys Glu Gln Asn Lys Gly Asn Val Ser Ala Phe Glu Arg Arg  
1775 1780 1785

Leu Arg Ala His Asn Arg Asn Leu Leu Ser Ile Asp Phe Asp His  
1790 1795 1800

Ile Thr Arg Thr Gly Lys Ile Tyr Asp Asp His Arg Lys Phe Thr  
1805 1810 1815

Leu Arg Ile Leu Tyr Asp Gln Thr Gly Arg Pro Ile Leu Trp Ser  
1820 1825 1830

Pro Val Ser Arg Tyr Asn Glu Val Asn Ile Thr Tyr Ser Pro Ser  
1835 1840 1845

Gly Leu Val Thr Phe Ile Gln Arg Gly Thr Trp Asn Glu Lys Met  
1850 1855 1860

Glu Tyr Asp Gln Ser Gly Lys Ile Ile Ser Arg Thr Trp Ala Asp  
1865 1870 1875

Gly Lys Ile Trp Ser Tyr Thr Tyr Leu Glu Lys Ser Val Met Leu  
1880 1885 1890

Leu Leu His Ser Gln Arg Arg Tyr Ile Phe Glu Tyr Asp Gln Ser  
1895 1900 1905

Asp Cys Leu Leu Ser Val Thr Met Pro Ser Met Val Arg His Ser  
1910 1915 1920

Leu Gln Thr Met Leu Ser Val Gly Tyr Tyr Arg Asn Ile Tyr Thr  
1925 1930 1935

Pro Pro Asp Ser Ser Thr Ser Phe Ile Gln Asp Tyr Ser Arg Asp  
1940 1945 1950

Gly Arg Leu Leu Gln Thr Leu His Leu Gly Thr Gly Arg Arg Val  
1955 1960 1965

Leu Tyr Lys Tyr Thr Lys Gln Ala Arg Leu Ser Glu Val Leu Tyr  
1970 1975 1980

Asp Thr Thr Gln Val Thr Leu Thr Tyr Glu Glu Ser Ser Gly Val  
1985 1990 1995

Ile Lys Thr Ile His Leu Met His Asp Gly Phe Ile Cys Thr Ile  
2000 2005 2010

Arg Tyr Arg Gln Thr Gly Pro Leu Ile Gly Arg Gln Ile Phe Arg

2015

2020

2025

Phe Ser Glu Glu Gly Leu Val Asn Ala Arg Phe Asp Tyr Ser Tyr  
2030 2035 2040

Asn Asn Phe Arg Val Thr Ser Met Gln Ala Val Ile Asn Glu Thr  
2045 2050 2055

Pro Leu Pro Ile Asp Leu Tyr Arg Tyr Val Asp Val Ser Gly Arg  
2060 2065 2070

Thr Glu Gln Phe Gly Lys Phe Ser Val Ile Asn Tyr Asp Leu Asn  
2075 2080 2085

Gln Val Ile Thr Thr Thr Val Met Lys His Thr Lys Ile Phe Ser  
2090 2095 2100

Ala Asn Gly Gln Val Ile Glu Val Gln Tyr Glu Ile Leu Lys Ala  
2105 2110 2115

Ile Ala Tyr Trp Met Thr Ile Gln Tyr Asp Asn Val Gly Arg His  
2120 2125 2130

Gly Asn Met Cys Ile Arg Val Gly Val Asp Ala Asn Ile Thr Arg  
2135 2140 2145

Tyr Phe Tyr Glu Tyr Asp Ala Asp Gly Gln Leu Gln Thr Val Ser  
2150 2155 2160

Val Asn Asp Lys Thr Gln Trp Arg Tyr Ser Tyr Asp Leu Asn Gly  
2165 2170 2175

Asp Ile Asn Leu Leu Ser His Gly Lys Ser Ala Arg Leu Thr Pro  
2180 2185 2190

Leu Arg Tyr Asp Leu Arg Asp Arg Ile Thr Arg Leu Gly Glu Ile  
2195 2200 2205

Gln Tyr Lys Met Asp Glu Asp Gly Phe Leu Arg Gln Arg Gly Asn  
2210 2215 2220

Asp Ile Phe Glu Tyr Asn Ser Asn Gly Leu Leu Gln Lys Ala Tyr  
2225 2230 2235

Asn Lys Ala Ser Gly Trp Thr Val Gln Tyr Tyr Tyr Asp Gly Leu  
2240 2245 2250

Gly Arg Arg Val Ala Ser Lys Ser Ser Leu Gly Gln His Leu Gln  
2255 2260 2265

Phe Phe Val Asp Ala Thr Ala Asn Pro Ile Arg Val Thr His Leu  
2270 2275 2280

Tyr Asn His Thr Ser Ser Glu Ile Thr Ser Leu Tyr Tyr Asp Leu  
2285 2290 2295

Gln Gly His Leu Ile Ala Met Glu Leu Ser Ser Gly Glu Glu Tyr  
2300 2305 2310

Tyr Val Ala Cys Asp Asn Thr Gly Thr Pro Leu Ala Val Phe Ser  
2315 2320 2325

Ser Arg Gly Gln Val Ile Lys Glu Ile Leu Tyr Thr Pro Tyr Gly  
2330 2335 2340

Asp Ile Tyr His Asp Thr Tyr Pro Asp Phe Gln Val Ile Ile Gly  
2345 2350 2355

Phe His Gly Gly Leu Tyr Asp Phe Leu Thr Lys Leu Val His Leu  
2360 2365 2370

Gly Gln Arg Asp Tyr Asp Val Val Ala Gly Arg Trp Thr Thr Ala  
2375 2380 2385

Tyr His His Ile Trp Lys Gln Leu Asn Leu Leu Pro Lys Pro Phe  
2390 2395 2400

Asn Leu Tyr Ser Phe Glu Asn Asn Tyr Pro Val Gly Lys Ile Gln  
2405 2410 2415

Asp Val Ala Lys Tyr Thr Thr Asp Ile Arg Ser Trp Leu Glu Leu  
2420 2425 2430

Phe Gly Phe Gln Leu His Asn Val Leu Pro Gly Phe Pro Lys Pro  
2435 2440 2445

Glu Leu Glu Asn Leu Glu Leu Thr Tyr Glu Leu Leu Arg Leu Gln  
2450 2455 2460

Thr Lys Thr Gln Glu Trp Asp Pro Gly Lys Thr Ile Leu Gly Ile  
2465 2470 2475

Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe Ile Ser Leu Asp  
2480 2485 2490

Gln Leu Pro Met Thr Pro Arg Tyr Asn Asp Gly Arg Cys Leu Glu  
2495 2500 2505

Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val Phe Gly  
2510 2515 2520

Lys Gly Ile Lys Phe Ala Ile Lys Asp Gly Ile Val Thr Ala Asp  
2525 2530 2535

Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile  
2540 2545 2550

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu  
2555 2560 2565

Gly Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu  
2570 2575 2580

Asp Leu Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu  
2585 2590 2595

Asn Gly Val Asn Val Thr Val Ser Gln Met Thr Ser Leu Leu Asn  
2600 2605 2610

Gly Arg Thr Arg Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala  
2615 2620 2625

Leu Cys Phe Asn Ile Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys  
2630 2635 2640

Asn His Val Leu Glu Ile Ala Arg Gln Arg Ala Val Ala Gln Ala  
2645 2650 2655

Trp Thr Lys Glu Gln Arg Arg Leu Gln Glu Gly Glu Glu Gly Ile  
2660 2665 2670

Arg Ala Trp Thr Glu Gly Glu Lys Gln Gln Leu Leu Ser Thr Gly  
2675 2680 2685

Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val Leu Ser Val Glu Gln  
2690 2695 2700

Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile His Phe Met Arg  
2705 2710 2715

Gln Ser Glu Ile Gly Arg Arg  
2720 2725

<210> 231  
<211> 4930  
<212> DNA  
<213> human organism

<400> 231  
ctcagccttc ccgggttcggg aaaggggaag aatgcaggag gggtaggatt tctttcctga 60  
taggatcggt tggaaagac cgcgcgtgt gtgtgtctt cccttcgacc aaggtgtctg 120  
ttgctccgta aataaaacgt cccactgcct tctgagagcg ctataaaggc agcggaaagg 180  
tagtccgcgg ggcattccgg gcggggcgcg agcagagaca ggtcatggca ggcgcaggcg 240  
gcagggtcgga gccgcgcag ctccccgagt acagctgcag ctacatggtg tcgcggccgg 300  
tctacagcga gctcgcttc cagcaacagc acgagcggcg cctgcaggag cgcaagacgc 360  
tgccggagag cctggccaag tgctgcagtt gttcaagaaa gagagcctt ggtgtgctaa 420  
agactcttgt gcccatttg gagtggtcc ccaaataccg agtcaaggaa tggctgctta 480  
gtgacgtcat ttccggagtt agtactggc tagtgccac gctgcaaggg atggcatatg 540  
ccctactagc tgcagttcct gtcggatatg gtctctactc tgcttttcc cctatcctga 600  
catactttat ctttggaaaca tcaagacata tctcagttgg acctttcca gtggtgagtt 660  
taatggtggg atctgttgtt ctgagcatgg ccccccacga acactttctc gtatccagca 720  
gcaatggAAC tgtattaaat actactatga tagacactgc agctagagat acagctagag 780  
tcctgattgc cagtgcctg actctgctgg ttggaattat acagttgata tttggtggt 840  
tgcagattgg attcatagtg aggtacttgg cagatcctt ggttggtggc ttcacaacag 900  
ctgctgcctt ccaagtgcgt gtctcacagc taaagattgt cctcaatgtt tcaaccaaaa 960

actacaatgg agttctctt attatctata cgctgggtga gattttcaa aatattggtg 1020  
ataccaatct tgctgatttc actgctggat tgctcaccat tgcgtctgt atggcagttt 1080  
aggaattaaa tgatcggttt agacacaaaaa tcccagtcgg tattcctata gaagtaattg 1140  
tgacgataat tgctactgcc atttcataatg gagccaacct ggaaaaaaaaat tacaatgctg 1200  
gcattgttaa atccatccca agggggtttt tgccctcctga acttccacct gtgagcttgt 1260  
tctcgagat gctggctgca tcatttcca tcgctgtggt ggcttatgct attgcagtgt 1320  
cagtaggaaa agtataatgcc accaagtatg attacaccat cgatggaaac caggaattca 1380  
ttgcctttgg gatcagcaac atcttctcag gattcttcctc ttgtttgtg gccaccactg 1440  
ctcttccccg cacggccggtc caggagagca ctggaggaaa gacacaggtt gctggcatca 1500  
tctctgctgc gattgtgatg atcgccattc ttgcctcggg gaagcttctg gaacccttgc 1560  
agaagtcggt cttggcagct gttgtattt ccaacctgaa agggatgttt atgcagctgt 1620  
gtgacattcc tcgtctgtgg agacagaata agattgatgc tgatatctgg gtgtttacgt 1680  
gtatagtgtc catcattctg gggctggatc tcggttact agctggcctt atattggac 1740  
tgttgactgt ggtcctgaga gttcagttt cttcttgaa tggccttggaa agcatcccta 1800  
gcacagatata ctacaaaagt accaagaatt acaaaaaacat tgaagaacct caaggagtga 1860  
agattcttag atttccagt cctatttct atggcaatgt cgatggtttt aaaaaatgtt 1920  
tcaagtccac agttggattt gatgccatta gatgtataaa taaggaggctg aaagcgctga 1980  
ggaaaataca gaaactaata aaaagtggac aattaagagc aacaaagaat ggcataa 2040  
gtgatgctgt ttcaacaaat aatgcttttgc agcctgatga ggatattgaa gatctggagg 2100  
aacttgatata cccaaaccaag gaaatagaga ttcaagtggaa ttggaaactct gagttccag 2160  
tcaaagtggaa cgttccaaa gtgccaatcc atagccttgt gcttgactgt ggagctataat 2220  
ctttccttggaa cgttggggatcac tgcgggtgat tgtcaaagaa ttccaaagaa 2280  
ttgatgtggaa tgtgtatccc gcatcacttc aagattatgt gatagaaaag ctggagcaat 2340  
gcgggttctt tgacgacaac attagaaaagg acacattttt tttgacggtc catgatgcta 2400  
tactctatct acagaaccaa gtgaaatctc aagagggtca aggttccatt ttagaaaacgaa 2460  
tcactctcat tcaggattgt aaagataccctt ttgaatataat agaaacagag ctgacggaa 2520  
aagaacttga tgtccaggat gaggctatgc gtacacttgc atcctgaaag tgggttcggg 2580  
aggctctat gagcaaggaa tacaagacaa aacttcctca atgcattgac tatttcttca 2640

gactcaaaac actcattctt ttttctatta agccattgaa agagaagcac taagactgct 2700  
tctaggctt atttataaaa taaacacctt atccctaaca tgggcaaaat ggctagaatt 2760  
attcagacga tttggcagcg tccaggtaa gctgggtta taatacgctg ctgatctaca 2820  
tcacagattt gctaataatg ttcacgtggg ccctggcata tctctgttca gtagagtga 2880  
gtgctgaccc aacagcctct gtggtaaagc gagtcacgaa tgattaatca taaagaaaaa 2940  
tcagttttg actgacctgg atatccatga gctgcactga tcaccatgta aggtcacatt 3000  
tagtaaatgc tgaaataaaa tgattaatgc atttatcaat aaaagcctt gaaaatactt 3060  
tggataataa attggagttt taaaaatgca aatttgctt gatctaata atgaagtgtt 3120  
attacatata gccggaattt agatctctt tgatccttga aatggtttac ctaaaagcta 3180  
cagaaccagg ccaatatatt ttgaaatatt gatgcagaca aatgaaataa taaagagatt 3240  
ttcatggttt ataaaaatct ttttgatat gataataatc atgatcacaa ctgagatcaa 3300  
aaaaatataat gacagattat ttgtttaaa aatgcagttt taattatctt agtctataga 3360  
aatgatcatt gcatggaggc atgtataggt atgatctgtg taaaatctga cataaaaaca 3420  
gtgctattct gagtggaaat tttttgatg tgcttacata accatggtga taaaatgag 3480  
tttatatttt ttctcaaaaaa ttttagcagt gtgtaaagta agtaatctt aactgaactc 3540  
tgaccactta aaaaaaaaaatc taaaattga actacctata gtagtctgtg tttaaagtga 3600  
attttaaag acaaagcatt ctaaatgaac tcaatataaa aacattcatt tggaatgtac 3660  
atactgaaaa atacaggttt tttgaccaa aagttttat atctttctt tttatattt 3720  
ttttcctaa gtgccaacaa tttcttagat attatataca acacaggctt tgatcttggg 3780  
gactttccc atatattca cactggagtg aatgaagttg tacttcattt ctagagaaaa 3840  
gttataccca ggtccccat tgagaatgtc ttgcttgatt gaaaacgaca tcatcccttg 3900  
gtatactcca gggattggtt tcaggacccc tgcatttacc aaaatttgc cacactcaag 3960  
tcctgcagtc acccctgcct aaagatagaa tggcttctct gttttcttc tgaaatacaa 4020  
ccagaaacaa tgtgtctatt tctgaaagaa taggattaat gatcatacaa atgggttaat 4080  
cctgaattct gggtgtaaat ctggttacag cataactagg attataatgc tgcctcattt 4140  
tcacagcact acttgcttattt attgacaaca aatcatctcg ctaaagagtg aatgtaggcc 4200  
aggcgccgtg gctcatgcct gtaatcccag cactttggga ggccgaggcg ggtggatcac 4260  
gaggtcagga gatcgagacc atcctggcta acatggtaaa accccgtctc tactaaaaat 4320  
agaaaaaaaag aaattagcct agcgtggtgg ctggcggcgc cctgttagtcc cagctattt 4380

ggaggcataag	gcaggagaat	ggcgtgaacc	cgggaggcg	agcttgcagt	gagccgaggt	4440
cgtgccactg	cactccagcc	tggcgacag	agcaagactc	cgtctaaaaa	aaaaaaaaaa	4500
aaaaaaaaaa	agagtgaatg	taatagtctt	gcagaaaatg	aatgaatacc	tttgttcaat	4560
aaaggaaata	tgcactgctc	actttttga	aggaaatgcc	aaagttacgt	tttacaacaa	4620
ggctagagtt	tgtaaattct	gggttcattt	gtgatgacat	aagtcagcaa	actgcggaa	4680
tactgtctct	tctatgtatt	ttgtgaatag	taagcataat	tttagtttg	tattatcaat	4740
gaaaatttca	cttgaattta	aagctgcctt	ttgttatatt	tttaacctat	aggataagat	4800
tccagtattg	tatatgagtt	ttaacaaatt	aaaaaatcaa	atcatgtaca	tttggaaata	4860
tttgcacaca	tttaaaaata	aatgtaaagt	tgtctttaa	actactcgga	tgtgtccctt	4920
ctgaacaaaaa						4930

<210> 232  
 <211> 790  
 <212> PRT  
 <213> human organism

<400> 232

Met	Ala	Ala	Pro	Gly	Gly	Arg	Ser	Glu	Pro	Pro	Gln	Leu	Pro	Glu	Tyr
1															15

Ser	Cys	Ser	Tyr	Met	Val	Ser	Arg	Pro	Val	Tyr	Ser	Glu	Leu	Ala	Phe
				20					25						30

Gln	Gln	Gln	His	Glu	Arg	Arg	Leu	Gln	Glu	Arg	Lys	Thr	Leu	Arg	Glu
				35				40							45

Ser	Leu	Ala	Lys	Cys	Cys	Ser	Cys	Ser	Arg	Lys	Arg	Ala	Phe	Gly	Val
				50				55							60

Leu	Lys	Thr	Leu	Val	Pro	Ile	Leu	Glu	Trp	Leu	Pro	Lys	Tyr	Arg	Val
				65				70							80

Lys	Glu	Trp	Leu	Leu	Ser	Asp	Val	Ile	Ser	Gly	Val	Ser	Thr	Gly	Leu
				85				90							95

Val	Ala	Thr	Leu	Gln	Gly	Met	Ala	Tyr	Ala	Leu	Ala	Ala	Val	Pro	
				100				105							110

Val Gly Tyr Gly Leu Tyr Ser Ala Phe Phe Pro Ile Leu Thr Tyr Phe  
115 120 125

Ile Phe Gly Thr Ser Arg His Ile Ser Val Gly Pro Phe Pro Val Val  
130 135 140

Ser Leu Met Val Gly Ser Val Val Leu Ser Met Ala Pro Asp Glu His  
145 150 155 160

Phe Leu Val Ser Ser Ser Asn Gly Thr Val Leu Asn Thr Thr Met Ile  
165 170 175

Asp Thr Ala Ala Arg Asp Thr Ala Arg Val Leu Ile Ala Ser Ala Leu  
180 185 190

Thr Leu Leu Val Gly Ile Ile Gln Leu Ile Phe Gly Gly Leu Gln Ile  
195 200 205

Gly Phe Ile Val Arg Tyr Leu Ala Asp Pro Leu Val Gly Gly Phe Thr  
210 215 220

Thr Ala Ala Ala Phe Gln Val Leu Val Ser Gln Leu Lys Ile Val Leu  
225 230 235 240

Asn Val Ser Thr Lys Asn Tyr Asn Gly Val Leu Ser Ile Ile Tyr Thr  
245 250 255

Leu Val Glu Ile Phe Gln Asn Ile Gly Asp Thr Asn Leu Ala Asp Phe  
260 265 270

Thr Ala Gly Leu Leu Thr Ile Val Val Cys Met Ala Val Lys Glu Leu  
275 280 285

Asn Asp Arg Phe Arg His Lys Ile Pro Val Pro Ile Pro Ile Glu Val  
290 295 300

Ile Val Thr Ile Ile Ala Thr Ala Ile Ser Tyr Gly Ala Asn Leu Glu  
305 310 315 320

Lys Asn Tyr Asn Ala Gly Ile Val Lys Ser Ile Pro Arg Gly Phe Leu  
325 330 335

Pro Pro Glu Leu Pro Pro Val Ser Leu Phe Ser Glu Met Leu Ala Ala

340

345

350

Ser Phe Ser Ile Ala Val Val Ala Tyr Ala Ile Ala Val Ser Val Gly  
355 360 365

Lys Val Tyr Ala Thr Lys Tyr Asp Tyr Thr Ile Asp Gly Asn Gln Glu  
370 375 380

Phe Ile Ala Phe Gly Ile Ser Asn Ile Phe Ser Gly Phe Phe Ser Cys  
385 390 395 400

Phe Val Ala Thr Thr Ala Leu Ser Arg Thr Ala Val Gln Glu Ser Thr  
405 410 415

Gly Gly Lys Thr Gln Val Ala Gly Ile Ile Ser Ala Ala Ile Val Met  
420 425 430

Ile Ala Ile Leu Ala Leu Gly Lys Leu Leu Glu Pro Leu Gln Lys Ser  
435 440 445

Val Leu Ala Ala Val Val Ile Ala Asn Leu Lys Gly Met Phe Met Gln  
450 455 460

Leu Cys Asp Ile Pro Arg Leu Trp Arg Gln Asn Lys Ile Asp Ala Val  
465 470 475 480

Ile Trp Val Phe Thr Cys Ile Val Ser Ile Ile Leu Gly Leu Asp Leu  
485 490 495

Gly Leu Leu Ala Gly Leu Ile Phe Gly Leu Leu Thr Val Val Leu Arg  
500 505 510

Val Gln Phe Pro Ser Trp Asn Gly Leu Gly Ser Ile Pro Ser Thr Asp  
515 520 525

Ile Tyr Lys Ser Thr Lys Asn Tyr Lys Asn Ile Glu Glu Pro Gln Gly  
530 535 540

Val Lys Ile Leu Arg Phe Ser Ser Pro Ile Phe Tyr Gly Asn Val Asp  
545 550 555 560

Gly Phe Lys Lys Cys Ile Lys Ser Thr Val Gly Phe Asp Ala Ile Arg  
565 570 575

Val Tyr Asn Lys Arg Leu Lys Ala Leu Arg Lys Ile Gln Lys Leu Ile  
580 585 590

Lys Ser Gly Gln Leu Arg Ala Thr Lys Asn Gly Ile Ile Ser Asp Ala  
595 600 605

Val Ser Thr Asn Asn Ala Phe Glu Pro Asp Glu Asp Ile Glu Asp Leu  
610 615 620

Glu Glu Leu Asp Ile Pro Thr Lys Glu Ile Glu Ile Gln Val Asp Trp  
625 630 635 640

Asn Ser Glu Leu Pro Val Lys Val Asn Val Pro Lys Val Pro Ile His  
645 650 655

Ser Leu Val Leu Asp Cys Gly Ala Ile Ser Phe Leu Asp Val Val Gly  
660 665 670

Val Arg Ser Leu Arg Val Ile Val Lys Glu Phe Gln Arg Ile Asp Val  
675 680 685

Asn Val Tyr Phe Ala Ser Leu Gln Asp Tyr Val Ile Glu Lys Leu Glu  
690 695 700

Gln Cys Gly Phe Asp Asn Ile Arg Lys Asp Thr Phe Phe Leu  
705 710 715 720

Thr Val His Asp Ala Ile Leu Tyr Leu Gln Asn Gln Val Lys Ser Gln  
725 730 735

Glu Gly Gln Gly Ser Ile Leu Glu Thr Ile Thr Leu Ile Gln Asp Cys  
740 745 750

Lys Asp Thr Leu Glu Leu Ile Glu Thr Glu Leu Thr Glu Glu Glu Leu  
755 760 765

Asp Val Gln Asp Glu Ala Met Arg Thr Leu Ala Ser Gln Asp Glu Ala  
770 775 780

Met Arg Thr Leu Ala Ser  
785 790

<210> 233  
 <211> 1282  
 <212> DNA  
 <213> human organism

<400> 233  
 ctgcgatccc gcagggcagc gacgcgactc tggtgccggc cgtcttcttc cccccgagct 60  
 gggcggtgcgc ggccgcaatg aactgggagc tgctgctgtg gctgctggcg ctgtgcgcgc 120  
 tgctcctgct cttgggtgcag ctgctgcgc tcctgagggc tgacggcgac ctgacgctac 180  
 tatgggccga gtggcaggga cgacgcccag aatgggagct gactgatatg gtggtgtggg 240  
 tgactggagc ctgcgagtggaa attggtgagg agctggctta ccagttgtct aaactaggag 300  
 ttctcttgcgt gctgtcagcc agaagagtgc atgagctggaa aagggtgaaa agaagatgcc 360  
 tagagaatgg caatttaaaa gaaaaagata tacttgggg gccccttgac ctgaccgaca 420  
 ctgggtccca tgaagcggct accaaagctg ttctccagga gtttggtaga atcgacattc 480  
 tggtaaccaa tggtgaaatg tcccagcggt ctctgtgcatt ggataccagc ttggatgtct 540  
 acagaaagct aatagagctt aactacttag ggacgggtgc cttgacaaaaa tgtgttctgc 600  
 ctcacatgtat cgagaggaag caaggaaaga ttgttactgt gaatagcatc ctgggtatca 660  
 tatctgttacc tctttccatt ggatactgtg cttagcaagca tgctctccgg ggtttttta 720  
 atggccttcg aacagaactt gccacatacc caggtataat agtttctaac atttgcccg 780  
 gacctgtgca atcaaataattt gtggagaatt ccctagctgg agaagtcaca aagactata 840  
 gcaataatgg agaccagtcc cacaagatga caaccagtcg ttgtgtgcgg ctgatgtaa 900  
 tcagcatggc caatgatttg aaagaagttt ggatctcaga acaaccttgc ttgttagtaa 960  
 catatttgcgt gcaatacatg ccaacctggg cctgggtggat aaccaacaag atggggaa 1020  
 aaaggattga gaactttaag agtgggtgtgg atgcagactc ttcttatttt aaaatctta 1080  
 agacaaaaca tgactgaaaaa gagcacctgt actttcaag ccactggagg gagaaatgg 1140  
 aaacatgaaa acagcaatct tcttatgctt ctgaataatc aaagactaat ttgtgatttt 1200  
 acttttaat agatatgact ttgcttccaa catggaaatga aataaaaaat aaataataaa 1260  
 agattgccat gaatctgca aa 1282

<210> 234  
 <211> 339  
 <212> PRT  
 <213> human organism

<400> 234

Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu  
1 5 10 15

Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu  
20 25 30

Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu  
35 40 45

Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu  
50 55 60

Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser  
65 70 75 80

Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu  
85 90 95

Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu  
100 105 110

Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu  
115 120 125

Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly Met Ser Gln Arg  
130 135 140

Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg Lys Leu Ile Glu  
145 150 155 160

Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His  
165 170 175

Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu  
180 185 190

Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His  
195 200 205

Ala Leu Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr  
210 215 220

Pro Gly Ile Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn  
225 230 235 240

Ile Val Glu Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn  
245 250 255

Asn Gly Asp Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu  
260 265 270

Met Leu Ile Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu  
275 280 285

Gln Pro Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp  
290 295 300

Ala Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe  
305 310 315 320

Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys Thr  
325 330 335

Lys His Asp

<210> 235  
<211> 1833  
<212> DNA  
<213> human organism

<400> 235  
atgattgctt cacagtttct ctcagctctc actttgggtgc ttctcattaa agagagtggaa 60  
gcctggtctt acaacacacctc cacggaagct atgacttatg atgaggccag tgcttattgt 120  
cagcaaaggta acacacacactt ggttgcattt caaaaacaaag aagagattga gtacctaacc 180  
tccatattga gctattcacc aagtttattac tggattggaa tcagaaaagt caacaatgtg 240  
tgggtctggg taggaaccca gaaacctctg acagaagaag ccaagaactg ggctccaggt 300  
gaacccaaaca ataggcaaaa agatgaggac tgcgtggaga tctacatcaa gagagaaaaaa 360  
gatgtgggca tgtggaatga tgagaggtgc agcaagaaga agcttgcctt atgctacaca 420  
gctgcctgta ccaatacatc ctgcagtggc cacggtaat gtgttagagac catcaataat 480  
tacacttgca agtgtgaccc tggcttcagt ggactcaagt gtgagcaaat tgtgaactgt 540

acagccctgg	aatcccctga	gcatggaagc	ctggtttgc	gtcacccact	gggaaacttc	600
agctacaatt	cttcctgctc	tatcagctgt	gataggggtt	acctgccaag	cagcatggag	660
accatgcagt	gtatgtcctc	tggagaatgg	agtgcctcta	ttccagcctg	caatgtggtt	720
gagtgtgatg	ctgtgacaaa	tccagccaat	gggttcgtgg	aatgtttcca	aaaccctgga	780
agcttcccat	ggaacacaac	ctgtacattt	gactgtgaag	aaggatttg	actaatggga	840
gcccgagcc	ttcagtgtac	ctcatctggg	aattgggaca	acgagaagcc	aacgtgtaaa	900
gctgtgacat	gcagggccgt	ccgccagcct	cagaatggct	ctgtgaggtg	cagccattcc	960
cctgctggag	agttcacctt	caaatcatcc	tgcaacttca	cctgtgagga	aggcttcatg	1020
ttgcaggac	cagcccaggt	tgaatgcacc	actcaagggc	agtggacaca	gcaaatccca	1080
gtttgtgaag	ctttccagtg	cacagccttg	tccaaaccccg	agcgaggcta	catgaattgt	1140
cttccttagtg	cttctggcag	tttccgttat	gggtccagct	gtgagttctc	ctgtgagcag	1200
ggttttgtgt	tgaaggatc	caaaggctc	caatgtggcc	ccacagggga	gtggacaac	1260
gagaagccca	catgtgaagc	tgtgagatgc	gatgctgtcc	accagcccc	gaagggtttg	1320
tgtaggtgtg	ctcattcccc	tattggagaa	ttcacctaca	agtccctttg	tgccttcagc	1380
tgtgaggagg	gatttgaatt	atatggatca	actcaacttg	agtgcacatc	tcagggacaa	1440
tggacagaag	aggttccttc	ctgccaagtg	gtaaaatgtt	caagcctggc	agttccggga	1500
aagatcaaca	tgagctgcag	tggggagccc	gtgttggca	ctgtgtgcaa	gttcgcctgt	1560
cctgaaggat	ggacgctcaa	tggctctgca	gctcgacat	gtggagccac	aggacactgg	1620
tctggcctgc	tacctacctg	tgaagctccc	actgagtc	acattccctt	ggtagctgga	1680
ctttctgctg	ctggactctc	cctcctgaca	ttagcaccat	ttctcctctg	gcttcggaaa	1740
tgcttacgga	aagcaaagaa	atttgttccct	gccagcagct	gccaaagcct	tgaatcagac	1800
ggaagctacc	aaaagccttc	ttacatcctt	taa			1833

<210> 236  
 <211> 610  
 <212> PRT  
 <213> human organism

<400> 236

Met Ile Ala Ser Gln Phe Leu Ser Ala Leu Thr Leu Val Leu Leu Ile  
 1 5 10 15

Lys Glu Ser Gly Ala Trp Ser Tyr Asn Thr Ser Thr Glu Ala Met Thr

20

25

30

Tyr Asp Glu Ala Ser Ala Tyr Cys Gln Gln Arg Tyr Thr His Leu Val  
35 40 45

Ala Ile Gln Asn Lys Glu Glu Ile Glu Tyr Leu Asn Ser Ile Leu Ser  
50 55 60

Tyr Ser Pro Ser Tyr Tyr Trp Ile Gly Ile Arg Lys Val Asn Asn Val  
65 70 75 80

Trp Val Trp Val Gly Thr Gln Lys Pro Leu Thr Glu Glu Ala Lys Asn  
85 90 95

Trp Ala Pro Gly Glu Pro Asn Asn Arg Gln Lys Asp Glu Asp Cys Val  
100 105 110

Glu Ile Tyr Ile Lys Arg Glu Lys Asp Val Gly Met Trp Asn Asp Glu  
115 120 125

Arg Cys Ser Lys Lys Leu Ala Leu Cys Tyr Thr Ala Ala Cys Thr  
130 135 140

Asn Thr Ser Cys Ser Gly His Gly Glu Cys Val Glu Thr Ile Asn Asn  
145 150 155 160

Tyr Thr Cys Lys Cys Asp Pro Gly Phe Ser Gly Leu Lys Cys Glu Gln  
165 170 175

Ile Val Asn Cys Thr Ala Leu Glu Ser Pro Glu His Gly Ser Leu Val  
180 185 190

Cys Ser His Pro Leu Gly Asn Phe Ser Tyr Asn Ser Ser Cys Ser Ile  
195 200 205

Ser Cys Asp Arg Gly Tyr Leu Pro Ser Ser Met Glu Thr Met Gln Cys  
210 215 220

Met Ser Ser Gly Glu Trp Ser Ala Pro Ile Pro Ala Cys Asn Val Val  
225 230 235 240

Glu Cys Asp Ala Val Thr Asn Pro Ala Asn Gly Phe Val Glu Cys Phe  
245 250 255

Gln Asn Pro Gly Ser Phe Pro Trp Asn Thr Thr Cys Thr Phe Asp Cys  
260 265 270

Glu Glu Gly Phe Glu Leu Met Gly Ala Gln Ser Leu Gln Cys Thr Ser  
275 280 285

Ser Gly Asn Trp Asp Asn Glu Lys Pro Thr Cys Lys Ala Val Thr Cys  
290 295 300

Arg Ala Val Arg Gln Pro Gln Asn Gly Ser Val Arg Cys Ser His Ser  
305 310 315 320

Pro Ala Gly Glu Phe Thr Phe Lys Ser Ser Cys Asn Phe Thr Cys Glu  
325 330 335

Glu Gly Phe Met Leu Gln Gly Pro Ala Gln Val Glu Cys Thr Thr Gln  
340 345 350

Gly Gln Trp Thr Gln Gln Ile Pro Val Cys Glu Ala Phe Gln Cys Thr  
355 360 365

Ala Leu Ser Asn Pro Glu Arg Gly Tyr Met Asn Cys Leu Pro Ser Ala  
370 375 380

Ser Gly Ser Phe Arg Tyr Gly Ser Ser Cys Glu Phe Ser Cys Glu Gln  
385 390 395 400

Gly Phe Val Leu Lys Gly Ser Lys Arg Leu Gln Cys Gly Pro Thr Gly  
405 410 415

Glu Trp Asp Asn Glu Lys Pro Thr Cys Glu Ala Val Arg Cys Asp Ala  
420 425 430

Val His Gln Pro Pro Lys Gly Leu Val Arg Cys Ala His Ser Pro Ile  
435 440 445

Gly Glu Phe Thr Tyr Lys Ser Ser Cys Ala Phe Ser Cys Glu Glu Gly  
450 455 460

Phe Glu Leu Tyr Gly Ser Thr Gln Leu Glu Cys Thr Ser Gln Gly Gln  
465 470 475 480

Trp Thr Glu Glu Val Pro Ser Cys Gln Val Val Lys Cys Ser Ser Leu  
485 490 495

Ala Val Pro Gly Lys Ile Asn Met Ser Cys Ser Gly Glu Pro Val Phe  
500 505 510

Gly Thr Val Cys Lys Phe Ala Cys Pro Glu Gly Trp Thr Leu Asn Gly  
515 520 525

Ser Ala Ala Arg Thr Cys Gly Ala Thr Gly His Trp Ser Gly Leu Leu  
530 535 540

Pro Thr Cys Glu Ala Pro Thr Glu Ser Asn Ile Pro Leu Val Ala Gly  
545 550 555 560

Leu Ser Ala Ala Gly Leu Ser Leu Leu Thr Leu Ala Pro Phe Leu Leu  
565 570 575

Trp Leu Arg Lys Cys Leu Arg Lys Ala Lys Lys Phe Val Pro Ala Ser  
580 585 590

Ser Cys Gln Ser Leu Glu Ser Asp Gly Ser Tyr Gln Lys Pro Ser Tyr  
595 600 605

Ile Leu  
610

<210> 237  
<211> 3793  
<212> DNA  
<213> human organism

<400> 237  
atgatgtgtg aagtgtatgcc cacgattaat gaggacaccc caatgagcca aagggggtcc 60  
caaaggcagtg gctcgactc agactcccat tttgagcagc tgatggtaaa tatgttagat 120  
gaaaggatc gtcttctaga cacccttcgg gagaccagg aaagcctctc acttgccag 180  
caaagacttc aggatgtcat ctatgaccga gactcactcc agagacagct caattcagcc 240  
ctgccacagg atatcgaatc cctaacagga gggctggctg gttctaagggg ggctgatcca 300  
ccggaatttg ctgcactgac aaaagaatta aatgcctgca gggacaact tctagaaaag 360  
gaagaagaaa tctctgaact taaagctgaa agaaacaaca caagactatt actggagcat 420

ttggagtgcc ttgtgtcacg acatgaaaga tcactaagaa tgacggtggt aaaacggcaa 480  
gcccagtctc cctcaggagt atccagtcaa gttgaagttc tcaaggcact gaaatcttg 540  
ttttagcacc acaaggcctt ggatgaaaag gtaagggagc gactgagggt ttcttagaa 600  
agagtctctg cactggaaga agaactagct gctgctaattc aggagattgt tgccttcgt 660  
gaacaaaatg ttcatataca aagaaaaatg gcatcaagcg agggatccac agagtcagaa 720  
catcttgaag ggatggaacc tggacagaaa gtccatgaga agcgttgtc caatggttct 780  
atagactcaa ccgatgaaac tagtcaaata gttgaactac aagaattgtc tgaaaagcaa 840  
aactatgaaa tggcccagat gaaagaacgt ttagcagccc tttcttcccg agtgggagag 900  
gtggaacagg aagcagagac agcaagaaag gatctcatta aaacagaaga aatgaacacc 960  
aagtatcaaa gggacattag ggaggccatg gcacaaaagg aagatatgga agaaagaatt 1020  
acaacccttg aaaagcgta cctcagtgtc cagagagaat ctacctccat acatgacatg 1080  
aatgataaac tagaaaatga gttgcaaat aaagaagcta tcctacggca gatggaagag 1140  
aaaaacagac agttacaaga acgtcttgag ctagctgaac aaaagttgca gcagaccatg 1200  
agaaaggctg aaaccttgcc tgaagtagag gctgaactgg ctcagagaat tgcagcccta 1260  
accaaggctg aagagagaca tggaaatatt gaagaacgta tgagacattt agagggtcaa 1320  
cttgaagaga agaatcaaga acttcaaaga gctaggcaaa gagagaaaat gaatgaggag 1380  
cataacaaga gattatcggc tacgggttat agacttctga ctgaatccaa tgaacgccta 1440  
caactacact taaagggaaag aatggctgct cttagaagaaa agaatgttt aattcaagaa 1500  
tcagaaactt tcagaaagaa tcttgaagaa tctttacatg ataaggaaag attagcagaa 1560  
gaaattgaaa agctgagatc tgaacttgac caattgaaaa tgagaactgg ctcttaatt 1620  
gaacccacaa tbeccaacac tcacccatgac acctcagctg agttgcggta ctcagtgg 1680  
tccctagtgg acagccagtc tgattacaga acaactaaag taataagaag accaaggaga 1740  
ggccgcattgg gtgtgcgaag agatgagcca aaggtgaaat ctcttggggta tcacgagtgg 1800  
aatagaactc aacagattgg agtactaagc agccaccctt ttgaaagtga cactgaaatg 1860  
tctgatattt atgatgatga cagagaaaca attttagct caatggatct tctcttc 1920  
agtggtcatt ccgatgccc gacgctagcc atgatgcttc aggaacaatt ggatgccatc 1980  
aacaaagaaa tcaggctaat tcaggaagaa aaagaatcta cagagttgcg tgctgaagaa 2040  
attgaaaata gagtggctag tgtgagcctc gaaggcctga atttgcaag ggtccaccca 2100  
ggtacctcca ttactgcctc ttttacagct tcacccatg ccccccagt 2160

ggacactcaa ctccaaagct caccctcgaa agccctgccaa gggaaatggaa tcggatggga 2220  
gtcatgacac tgccaagtga tctgaggaaa catcgagaa agattgcagt tgtgaaagaa 2280  
gatggtcgag aggacaaagc aacaattaaa tgtgaaactt ctccctcctcc tacccctaga 2340  
gccctcagaa tgactcacac tctcccttct tcctaccaca atgatgctcg aagtagttta 2400  
tctgtctctc ttgagccaga aagcctcgaaa cttggtagtg ccaacagcag ccaagactct 2460  
cttcacaaag cccccaaagaa gaaaggaatc aagtcttcaa taggacgttt gtttggtaaa 2520  
aaagaaaaaaag ctcgacttgg gcagctccgaa ggctttatgg agactgaagc tgcagctcag 2580  
gagtccctgg ggttaggcaa actcggaact caagctgaga agatcgaag actaaagaaa 2640  
aagcatgaac ttcttgaaga agctcgagaa aagggattac ctttgccca gtggatggg 2700  
ccaactgtgg tcgcatggct agagcttgg ttggaaatgc ctgcgtggta cgtggcagcc 2760  
tgccgagcca acgtgaagag tgggccatc atgtctgctt tatctgacac tgagatccag 2820  
agagaaaattt gaatcagcaa tccactgcat cgcttaaaac ttcgattagc aatccaggag 2880  
atggtttccc taacaagtcc ttcaagtcct ccaacatctc gaactccttc aggcaacgtt 2940  
tgggtgactc atgaagaaat gggaaatctt gcagctccag caaaaacgaa agaatctgag 3000  
gaaggaagct gggcccagtg tccggttttt ctacagaccc tggcttatgg agatatgaat 3060  
catgagtggaa ttggaaatga atggcttccc agcttgggt tacctcagta cagaagttac 3120  
tttatggaaat gcttgtaga tgcaagaatg ttagatcacc taacaaaaaaaaa agatctccgt 3180  
gtccatttaa aaatggtaga tagttccat cgaacaagtt tacaatatgg aattatgtgc 3240  
ttaaagaggt tgaattatga cagaaaaagaa ctagaaagaa gacgggaagc aagccaacat 3300  
gaaataaaag acgtgttgggt gtggagcaat gaccgaatta ttcgctggat acaagcaatt 3360  
ggacttcgag aatatgc当地 taatatactt gagagcggtg tgc当地ggctc acttatagcc 3420  
ctggatgaaa actttgacta cagcagcttta actttattat tacagattcc aacacagaac 3480  
accaggcaa ggcagattct tgaaagagaa tacaataacc tcttggccct gggaaactgaa 3540  
aggcgactgg atgaaagtga tgacaagaac ttcaagacgtg gatcaacctg gagaaggcag 3600  
tttcctcctc gtgaagtaca tggaatcagc atgatgcctg ggtcctcaga aacattacca 3660  
gctggattta ggttaaccac aacctctggg caatcaagaa aaatgacaac agatgttgct 3720  
tcatcaagac tgcagagggtt agacaactcc actgttcgca cataactcatg tctcgagtaa 3780  
gcggcccgctt taa 3793

<210> 238  
<211> 1259  
<212> PRT  
<213> human organism

<400> 238

Met Met Cys Glu Val Met Pro Thr Ile Asn Glu Asp Thr Pro Met Ser  
1 5 10 15

Gln Arg Gly Ser Gln Ser Ser Gly Ser Asp Ser Asp Ser His Phe Glu  
20 25 30

Gln Leu Met Val Asn Met Leu Asp Glu Arg Asp Arg Leu Leu Asp Thr  
35 40 45

Leu Arg Glu Thr Gln Glu Ser Leu Ser Leu Ala Gln Gln Arg Leu Gln  
50 55 60

Asp Val Ile Tyr Asp Arg Asp Ser Leu Gln Arg Gln Leu Asn Ser Ala  
65 70 75 80

Leu Pro Gln Asp Ile Glu Ser Leu Thr Gly Gly Leu Ala Gly Ser Lys  
85 90 95

Gly Ala Asp Pro Pro Glu Phe Ala Ala Leu Thr Lys Glu Leu Asn Ala  
100 105 110

Cys Arg Glu Gln Leu Leu Glu Lys Glu Glu Glu Ile Ser Glu Leu Lys  
115 120 125

Ala Glu Arg Asn Asn Thr Arg Leu Leu Leu Glu His Leu Glu Cys Leu  
130 135 140

Val Ser Arg His Glu Arg Ser Leu Arg Met Thr Val Val Lys Arg Gln  
145 150 155 160

Ala Gln Ser Pro Ser Gly Val Ser Ser Glu Val Glu Val Leu Lys Ala  
165 170 175

Leu Lys Ser Leu Phe Glu His His Lys Ala Leu Asp Glu Lys Val Arg  
180 185 190

Glu Arg Leu Arg Val Ser Leu Glu Arg Val Ser Ala Leu Glu Glu Glu

195

200

205

Leu Ala Ala Ala Asn Gln Glu Ile Val Ala Leu Arg Glu Gln Asn Val  
210 215 220

His Ile Gln Arg Lys Met Ala Ser Ser Glu Gly Ser Thr Glu Ser Glu  
225 230 235 240

His Leu Glu Gly Met Glu Pro Gly Gln Lys Val His Glu Lys Arg Leu  
245 250 255

Ser Asn Gly Ser Ile Asp Ser Thr Asp Glu Thr Ser Gln Ile Val Glu  
260 265 270

Leu Gln Glu Leu Leu Glu Lys Gln Asn Tyr Glu Met Ala Gln Met Lys  
275 280 285

Glu Arg Leu Ala Ala Leu Ser Ser Arg Val Gly Glu Val Glu Gln Glu  
290 295 300

Ala Glu Thr Ala Arg Lys Asp Leu Ile Lys Thr Glu Glu Met Asn Thr  
305 310 315 320

Lys Tyr Gln Arg Asp Ile Arg Glu Ala Met Ala Gln Lys Glu Asp Met  
325 330 335

Glu Glu Arg Ile Thr Thr Leu Glu Lys Arg Tyr Leu Ser Ala Gln Arg  
340 345 350

Glu Ser Thr Ser Ile His Asp Met Asn Asp Lys Leu Glu Asn Glu Leu  
355 360 365

Ala Asn Lys Glu Ala Ile Leu Arg Gln Met Glu Glu Lys Asn Arg Gln  
370 375 380

Leu Gln Glu Arg Leu Glu Leu Ala Glu Gln Lys Leu Gln Gln Thr Met  
385 390 395 400

Arg Lys Ala Glu Thr Leu Pro Glu Val Glu Ala Glu Leu Ala Gln Arg  
405 410 415

Ile Ala Ala Leu Thr Lys Ala Glu Glu Arg His Gly Asn Ile Glu Glu  
420 425 430

Arg Met Arg His Leu Glu Gly Gln Leu Glu Glu Lys Asn Gln Glu Leu  
435 440 445

Gln Arg Ala Arg Gln Arg Glu Lys Met Asn Glu Glu His Asn Lys Arg  
450 455 460

Leu Ser Asp Thr Val Asp Arg Leu Leu Thr Glu Ser Asn Glu Arg Leu  
465 470 475 480

Gln Leu His Leu Lys Glu Arg Met Ala Ala Leu Glu Glu Lys Asn Val  
485 490 495

Leu Ile Gln Glu Ser Glu Thr Phe Arg Lys Asn Leu Glu Glu Ser Leu  
500 505 510

His Asp Lys Glu Arg Leu Ala Glu Glu Ile Glu Lys Leu Arg Ser Glu  
515 520 525

Leu Asp Gln Leu Lys Met Arg Thr Gly Ser Leu Ile Glu Pro Thr Ile  
530 535 540

Pro Arg Thr His Leu Asp Thr Ser Ala Glu Leu Arg Tyr Ser Val Gly  
545 550 555 560

Ser Leu Val Asp Ser Gln Ser Asp Tyr Arg Thr Thr Lys Val Ile Arg  
565 570 575

Arg Pro Arg Arg Gly Arg Met Gly Val Arg Arg Asp Glu Pro Lys Val  
580 585 590

Lys Ser Leu Gly Asp His Glu Trp Asn Arg Thr Gln Gln Ile Gly Val  
595 600 605

Leu Ser Ser His Pro Phe Glu Ser Asp Thr Glu Met Ser Asp Ile Asp  
610 615 620

Asp Asp Asp Arg Glu Thr Ile Phe Ser Ser Met Asp Leu Leu Ser Pro  
625 630 635 640

Ser Gly His Ser Asp Ala Gln Thr Leu Ala Met Met Leu Gln Glu Gln  
645 650 655

Leu Asp Ala Ile Asn Lys Glu Ile Arg Leu Ile Gln Glu Glu Lys Glu  
660 665 670

Ser Thr Glu Leu Arg Ala Glu Glu Ile Glu Asn Arg Val Ala Ser Val  
675 680 685

Ser Leu Glu Gly Leu Asn Leu Ala Arg Val His Pro Gly Thr Ser Ile  
690 695 700

Thr Ala Ser Val Thr Ala Ser Ser Leu Ala Ser Ser Ser Pro Pro Ser  
705 710 715 720

Gly His Ser Thr Pro Lys Leu Thr Pro Arg Ser Pro Ala Arg Glu Met  
725 730 735

Asp Arg Met Gly Val Met Thr Leu Pro Ser Asp Leu Arg Lys His Arg  
740 745 750

Arg Lys Ile Ala Val Val Glu Glu Asp Gly Arg Glu Asp Lys Ala Thr  
755 760 765

Ile Lys Cys Glu Thr Ser Pro Pro Pro Thr Pro Arg Ala Leu Arg Met  
770 775 780

Thr His Thr Leu Pro Ser Ser Tyr His Asn Asp Ala Arg Ser Ser Leu  
785 790 795 800

Ser Val Ser Leu Glu Pro Glu Ser Leu Gly Leu Gly Ser Ala Asn Ser  
805 810 815

Ser Gln Asp Ser Leu His Lys Ala Pro Lys Lys Lys Gly Ile Lys Ser  
820 825 830

Ser Ile Gly Arg Leu Phe Gly Lys Lys Glu Lys Ala Arg Leu Gly Gln  
835 840 845

Leu Arg Gly Phe Met Glu Thr Glu Ala Ala Ala Gln Glu Ser Leu Gly  
850 855 860

Leu Gly Lys Leu Gly Thr Gln Ala Glu Lys Asp Arg Arg Leu Lys Lys  
865 870 875 880

Lys His Glu Leu Leu Glu Glu Ala Arg Arg Lys Gly Leu Pro Phe Ala  
885 890 895

Gln Trp Asp Gly Pro Thr Val Val Ala Trp Leu Glu Leu Trp Leu Gly  
900 905 910

Met Pro Ala Trp Tyr Val Ala Ala Cys Arg Ala Asn Val Lys Ser Gly  
915 920 925

Ala Ile Met Ser Ala Leu Ser Asp Thr Glu Ile Gln Arg Glu Ile Gly  
930 935 940

Ile Ser Asn Pro Leu His Arg Leu Lys Leu Arg Leu Ala Ile Gln Glu  
945 950 955 960

Met Val Ser Leu Thr Ser Pro Ser Ala Pro Pro Thr Ser Arg Thr Pro  
965 970 975

Ser Gly Asn Val Trp Val Thr His Glu Glu Met Glu Asn Leu Ala Ala  
980 985 990

Pro Ala Lys Thr Lys Glu Ser Glu Glu Gly Ser Trp Ala Gln Cys Pro  
995 1000 1005

Val Phe Leu Gln Thr Leu Ala Tyr Gly Asp Met Asn His Glu Trp  
1010 1015 1020

Ile Gly Asn Glu Trp Leu Pro Ser Leu Gly Leu Pro Gln Tyr Arg  
1025 1030 1035

Ser Tyr Phe Met Glu Cys Leu Val Asp Ala Arg Met Leu Asp His  
1040 1045 1050

Leu Thr Lys Lys Asp Leu Arg Val His Leu Lys Met Val Asp Ser  
1055 1060 1065

Phe His Arg Thr Ser Leu Gln Tyr Gly Ile Met Cys Leu Lys Arg  
1070 1075 1080

Leu Asn Tyr Asp Arg Lys Glu Leu Glu Arg Arg Arg Glu Ala Ser  
1085 1090 1095

Gln His Glu Ile Lys Asp Val Leu Val Trp Ser Asn Asp Arg Ile

1100	1105	1110				
Ile Arg Trp Ile Gln Ala Ile Gly Leu Arg Glu Tyr Ala Asn Asn						
1115	1120	1125				
Ile Leu Glu Ser Gly Val His Gly Ser Leu Ile Ala Leu Asp Glu						
1130	1135	1140				
Asn Phe Asp Tyr Ser Ser Leu Thr Leu Leu Leu Gln Ile Pro Thr						
1145	1150	1155				
Gln Asn Thr Gln Ala Arg Gln Ile Leu Glu Arg Glu Tyr Asn Asn						
1160	1165	1170				
Leu Leu Ala Leu Gly Thr Glu Arg Arg Leu Asp Glu Ser Asp Asp						
1175	1180	1185				
Lys Asn Phe Arg Arg Gly Ser Thr Trp Arg Arg Gln Phe Pro Pro						
1190	1195	1200				
Arg Glu Val His Gly Ile Ser Met Met Pro Gly Ser Ser Glu Thr						
1205	1210	1215				
Leu Pro Ala Gly Phe Arg Leu Thr Thr Thr Ser Gly Gln Ser Arg						
1220	1225	1230				
Lys Met Thr Thr Asp Val Ala Ser Ser Arg Leu Gln Arg Leu Asp						
1235	1240	1245				
Asn Ser Thr Val Arg Thr Tyr Ser Cys Leu Glu						
1250	1255					
<210> 239						
<211> 1134						
<212> DNA						
<213> human organism						
<400> 239						
atgaggcgac	tgaatcgaa	aaaaacttta	agtttgtaa	aagagttgga	tgcctttccg	60
aaggttcctg	agagctatgt	agagacttca	gccagtggag	gtacagtttc	tctaatacgca	120
tttacaacta	tggcttattt	aaccataatg	gaattctcag	tatatcaaga	tacatggatg	180
aagtatgaat	acgaagttaga	caaggatttt	tctagcaaat	taagaattaa	tatagatatt	240

actgttgcca tgaagtgtca atatgttggaa gcggatgtat tggatttagc agaaaacaatg	300
gttgcacatctg cagatggttt agtttatgaa ccaacagtat ttgatcttc accacacgag	360
aaagagtgcc agaggatgct gcagctgatt cagagtaggc tacaagaaga gcattcactt	420
caagatgtga tatttaaaag tgctttaaa agtacatcaa cagctttcc accaagagaa	480
gatgattcat cacagtcctcc aaatgcacatgc agaattcatg gccatctata tgtcaataaa	540
gtagcaggaa attttcacat aacagtggc aaggcaattc cacatcctcg tggcatgca	600
catttggcag cacttgtcaa ccatgaatct tacaattttt ctcatagaat agatcattt	660
tctttggag agcttggcc agcaatttatt aatccttttag atggaactga aaaaattgct	720
atagatcaca accagatgtt ccaatattttt attacagttg tgccaacaaa actacataca	780
tataaaatat cagcagacac ccatcagttt tctgtgacag aaaggaaacg tatcattaac	840
catgctgcag gcagccatgg agtctctggg atatttatga aatatgatct cagttctctt	900
atggtgacag ttactgagga gcacatgcca ttctggcagt tttttaag actctgtggt	960
attgttggag gaatctttc aacaacagggc atgttacatg gaattggaaa atttatagtt	1020
gaaataattt gctgtcgaaa cagacttggaa tcctataaac ctgtcaattc tgccctttt	1080
gaggatggcc acacagacaa ccacttacact ctttttagaaa ataatacaca ttga	1134

<210> 240

<211> 377

<212> PRT

<213> human organism

<400> 240

Met Arg Arg Leu Asn Arg Lys Lys Thr Leu Ser Leu Val Lys Glu Leu			
1	5	10	15

Asp Ala Phe Pro Lys Val Pro Glu Ser Tyr Val Glu Thr Ser Ala Ser		
20	25	30

Gly Gly Thr Val Ser Leu Ile Ala Phe Thr Thr Met Ala Leu Leu Thr		
35	40	45

Ile Met Glu Phe Ser Val Tyr Gln Asp Thr Trp Met Lys Tyr Glu Tyr		
50	55	60

Glu Val Asp Lys Asp Phe Ser Ser Lys Leu Arg Ile Asn Ile Asp Ile			
65	70	75	80

Thr Val Ala Met Lys Cys Gln Tyr Val Gly Ala Asp Val Leu Asp Leu  
85 90 95

Ala Glu Thr Met Val Ala Ser Ala Asp Gly Leu Val Tyr Glu Pro Thr  
100 105 110

Val Phe Asp Leu Ser Pro Gln Gln Lys Glu Trp Gln Arg Met Leu Gln  
115 120 125

Leu Ile Gln Ser Arg Leu Gln Glu Glu His Ser Leu Gln Asp Val Ile  
130 135 140

Phe Lys Ser Ala Phe Lys Ser Thr Ser Thr Ala Leu Pro Pro Arg Glu  
145 150 155 160

Asp Asp Ser Ser Gln Ser Pro Asn Ala Cys Arg Ile His Gly His Leu  
165 170 175

Tyr Val Asn Lys Val Ala Gly Asn Phe His Ile Thr Val Gly Lys Ala  
180 185 190

Ile Pro His Pro Arg Gly His Ala His Leu Ala Ala Leu Val Asn His  
195 200 205

Glu Ser Tyr Asn Phe Ser His Arg Ile Asp His Leu Ser Phe Gly Glu  
210 215 220

Leu Val Pro Ala Ile Ile Asn Pro Leu Asp Gly Thr Glu Lys Ile Ala  
225 230 235 240

Ile Asp His Asn Gln Met Phe Gln Tyr Phe Ile Thr Val Val Pro Thr  
245 250 255

Lys Leu His Thr Tyr Lys Ile Ser Ala Asp Thr His Gln Phe Ser Val  
260 265 270

Thr Glu Arg Glu Arg Ile Ile Asn His Ala Ala Gly Ser His Gly Val  
275 280 285

Ser Gly Ile Phe Met Lys Tyr Asp Leu Ser Ser Leu Met Val Thr Val  
290 295 300

Thr Glu Glu His Met Pro Phe Trp Gln Phe Phe Val Arg Leu Cys Gly  
305 310 315 320

Ile Val Gly Gly Ile Phe Ser Thr Thr Gly Met Leu His Gly Ile Gly  
325 330 335

Lys Phe Ile Val Glu Ile Ile Cys Cys Arg Phe Arg Leu Gly Ser Tyr  
340 345 350

Lys Pro Val Asn Ser Val Pro Phe Glu Asp Gly His Thr Asp Asn His  
355 360 365

Leu Pro Leu Leu Glu Asn Asn Thr His  
370 375

<210> 241

<211> 4298

<212> DNA

<213> human organism

<400> 241

aattcgcctt tgcttaatta agcatgttta ctttcctgtc atctgtcaact gctgctgtca 60

gtggcctcctt ggtgggttat gaacttggga tcatctctgg ggctcttctt cagatcaaaa 120

ccttatttagc cctgagctgc catgaggcagg aaatggttgt gagctccctc gtcattggag 180

ccctccttgc ctcactcacc ggaggggtcc tgatagacag atatgaaaga aggacagcaa 240

tcatcttgta atcctgcctg ctggactcg gaagcttagt cttgatcctc agtttatacct 300

acacggttct tatagtggga cgcatggcca taggggttcc catctccctc tcttccattg 360

ccacttgtt ttacatcgca gagattgctc ctcaacacag aagaggcctt cttgtgtcac 420

tgaatgagct gatgattgtc atcggcattc tttctgccta tatttcaaata tacgcatttg 480

ccaatgtttt ccatggctgg aagtacatgt ttggcttgc gattcccttg ggagttttgc 540

aagcaattgc aatgtatccc ctcctccaa gccctcggtt tctggatgaaaggacaag 600

aggagctgc tagcaagggtt ctggaaaggtaaagagact ctcagataca actgaggaac 660

tcactgtgat caaatcctcc ctgaaagatg aatatcagta cagttttgg gatctgttc 720

gttcaaaaga caacatgcgg acccgaataa tgataggact aacactagta tttttgtac 780

aaatcactgg ccaaccaaac atattgttct atgcatcaac tgtttgaag tcagttggat 840

ttcaaaagcaa tgagggcagct agcctgcctt ccactgggtt tggagtcgtc aaggtcatta 900

gcaccatccc tgccactctt ctgttagacc atgtcggcag caaaacattc ctctgcattg 960

gctcctctgt gatggcagct tcgttggtga ccatggccat cgtaaatctc aacatccaca 1020  
tgaacttcac ccatatctgc agaagccaca attctatcaa ccagtccttg gatgagtctg 1080  
tgatttatgg accagggaaac ctgtcaacca acaacaatac tctcagagac cacttcaaag 1140  
ggatttcttc ccatagcaga agctcactca tgcccctgag aaatgatgtg gataagagag 1200  
gggagacgac ctcagcatcc ttgctaaatg ctggattaag ccacactgaa taccagatag 1260  
tcacagacccc tggggacgtc ccagtttt tgaaatggct gtccttagcc agcttgcttg 1320  
tttatgttgc tgcttttca attggtctag gaccaatgcc ctggctggc ctcagcgaga 1380  
tcttcctgg tgggatcaga ggacgagcca tggcttaac ttcttagcatg aactggggca 1440  
tcaatctcct catctcgctg acattttga ctgtaactga tcttattggc ctgccatggg 1500  
tgtgctttat atatacaatc atgagtctag atcttattgg cctgccccatgg gtgtgcttta 1560  
tatatacaat catgagtcata gcatccctgc tttttgttgt tatgtttata cctgagacaa 1620  
aggatgctc tttggaacaa atatcaatgg agctagcaaa agtgaactat gtgaaaaaca 1680  
acattttgttt tatgagtcat caccaagaag aatttagtgcc aaaacagcct caaaaaagaa 1740  
aaccccagga gcagctttg gagtgtaaca agctgtgtgg taggggccaa tccaggcagc 1800  
tttctccaga gacctaattgg cctcaacacc ttctgaacgt ggatagtgcc agaacactta 1860  
ggaggggtgtc tttggaccaa tgcatacgatgg cgactcctgt gctctttt cagtgtcatg 1920  
gaactggttt tgaagagaca ctctgaaatg ataaagacag ccttaatcc ccctccctmc 1980  
cagaaggaac ctcaaaaagg agatgaggta caaggtccta agtgatctt tttctgagc 2040  
agatatacg gttaaaaaaaaaaa aaaaagttact ggctggtta atacttctta ctttcttcac 2100  
agagcagcct ttgaatagac tatgtcctag tgaagacatc aaccccgcc ttaagctatg 2160  
tatgtatggc ggccagtcgc agcttttatta tgcagacaca caagtggctc ggacatgagg 2220  
gtacagtttgc tgcctaccaa gacactactt gcactggatc ttacgcaaaa aagaaccaga 2280  
acacacagtg tggacaactg cccatatatt ctatctagat taggagaggg tcctggctag 2340  
gattttatgt gtaattccctt gttacattca acaagtataa agattataga gcttattttt 2400  
tgaactataa actataattt aatgcaaaaat atcctttat gaatttcatg ttaatattgt 2460  
gaaatattaa aataattccr caatagttga gaaaaatgag cattttttc cattttaaa 2520  
aaatgcatac aaaagacaat tttaaaatcc tggaccata tttatgttgc agtagctgtt 2580  
agtaaaaacat tagaaaagga gtcaggccat taggttattt atccaaatct ctaagcaatt 2640

aggttgaagt tattaagtca agcctagaaa agctgcctcc ttgtaaggct ttcatgacaa 2700  
tgtatagtaa tccacagtgt ccaattcttc acactcctca ggaatatcac tacctcaggt 2760  
tacggtagac aggctataat tgatgatgat gttcagataa ctgaagacac aataaatgac 2820  
attcagacat caggamaaww ccctcatgtt ctttctatg atggccacct gtaccagcaa 2880  
cgtaggtttc acccacacaa cgatgaactg ttctcttact tctccagttg attttaaga 2940  
cttgtaaga ggtcttacta ataaaatttg ggtatgatag aaaawccaca atcaaawctt 3000  
gaaccaaata acatattaaa ttactaatat ttaagtgatg gaagacacac aaaaaactta 3060  
aaagcacgaa caacctaact tgaaaaagaa tttaaaata tgattaacct gaagaaaaga 3120  
gaatcctaag agccaaagct ccttttatt tagcttgaa tttcctatt ggccctaac 3180  
aaactgtccc aatgtcatat aaggaaacat gatctattac attcctttat aacaatgtgg 3240  
agagactata aacctatgta agtagtaaaa ctatatyaga gactcaggag actgactaaa 3300  
aggcctggat ctgcagtgtt ttatctgtat aaaaattggc agggggaaagc taaaaggaaa 3360  
ggagattgga gatctcaatt ctatcatggt gtatttcata cgcaaatcag agcatgcatt 3420  
gtttttgtt tttggaaaga gaaggaaagt gtgttctgcc ccatgtttcc ttccgtgttt 3480  
atagttcaaa ctctatatat acttcaggta tttttgttt agcccttcata tataaatggg 3540  
cagaaattt tttatcaacc tagccagttt attactagtg accttgactt cagttcttgc 3600  
agcattcttt tatatttttc ttttattatc ctgagtcgt aactaaacaa ttttgtttcc 3660  
aaatttttat ccaatatcca ttgcaccaca ccaaatcaag cttcttgatt ttcaaaaata 3720  
aaaagggggaa aataacttaca acttgtacat atatattcac agtttttatt tataaaaaaaa 3780  
attacagta cttatggaga gccagcagaa gacatcagag cactcaattc ttcccatctt 3840  
tgttaagggtt agcgaattac ccatggacac tggtaggtga ggctcattcg gcagccctga 3900  
aaacaaacactg tctttaccct ctcccttcag ataaagcact tcgattatct 3960  
attgatctgc ccagtttca agtcatgcga atactaaaaa ggttacatca tctggatctg 4020  
tacctggct atataagcat gttttcccccc tattctatgt ttctttttt ggtgaacatt 4080  
gaaaaacagg aggtgactta ttactgttaa taaaactaa atgaaaaatg tcaagtctt 4140  
aaaacagtga gcttgtaact ctttcatgtt attttattct ctatgaattt ggctatccta 4200  
ctgaatctt aaataaagga aataaacact ttttttwaa aaaaaggaa aaatamaarw 4260  
mwaaaaaatct caatgaaata tttcacaaga agaaaaaa 4298

<210> 242  
<211> 597  
<212> PRT  
<213> human organism

<400> 242

Met Phe Thr Phe Leu Ser Ser Val Thr Ala Ala Val Ser Gly Leu Leu  
1 5 10 15

Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala Leu Leu Gln Ile Lys  
20 25 30

Thr Leu Leu Ala Leu Ser Cys His Glu Gln Glu Met Val Val Ser Ser  
35 40 45

Leu Val Ile Gly Ala Leu Leu Ala Ser Leu Thr Gly Gly Val Leu Ile  
50 55 60

Asp Arg Tyr Gly Arg Arg Thr Ala Ile Ile Leu Ser Ser Cys Leu Leu  
65 70 75 80

Gly Leu Gly Ser Leu Val Leu Ile Leu Ser Leu Ser Tyr Thr Val Leu  
85 90 95

Ile Val Gly Arg Ile Ala Ile Gly Val Ser Ile Ser Leu Ser Ser Ile  
100 105 110

Ala Thr Cys Val Tyr Ile Ala Glu Ile Ala Pro Gln His Arg Arg Gly  
115 120 125

Leu Leu Val Ser Leu Asn Glu Leu Met Ile Val Ile Gly Ile Leu Ser  
130 135 140

Ala Tyr Ile Ser Asn Tyr Ala Phe Ala Asn Val Phe His Gly Trp Lys  
145 150 155 160

Tyr Met Phe Gly Leu Val Ile Pro Leu Gly Val Leu Gln Ala Ile Ala  
165 170 175

Met Tyr Phe Leu Pro Pro Ser Pro Arg Phe Leu Val Met Lys Gly Gln  
180 185 190

Glu Gly Ala Ala Ser Lys Val Leu Gly Arg Leu Arg Ala Leu Ser Asp  
195 200 205

Thr Thr Glu Glu Leu Thr Val Ile Lys Ser Ser Leu Lys Asp Glu Tyr  
210 215 220

Gln Tyr Ser Phe Trp Asp Leu Phe Arg Ser Lys Asp Asn Met Arg Thr  
225 230 235 240

Arg Ile Met Ile Gly Leu Thr Leu Val Phe Phe Val Gln Ile Thr Gly  
245 250 255

Gln Pro Asn Ile Leu Phe Tyr Ala Ser Thr Val Leu Lys Ser Val Gly  
260 265 270

Phe Gln Ser Asn Glu Ala Ala Ser Leu Ala Ser Thr Gly Val Gly Val  
275 280 285

Val Lys Val Ile Ser Thr Ile Pro Ala Thr Leu Leu Val Asp His Val  
290 295 300

Gly Ser Lys Thr Phe Leu Cys Ile Gly Ser Ser Val Met Ala Ala Ser  
305 310 315 320

Leu Val Thr Met Gly Ile Val Asn Leu Asn Ile His Met Asn Phe Thr  
325 330 335

His Ile Cys Arg Ser His Asn Ser Ile Asn Gln Ser Leu Asp Glu Ser  
340 345 350

Val Ile Tyr Gly Pro Gly Asn Leu Ser Thr Asn Asn Asn Thr Leu Arg  
355 360 365

Asp His Phe Lys Gly Ile Ser Ser His Ser Arg Ser Ser Leu Met Pro  
370 375 380

Leu Arg Asn Asp Val Asp Lys Arg Gly Glu Thr Thr Ser Ala Ser Leu  
385 390 395 400

Leu Asn Ala Gly Leu Ser His Thr Glu Tyr Gln Ile Val Thr Asp Pro  
405 410 415

Gly Asp Val Pro Ala Phe Leu Lys Trp Leu Ser Leu Ala Ser Leu Leu  
420 425 430

Val Tyr Val Ala Ala Phe Ser Ile Gly Leu Gly Pro Met Pro Trp Leu  
435 440 445

Val Leu Ser Glu Ile Phe Pro Gly Gly Ile Arg Gly Arg Ala Met Ala  
450 455 460

Leu Thr Ser Ser Met Asn Trp Gly Ile Asn Leu Leu Ile Ser Leu Thr  
465 470 475 480

Phe Leu Thr Val Thr Asp Leu Ile Gly Leu Pro Trp Val Cys Phe Ile  
485 490 495

Tyr Thr Ile Met Ser Leu Asp Leu Ile Gly Leu Pro Trp Val Cys Phe  
500 505 510

Ile Tyr Thr Ile Met Ser Leu Ala Ser Leu Leu Phe Val Val Met Phe  
515 520 525

Ile Pro Glu Thr Lys Gly Cys Ser Leu Glu Gln Ile Ser Met Glu Leu  
530 535 540

Ala Lys Val Asn Tyr Val Lys Asn Asn Ile Cys Phe Met Ser His His  
545 550 555 560

Gln Glu Glu Leu Val Pro Lys Gln Pro Gln Lys Arg Lys Pro Gln Glu  
565 570 575

Gln Leu Leu Glu Cys Asn Lys Leu Cys Gly Arg Gly Gln Ser Arg Gln  
580 585 590

Leu Ser Pro Glu Thr  
595

<210> 243  
<211> 979  
<212> DNA  
<213> human organism

<220>  
<221> misc\_feature  
<222> (17)..(17)  
<223> n is a, c, g, or t

<220>

```

<221> misc_feature
<222> (229)..(230)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (238)..(238)
<223> n is a, c, g, or t

<400> 243
tttagccacc agagganttc tcttcaaata cccaaaatcc atcagtatct tgaatcatgc      60
tggattttga agaattctta agaagccatg taaagggggc tctctggcct tgaaatagt
atgttttta tacagaaagg agaatgcaga atggtcagac tatcatgcac tgttaaattt      120
gatttcaaga aattacagga aaactttcca aagttccatc tcacagaann ttattncc      180
aagaattcca agataagttt agtttatgg aagactttt tgggtttt actcactctt      240
catctcagac atcgacagat gattacatca cttatagttc tagtaaattt attaatataa      300
aactcagaga cattccaata tccacattgc ttacaccatt aggcatagat tcagtgtcag      360
ctatgacaat tgaaaatgag ctgtttgtg atttaaaggt taaaatttct ctaaccaaac      420
tgcttgatcc agatgcagga ctgcaaatgt taatattgt tctggaagaa caatcaaata      480
agacttaaga ggaaaggaa tggccacaat ccacctgaaa tttttctta aaaagtgtgc      540
agcctactaa atcagaatga aaatagaagt acaagattt aaacaaaatg caatcaaact      600
tttcttaagc ttacctaaag ttatcatc tgaaaatttc aagcaacttt gttcaacatt      660
aaattgacaa tctaaactaa caagtctttt gaatttatgc atggtagtaa acattctctc      720
tattaacttt attacctaag gctaaaccta aaattttaa gcaaaattag aaaaatagtc      780
ttcactcatc aaaaaataaa gtttgtaca ttttagtattt tcccaataaa attggtcgtt      840
cttggttttt tatttgaga gtctgtgcaa aatgtcacta aaaataaatt agcactagaa      900
attatttcta aataccaaa                                         960
                                                               979

```

```

<210> 244
<211> 2443
<212> DNA
<213> human organism

<400> 244
aaatggcgtg cccgtctctc cgccggcccc ctgcctcgca gtggttctc ctgcagctcc      60
cctgggctcc gcggccagta gtgcagcccg tggagccgag gctttgcccg tctcctctgg      120
gtggcccccag tgcgcgggct gacactcatt cagccgggaa aggtgaggcg agtagaggct      180

```

ggtcggaac ttgcccccc cagcagcgcc ggcggctaa gcccaggccc gggcagacaa 240  
aaggaggccgc ccgcgttagga aggcacggcc ggcggccgcg gagcgcagcg atggccggc 300  
gagggggcag cgcgctgctg gctctgtgcg gggcaactggc tgcctgcggg tggctcctgg 360  
gcgccgaagc ccaggagccc gggcgcccg cggcggcat gaggcggcgc cggcggctgc 420  
agcaagagga cggcatctcc ttgcgttacc accgctaccc cgagctgcgc gaggcgctcg 480  
tgtccgtgtg gctgcagtgc accgccatca gcaggattt cacggtggg cgcagctcg 540  
aggccggga gctcctggc atcgagctgt ccgacaaccc tggcgtccat gagcctggg 600  
agcctgaatt taaatacatt gggatatgc atggaatga ggctgttgga cgagaactgc 660  
tcatttctt ggcccagtac ctatgcaacg aataccagaa ggggaacgag acaattgtca 720  
acctgatcca cagtacccgc attcacatca tgcctccct gaacccagat ggcttgaga 780  
aggcagcgtc tcagcctggt gaactcaagg actgggttgt gggtcgaagc aatgcccagg 840  
gaatagatct gaaccggaac ttccagacc tggataggat agtgtacgtg aatgagaaaag 900  
aagggtggcc aaataatcat ctgttggaaaa atatgaagaa aattgtggat caaaacacaa 960  
agcttgctcc tgagaccaag gctgtcattc attggattat ggatattcct tttgtgctt 1020  
ctgccaatct ccatggagga gaccttgtgg ccaattatcc atatgatgag acgcggagt 1080  
gtagtgctca cgaatacagc tcctccccag atgacccat tttccaaagc ttggccggg 1140  
catactcttc tttcaacccg gccatgtctg accccaatcg gccaccatgt cgcaagaatg 1200  
atgatgacag cagcttgta gatggAACCA ccaacgggtgg tgcttggtac agcgtacctg 1260  
gagggatgca agacttcaat taccttagca gcaactgttt tgagatcacc gtggagctt 1320  
gctgtgagaa gttcccacct gaagagactc tgaagaccta ctgggaggat aacaaaaact 1380  
ccctcattag ctaccttgag cagatacacc gaggagttaa aggatttgc cgagaccttc 1440  
aaggtaaccc aattgcgaat gccaccatct ccgtggagg aatagaccac gatgttacat 1500  
ccgcaaagga tggtgattac tggagattgc ttatacctgg aaactataaa cttacagcct 1560  
cagctccagg ctatctggca ataacaaaga aagtggcagt tccttacagc cctgtgctg 1620  
gggttgattt tgaactggag tcatTTCTG aaaggaaaga agaggagaag gaagaattga 1680  
tggaatggtg gaaaatgtg tcagaaactt taaatttttta aaaaggcttc tagttagctg 1740  
ctttaaatct atctatataa tggatgtatga tgtaatgtgg tctttttttt agatTTGTG 1800  
cagttataac ttaacattga ttatTTTTT aatcatttaa atattaatca actttcctta 1860  
aaataaaatag cctcttaggt aaaaatataa gaacttgata tatttcattc tcttatata 1920

tattcatttt cctacacctata ttacacaaaa aagtatagaa aagatccaag taatggcc	1980
atcctaggct taaatgcaat attcctggta ttatcacaa tgccagaattt tttgagtaat	2040
tcttagcttc aaaaatttgt gaagttcttt tactgttaatt ggtgacaatg tcacataatg	2100
aatgctattg aaaaggttaa cagatacago tcggagttgt gagcactcta ctgcaagact	2160
taaatagttc agtataaatt gtcgttttt tcttgtgctg actaactata agcatgatct	2220
tgttaatgca ttttgatgg gaagaaaagg tacatgtta caaagaggtt ttatgaaaag	2280
aataaaaatt gacttcttgc ttgtacatat aggagcaata ctattatatt atgttagtccg	2340
ttaacactac ttaaaagttt agggtttctt ctgggtgtta gagtggccca gaattgcatt	2400
ctgaatgaat aaaggttaaa aaaaaatccc cagtaaaaaa aaa	2443

<210> 245  
<211> 476  
<212> PRT  
<213> human organism

<400> 245

Met Ala Gly Arg Gly Gly Ser Ala Leu Leu Ala Leu Cys Gly Ala Leu			
1	5	10	15

Ala Ala Cys Gly Trp Leu Leu Gly Ala Glu Ala Gln Glu Pro Gly Ala		
20	25	30

Pro Ala Ala Gly Met Arg Arg Arg Arg Leu Gln Gln Glu Asp Gly		
35	40	45

Ile Ser Phe Glu Tyr His Arg Tyr Pro Glu Leu Arg Glu Ala Leu Val		
50	55	60

Ser Val Trp Leu Gln Cys Thr Ala Ile Ser Arg Ile Tyr Thr Val Gly			
65	70	75	80

Arg Ser Phe Glu Gly Arg Glu Leu Leu Val Ile Glu Leu Ser Asp Asn		
85	90	95

Pro Gly Val His Glu Pro Gly Glu Pro Glu Phe Lys Tyr Ile Gly Asn		
100	105	110

Met His Gly Asn Glu Ala Val Gly Arg Glu Leu Leu Ile Phe Leu Ala		
115	120	125

Gln Tyr Leu Cys Asn Glu Tyr Gln Lys Gly Asn Glu Thr Ile Val Asn  
130 135 140

Leu Ile His Ser Thr Arg Ile His Ile Met Pro Ser Leu Asn Pro Asp  
145 150 155 160

Gly Phe Glu Lys Ala Ala Ser Gln Pro Gly Glu Leu Lys Asp Trp Phe  
165 170 175

Val Gly Arg Ser Asn Ala Gln Gly Ile Asp Leu Asn Arg Asn Phe Pro  
180 185 190

Asp Leu Asp Arg Ile Val Tyr Val Asn Glu Lys Glu Gly Gly Pro Asn  
195 200 205

Asn His Leu Leu Lys Asn Met Lys Lys Ile Val Asp Gln Asn Thr Lys  
210 215 220

Leu Ala Pro Glu Thr Lys Ala Val Ile His Trp Ile Met Asp Ile Pro  
225 230 235 240

Phe Val Leu Ser Ala Asn Leu His Gly Gly Asp Leu Val Ala Asn Tyr  
245 250 255

Pro Tyr Asp Glu Thr Arg Ser Gly Ser Ala His Glu Tyr Ser Ser Ser  
260 265 270

Pro Asp Asp Ala Ile Phe Gln Ser Leu Ala Arg Ala Tyr Ser Ser Phe  
275 280 285

Asn Pro Ala Met Ser Asp Pro Asn Arg Pro Pro Cys Arg Lys Asn Asp  
290 295 300

Asp Asp Ser Ser Phe Val Asp Gly Thr Thr Asn Gly Gly Ala Trp Tyr  
305 310 315 320

Ser Val Pro Gly Gly Met Gln Asp Phe Asn Tyr Leu Ser Ser Asn Cys  
325 330 335

Phe Glu Ile Thr Val Glu Leu Ser Cys Glu Lys Phe Pro Pro Glu Glu  
340 345 350

Thr Leu Lys Thr Tyr Trp Glu Asp Asn Lys Asn Ser Leu Ile Ser Tyr  
355 360 365

Leu Glu Gln Ile His Arg Gly Val Lys Gly Phe Val Arg Asp Leu Gln  
370 375 380

Gly Asn Pro Ile Ala Asn Ala Thr Ile Ser Val Glu Gly Ile Asp His  
385 390 395 400

Asp Val Thr Ser Ala Lys Asp Gly Asp Tyr Trp Arg Leu Leu Ile Pro  
405 410 415

Gly Asn Tyr Lys Leu Thr Ala Ser Ala Pro Gly Tyr Leu Ala Ile Thr  
420 425 430

Lys Lys Val Ala Val Pro Tyr Ser Pro Ala Ala Gly Val Asp Phe Glu  
435 440 445

Leu Glu Ser Phe Ser Glu Arg Lys Glu Glu Glu Lys Glu Glu Leu Met  
450 455 460

Glu Trp Trp Lys Met Met Ser Glu Thr Leu Asn Phe  
465 470 475

<210> 246  
<211> 1926  
<212> DNA  
<213> human organism

<400> 246  
ggggcgacgt gagcgcgcag gggggcggcg gcctcgccctc gtctctctct ctgcgcctgg 60  
gtcgggtggg tgacgcccag agccagagag atgtcgatt tcgacagtaa cccgtttgcc 120  
gaccggatc tcaacaatcc cttcaaggat ccatcagtta cacaagtgac aagaatgtt 180  
ccaccaggac ttgatgaata taatccattc tcggattcta gaacacctcc accaggcggt 240  
gtgaagatgc ctaatgtacc caatacacaa ccagcaataa tgaaaccaac agaggaacat 300  
ccagcttata cacagattgc aaaggaacat gcattggccc aagctgaact tcttaagcgc 360  
caagaagaac tagaaagaaa agccgcagaa ttagatcgac gggAACGAGA aatgcaaaac 420  
ctcagtcaac atggtagaaa aaatatttgg ccaccccttc ctagcaattt tcctgtcgga 480  
ccttgtttct atcaggaatt ttctgttagac attccctgttag aattccaaaa gacagtaaag 540

cttatgtact	acttgtggat	gttccatgca	gtaacactgt	ttctaaatat	cttcggatgc	600
ttggcttggt	tttgtgttga	ttctgcaaga	gcgggtgatt	ttggatttag	tatcctgtgg	660
ttcttgcttt	ttactccttg	ttcatttgc	tgttgtaca	gaccactta	tggagcttc	720
aggagtgaca	gttcatttag	attcttgta	ttcttctcg	tctatatttgc	tcagttgct	780
gtacatgtac	tccaagctgc	aggatttcat	aactggggca	attgtggttg	gatttcatcc	840
cttactggtc	tcaacccaaa	tattcctgtt	ggaatcatga	tgataatcat	agcagcactt	900
ttcacagcat	cagcagtc	ctcactagtt	atgttcaaaa	aagtacatgg	actatatcgc	960
acaacaggtg	ctagtttga	gaaggcccaa	caggagtttgc	caacaggtgt	gatgtccaaac	1020
aaaactgtcc	agaccgcagc	tgcaaatgca	gcttcaactg	cagcatctag	tgcagctcag	1080
aatgcttca	aggtaacca	gatttaagaa	tcttcaaaca	atacactgtt	acctttgac	1140
tgtacctttt	tctccagttt	ctgtattcta	caaataatttt	tatgttcaaa	acacacagta	1200
cagacagcat	ggatatttcc	tgttcaacttgc	tgcattggct	aaaaccagga	aaacttcctt	1260
gtcttattac	tttaccta	atgttcttaa	tatttcagtg	ccccttgcag	aaaaaatatt	1320
acatgctaaa	taaatattct	ccatattttt	ggggatgac	attcagtgaa	ttatttcagt	1380
ggtgaccac	tgaaaattaa	taatggtact	tatgattaaa	aacgcattta	atactaactg	1440
cagtagttct	ttcaagaatc	tttagagata	aggattgcac	attggaaaag	taaaccatgt	1500
ttcattcctt	tttccctatt	tatattgaaa	gaaataggcc	agcagagact	tagggatttt	1560
aaattggctt	gcttttagc	tgtttcagtc	accagtgaag	gcctatgtg	cattttgtag	1620
tagataatgt	aaaatttgc	atcttttct	tttctttttt	ttagaatagc	tgatattttg	1680
ataacaatct	ctaatttgca	tgggcaccac	atttcttata	ttaaaagaat	tagtgttttgc	1740
gcttctgtac	tgcttatgg	tgttaggattc	aggggttaat	ggaatcacag	aaatgatatt	1800
ctgcaagaat	ttctttaaa	taaaaagttt	gggggtgcaa	tataagaagt	ttatataata	1860
tgcagtacat	tatccaaaag	agaaggtgt	taatgcagta	gaaagtagtg	gtaataattc	1920
cttttt						1926

<210> 247  
 <211> 338  
 <212> PRT  
 <213> human organism

<400> 247

Met Ser Asp Phe Asp Ser Asn Pro Phe Ala Asp Pro Asp Leu Asn Asn

1

5

10

15

Pro Phe Lys Asp Pro Ser Val Thr Gln Val Thr Arg Asn Val Pro Pro  
20 25 30

Gly Leu Asp Glu Tyr Asn Pro Phe Ser Asp Ser Arg Thr Pro Pro Pro  
35 40 45

Gly Gly Val Lys Met Pro Asn Val Pro Asn Thr Gln Pro Ala Ile Met  
50 55 60

Lys Pro Thr Glu Glu His Pro Ala Tyr Thr Gln Ile Ala Lys Glu His  
65 70 75 80

Ala Leu Ala Gln Ala Glu Leu Leu Lys Arg Gln Glu Glu Leu Glu Arg  
85 90 95

Lys Ala Ala Glu Leu Asp Arg Arg Glu Arg Glu Met Gln Asn Leu Ser  
100 105 110

Gln His Gly Arg Lys Asn Ile Trp Pro Pro Leu Pro Ser Asn Phe Pro  
115 120 125

Val Gly Pro Cys Phe Tyr Gln Glu Phe Ser Val Asp Ile Pro Val Glu  
130 135 140

Phe Gln Lys Thr Val Lys Leu Met Tyr Tyr Leu Trp Met Phe His Ala  
145 150 155 160

Val Thr Leu Phe Leu Asn Ile Phe Gly Cys Leu Ala Trp Phe Cys Val  
165 170 175

Asp Ser Ala Arg Ala Val Asp Phe Gly Leu Ser Ile Leu Trp Phe Leu  
180 185 190

Leu Phe Thr Pro Cys Ser Phe Val Cys Trp Tyr Arg Pro Leu Tyr Gly  
195 200 205

Ala Phe Arg Ser Asp Ser Ser Phe Arg Phe Phe Val Phe Phe Val  
210 215 220

Tyr Ile Cys Gln Phe Ala Val His Val Leu Gln Ala Ala Gly Phe His  
225 230 235 240

Asn Trp Gly Asn Cys Gly Trp Ile Ser Ser Leu Thr Gly Leu Asn Gln  
245 250 255

Asn Ile Pro Val Gly Ile Met Met Ile Ile Ile Ala Ala Leu Phe Thr  
260 265 270

Ala Ser Ala Val Ile Ser Leu Val Met Phe Lys Lys Val His Gly Leu  
275 280 285

Tyr Arg Thr Thr Gly Ala Ser Phe Glu Lys Ala Gln Gln Glu Phe Ala  
290 295 300

Thr Gly Val Met Ser Asn Lys Thr Val Gln Thr Ala Ala Ala Asn Ala  
305 310 315 320

Ala Ser Thr Ala Ala Ser Ser Ala Ala Gln Asn Ala Phe Lys Gly Asn  
325 330 335

Gln Ile

<210> 248  
<211> 615  
<212> DNA  
<213> human organism

<400> 248	
atgagagaca ataaatcgtg tgcttttgc atggaaaagt taaatgtttg ttttgaaggc	60
acagtaatag caggctattc agtgtttgc actacctgca tcattcatct ggctgttagct	120
agtgcactac aatttcctaa aaagtcttct caccctcaca ggactgctct acatctggcc	180
tctgccaatg gaaattcaga agtagtaaaa ctcctgctgg acagacgatg tcaacttaat	240
atccttgaca acaaaaagag gacagctctg acaaaggccg tacaatgcca ggaagatgaa	300
tgtgcgttaa tggtgctgga acatggact gatccgata ttccagatga gtatggaaat	360
accgctctac actatgctat ctacaatgaa gataaattaa tggccaaagc actgcttta	420
tacggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttggtgta	480
catgagcaaa aacagcaagt ggtgaaattt ttaatcaaga aaaaagcaaa tttaaatgca	540
ctggatagat atggaagggtg tgtgaccttg ggaacgttat ttaccaccaa atatgttgta	600
atatatgaaa agtag	615

<210> 249  
<211> 204  
<212> PRT  
<213> human organism

<400> 249

Met Arg Asp Asn Lys Ser Cys Ala Phe Phe Met Gly Lys Leu Asn Val  
1 5 10 15

Cys Phe Glu Gly Thr Val Ile Ala Gly Tyr Ser Val Phe Ala Thr Thr  
20 25 30

Cys Ile Ile His Leu Ala Val Ala Ser Ala Leu Gln Phe Pro Lys Lys  
35 40 45

Ser Ser His Pro His Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly  
50 55 60

Asn Ser Glu Val Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn  
65 70 75 80

Ile Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala Val Gln Cys  
85 90 95

Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro  
100 105 110

Asn Ile Pro Asp Glu Tyr Gly Asn Thr Ala Leu His Tyr Ala Ile Tyr  
115 120 125

Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp  
130 135 140

Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val  
145 150 155 160

His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala  
165 170 175

Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Cys Val Thr Leu Gly Thr  
180 185 190

Leu Phe Thr Thr Lys Tyr Val Val Ile Tyr Glu Lys  
195 200

<210> 250  
<211> 3342  
<212> DNA  
<213> human organism

<400> 250 atggatca tctatcttc tttctgcaat tattacatgg agttctacag agaagagctt 60  
ccccacattg actatttgat tgacattcg tttgcaacag gaaaggtag tcagccggga 120  
gaggacactt cctaccatca atgcgctcag cttgaagcca gagacgaagg caccgacagt 180  
ttattattaa acaatggcag cagcgccacg ctgaagacac gaacgcgctg ttatggaacc 240  
cccagaggta tccccatcg tagcctgctc cagccgactc cgcccacatg taaaacgaag 300  
atcaggagca gatttgaaga attacaaagt gaattggtag cagtcagcat gtcagagaca 360  
gaccacatag cctctacttc ctctgataaa aatgttggaa aaacacactga attaaaggaa 420  
gactcatgca acttgtttc tggcaatgaa agcagcaa at tagaaaatga gtccaaacta 480  
ttgtcattaa acactgataa aactttatgt caaccta atg agcataataa tcgaattgaa 540  
gcccgaggaaa attatattcc agatcatgg ggaggtgagg attcttgtag caaaacagac 600  
acaggctcag aaaattctga acaaatacg aatttccta gtggaaattt tgctaaacat 660  
atttcaaaaa caaatgaaac agaacagaaa gtaacacaaa tattggtagg attaaggta 720  
tctacatttc cagaatcagc taatgaaaag acttattcg aaagccctta tgatacagac 780  
tgcaccaaga aatttatttc aaaaataaaag agcgttcag catcagagga tttgttggaa 840  
gaaatagaat ctgagcttt atctacggag tttgcagaac atcgagtacc aaatggaaatg 900  
aataaggag aacatgcatt agttctgtt gaaaagtgtg tgcaagataa atatttgcag 960  
caggaacata tcataaaaaa gtttataaa gaaaataaga agcatcagga gctcttcgta 1020  
gacatttggc cagaaaaaga caatttaaga gaagaactaa agaaaagaac agaaactgag 1080  
aagcagcata tgaacacaat taaacagtta gaatcaagaa tagaagaact taataaagaa 1140  
gttaaagctt ccagagatca actaatagct caagacgtt cagctaaaaa tgctttcag 1200  
cagttacaca aagagatggc ccaacggatg gaacaggcca acaagaaaatg tgaagaggca 1260  
cgccaagaaa aagaagcaat ggtatgaaa tatgtaaagag gtgagaagga atcttttagat 1320  
cttcgaaagg aaaaagagac acttgagaaa aaacttagag atgcaaataa ggaacttgag 1380  
aaaaacacta acaaattaa gcagcttct caggagaaag gacggttgca ccagctgtat 1440

gaaactaagg aaggcgaaac gactagactc atcagagaaa tagacaatt aaaggaagac 1500  
atthaactctc acgtcatcaa agtaaagtgg gcacaaaaca aattaaaagc tgaaatggat 1560  
tcacacaagg aaaccaaaga taaactcaa gaaacaacaa caaaattaac acaagcaaag 1620  
gaagaagcag atcagatacg aaaaaactgt caggatatga taaaaacata tcaggagtca 1680  
gaagaaatta aatcaaatga gcttgatgca aagcttagag tcacaaaagg agaacttgaa 1740  
aaacaaatgc aagaaaaatc tgaccagcta gagatgcac tcgaaaaat aaaggaacta 1800  
gaagatctga agagaacatt taaggagggt atggatgagt taagaacact gagaacaaag 1860  
gtgaaatgtc tagaagatga acgattaaga acagaagatg aattatcaa atataaggaa 1920  
attattaatc gccaaaaagc taaaattcag aatttattgg acaagggtgaa aactgcagat 1980  
cagctacagg agcagctca aagaggtaa gaaatgggaaaatggaa agaagaagtg 2040  
gaaagtctta attcttgat taatgaccta caaaaagaca tcgaaggcag tagaaaaga 2100  
gaatctgagc tgctgctgtt tacagaaagg ctcactagta agaatgcaca gttcagtct 2160  
gaatccaatt ctgcagtc acaatttgat aaagttccct gtatgaaag tcagttacaa 2220  
agccagtgtg aacaaatgaa acagacaaat attaattgg aaagtaggtt gttgaaagag 2280  
gaagaactgc gaaaagagga agtccaaact ctgcaagctg aactcgctt tagacaaaca 2340  
gaagttaaag cattgagttac ccaggtagaa gaattaaaag atgagttat aactcagaga 2400  
cgtaaacatg cctctagtat caaggatctc accaaacaac ttcatcaagc acgaagaaaa 2460  
ttagatcagg ttgagagtgg aagctatgac aaagaagtca gcagcatggg aagtcgttct 2520  
atttcatcag ggtccctgaa tgctcgaagc agtgcagaag atcgatctcc agaaaatact 2580  
gggtccctcag tagctgtgaa taactttcca caagtagata aggccatgtt gattgagaga 2640  
atagttaggc tgcaaaaagc acatgcccgg aaaaatgaaa agatagaatt tatggaggac 2700  
cacatcaaac aactggtgga agaaattagg aaaaaacaa aaataattca aagttatatt 2760  
ttacgagaag aatcaggcac actttcttca gaggcatctg attttacaa agttcattta 2820  
atagacggg gtggcatcat ggcattttatacatccc atccagctga caatggatta 2880  
acattggagc tctctttgaa aatcaaccga aaattacagg ctgttttggg ggatacggtt 2940  
ctaaaaaata ttactttgaa ggaaaatcta caaacacttg gaacagaaat agaacgtctt 3000  
attnaacacc agcatgaact agaacagagg acaaagaaaa cctaaaacaa gcctcttgct 3060  
cagtaaagag acaaagcca cacaggagta ggtgccactg acctcttatttggagactt 3120

tgttccactt tttgtttcag ccagtaaaaa tattgtttg cttcatctgt acacaaaaaa 3180  
atacccttt acaatatgaa tgcattgctg tatatactgt aagactgaaa gctttgatga 3240  
aatttgggg tgtatggtgc aatatgacag cctgtcattg aatctaaaca acttaatttg 3300  
cttgttattca taagaagtgt tgaacattac aaggccttt at 3342

<210> 251  
<211> 1014  
<212> PRT  
<213> human organism

<400> 251

Met Val Ile Ile Tyr Leu Ser Phe Cys Asn Tyr Tyr Met Glu Phe Tyr  
1 5 10 15

Arg Glu Glu Leu Pro His Ile Asp Tyr Leu Ile Asp Ile Gln Phe Ala  
20 25 30

Thr Gly Lys Val Thr Gln Pro Gly Glu Asp Thr Ser Tyr His Gln Cys  
35 40 45

Ala Gln Leu Glu Ala Arg Asp Glu Gly Thr Asp Ser Leu Leu Leu Asn  
50 55 60

Asn Gly Ser Ser Ala Thr Leu Lys Thr Arg Thr Arg Cys Tyr Gly Thr  
65 70 75 80

Pro Arg Gly Leu Pro His Arg Ser Leu Leu Gln Pro Thr Pro Pro Thr  
85 90 95

Cys Lys Thr Lys Ile Arg Ser Arg Phe Glu Glu Leu Gln Ser Glu Leu  
100 105 110

Val Pro Val Ser Met Ser Glu Thr Asp His Ile Ala Ser Thr Ser Ser  
115 120 125

Asp Lys Asn Val Gly Lys Thr Pro Glu Leu Lys Glu Asp Ser Cys Asn  
130 135 140

Leu Phe Ser Gly Asn Glu Ser Ser Lys Leu Glu Asn Glu Ser Lys Leu  
145 150 155 160

Leu Ser Leu Asn Thr Asp Lys Thr Leu Cys Gln Pro Asn Glu His Asn

165

170

175

Asn Arg Ile Glu Ala Gln Glu Asn Tyr Ile Pro Asp His Gly Gly Gly  
180 185 190

Glu Asp Ser Cys Ala Lys Thr Asp Thr Gly Ser Glu Asn Ser Glu Gln  
195 200 205

Ile Ala Asn Phe Pro Ser Gly Asn Phe Ala Lys His Ile Ser Lys Thr  
210 215 220

Asn Glu Thr Glu Gln Lys Val Thr Gln Ile Leu Val Glu Leu Arg Ser  
225 230 235 240

Ser Thr Phe Pro Glu Ser Ala Asn Glu Lys Thr Tyr Ser Glu Ser Pro  
245 250 255

Tyr Asp Thr Asp Cys Thr Lys Lys Phe Ile Ser Lys Ile Lys Ser Val  
260 265 270

Ser Ala Ser Glu Asp Leu Leu Glu Glu Ile Glu Ser Glu Leu Leu Ser  
275 280 285

Thr Glu Phe Ala Glu His Arg Val Pro Asn Gly Met Asn Lys Gly Glu  
290 295 300

His Ala Leu Val Leu Phe Glu Lys Cys Val Gln Asp Lys Tyr Leu Gln  
305 310 315 320

Gln Glu His Ile Ile Lys Lys Leu Ile Lys Glu Asn Lys Lys His Gln  
325 330 335

Glu Leu Phe Val Asp Ile Cys Ser Glu Lys Asp Asn Leu Arg Glu Glu  
340 345 350

Leu Lys Lys Arg Thr Glu Thr Glu Lys Gln His Met Asn Thr Ile Lys  
355 360 365

Gln Leu Glu Ser Arg Ile Glu Glu Leu Asn Lys Glu Val Lys Ala Ser  
370 375 380

Arg Asp Gln Leu Ile Ala Gln Asp Val Thr Ala Lys Asn Ala Val Gln  
385 390 395 400

Gln Leu His Lys Glu Met Ala Gln Arg Met Glu Gln Ala Asn Lys Lys  
405 410 415

Cys Glu Glu Ala Arg Gln Glu Lys Glu Ala Met Val Met Lys Tyr Val  
420 425 430

Arg Gly Glu Lys Glu Ser Leu Asp Leu Arg Lys Glu Lys Glu Thr Leu  
435 440 445

Glu Lys Lys Leu Arg Asp Ala Asn Lys Glu Leu Glu Lys Asn Thr Asn  
450 455 460

Lys Ile Lys Gln Leu Ser Gln Glu Lys Gly Arg Leu His Gln Leu Tyr  
465 470 475 480

Glu Thr Lys Glu Gly Glu Thr Thr Arg Leu Ile Arg Glu Ile Asp Lys  
485 490 495

Leu Lys Glu Asp Ile Asn Ser His Val Ile Lys Val Lys Trp Ala Gln  
500 505 510

Asn Lys Leu Lys Ala Glu Met Asp Ser His Lys Glu Thr Lys Asp Lys  
515 520 525

Leu Lys Glu Thr Thr Lys Leu Thr Gln Ala Lys Glu Glu Ala Asp  
530 535 540

Gln Ile Arg Lys Asn Cys Gln Asp Met Ile Lys Thr Tyr Gln Glu Ser  
545 550 555 560

Glu Glu Ile Lys Ser Asn Glu Leu Asp Ala Lys Leu Arg Val Thr Lys  
565 570 575

Gly Glu Leu Glu Lys Gln Met Gln Glu Lys Ser Asp Gln Leu Glu Met  
580 585 590

His His Ala Lys Ile Lys Glu Leu Glu Asp Leu Lys Arg Thr Phe Lys  
595 600 605

Glu Gly Met Asp Glu Leu Arg Thr Leu Arg Thr Lys Val Lys Cys Leu  
610 615 620

Glu Asp Glu Arg Leu Arg Thr Glu Asp Glu Leu Ser Lys Tyr Lys Glu  
625 630 635 640

Ile Ile Asn Arg Gln Lys Ala Glu Ile Gln Asn Leu Leu Asp Lys Val  
645 650 655

Lys Thr Ala Asp Gln Leu Gln Glu Gln Leu Gln Arg Gly Lys Gln Glu  
660 665 670

Ile Glu Asn Leu Lys Glu Glu Val Glu Ser Leu Asn Ser Leu Ile Asn  
675 680 685

Asp Leu Gln Lys Asp Ile Glu Gly Ser Arg Lys Arg Glu Ser Glu Leu  
690 695 700

Leu Leu Phe Thr Glu Arg Leu Thr Ser Lys Asn Ala Gln Leu Gln Ser  
705 710 715 720

Glu Ser Asn Ser Leu Gln Ser Gln Phe Asp Lys Val Ser Cys Ser Glu  
725 730 735

Ser Gln Leu Gln Ser Gln Cys Glu Gln Met Lys Gln Thr Asn Ile Asn  
740 745 750

Leu Glu Ser Arg Leu Leu Lys Glu Glu Glu Leu Arg Lys Glu Glu Val  
755 760 765

Gln Thr Leu Gln Ala Glu Leu Ala Cys Arg Gln Thr Glu Val Lys Ala  
770 775 780

Leu Ser Thr Gln Val Glu Glu Leu Lys Asp Glu Leu Val Thr Gln Arg  
785 790 795 800

Arg Lys His Ala Ser Ser Ile Lys Asp Leu Thr Lys Gln Leu Gln Gln  
805 810 815

Ala Arg Arg Lys Leu Asp Gln Val Glu Ser Gly Ser Tyr Asp Lys Glu  
820 825 830

Val Ser Ser Met Gly Ser Arg Ser Ser Ser Ser Gly Ser Leu Asn Ala  
835 840 845

Arg Ser Ser Ala Glu Asp Arg Ser Pro Glu Asn Thr Gly Ser Ser Val  
 850 855 860  
  
 Ala Val Asp Asn Phe Pro Gln Val Asp Lys Ala Met Leu Ile Glu Arg  
 865 870 875 880  
  
 Ile Val Arg Leu Gln Lys Ala His Ala Arg Lys Asn Glu Lys Ile Glu  
 885 890 895  
  
 Phe Met Glu Asp His Ile Lys Gln Leu Val Glu Glu Ile Arg Lys Lys  
 900 905 910  
  
 Thr Lys Ile Ile Gln Ser Tyr Ile Leu Arg Glu Glu Ser Gly Thr Leu  
 915 920 925  
  
 Ser Ser Glu Ala Ser Asp Phe Asn Lys Val His Leu Ser Arg Arg Gly  
 930 935 940  
  
 Gly Ile Met Ala Ser Leu Tyr Thr Ser His Pro Ala Asp Asn Gly Leu  
 945 950 955 960  
  
 Thr Leu Glu Leu Ser Leu Glu Ile Asn Arg Lys Leu Gln Ala Val Leu  
 965 970 975  
  
 Glu Asp Thr Leu Leu Lys Asn Ile Thr Leu Lys Glu Asn Leu Gln Thr  
 980 985 990  
  
 Leu Gly Thr Glu Ile Glu Arg Leu Ile Lys His Gln His Glu Leu Glu  
 995 1000 1005  
  
 Gln Arg Thr Lys Lys Thr  
 1010

<210> 252  
 <211> 1491  
 <212> DNA  
 <213> human organism

<400> 252		
ttgccgtgaa gggctgtgcg gttcccggtgc gcgcggagc ctgctgtggc ctcttatgca		60
ctccaccacc cccatcagct ccctcttctc cttcaccaggc cccgcagtga agagactgct		120
aggctggaag caaggagatg aagaggaaaa gtgggcagag aaggcagtgg actctcttagt		180
gaagaagtta aagaagaaga agggagccat ggacgagctg gagagggctc tcagctgccc		240

ggggcagccc	agcaaatgcg	tcacgattcc	ccgctccctg	gacgggcggc	tgcagggtgc	300
ccaccgcaag	ggcctgcccc	atgtgattta	ctgtcgctg	tggcgctggc	cggatctgca	360
gtcccaccac	gagctgaagc	cgctggagtg	ctgtgagttc	ccatggct	ccaagcagaa	420
agaagtgtgc	attaaccctt	accactaccg	ccgggtggag	actccagttac	tgcctcctgt	480
gctcgtgcca	agacacagtg	aatataaccc	ccagctcagc	ctcctggcca	agttccgcag	540
cgccctccctg	cacagtgagc	cactcatgcc	acacaacgccc	acctatcctg	actctttcca	600
gcagcctccg	tgctctgcac	tccctccctc	acccagccac	gcgttctccc	agtccccgtg	660
cacggccagc	taccctcact	ccccaggaag	tccttctgag	ccagagagtc	cctatcaaca	720
ctcagttgac	acaccacccc	tgcctttatca	tgccacagaa	gcctctgaga	cccagagtgg	780
ccaacctgta	gatgccacag	ctgatagaca	tgttagtgcta	tcgataccaa	atggagactt	840
tcgaccagtt	tgttacgagg	agccccagca	ctggtgctcg	gtcgctact	atgaactgaa	900
caaccgagtt	ggggagacat	tcaggcttc	ctcccgaaagt	gtgctcatag	atggggtcac	960
cgacccttca	aataacagga	acagattctg	tcttggactt	ctttctaattg	taaacagaaa	1020
ctcaacgata	gaaaatacca	ggagacatat	aggaaagggt	gtgcacttgt	actacgtcgg	1080
gggagaggtg	tatgccgagt	gcgtgagtga	cagcagcatc	tttgcgcaga	gccggaactg	1140
caactatcaa	cacggottcc	acccagctac	cgtctgcaag	atccccagcg	gctgcagcct	1200
caaggtcttc	aacaaccagc	tcttcgctca	gctcctggcc	cagtcagttc	accacggctt	1260
tgaagtcgtg	tatgaactga	ccaagatgtg	tactatccgg	atgagttttg	ttaagggttg	1320
gggtgctgag	tatcatcgcc	aggatgtcac	cagcacccccc	tgctggattt	agattcatct	1380
tcatgggcca	ctgcagtggc	tggacaaagt	tctgactcag	atgggctctc	cacataaccc	1440
catttcttca	gtgtcttaac	agtcatgtct	taagctgcat	ttccatagga	t	1491

<210> 253  
 <211> 467  
 <212> PRT  
 <213> human organism

<400> 253

Met	His	Ser	Thr	Thr	Pro	Ile	Ser	Ser	Leu	Phe	Ser	Phe	Thr	Ser	Pro
1						5				10				15	

Ala	Val	Lys	Arg	Leu	Leu	Gly	Trp	Lys	Gln	Gly	Asp	Glu	Glu	Lys
								20		25		30		

Trp Ala Glu Lys Ala Val Asp Ser Leu Val Lys Lys Leu Lys Lys Lys  
35 40 45

Lys Gly Ala Met Asp Glu Leu Glu Arg Ala Leu Ser Cys Pro Gly Gln  
50 55 60

Pro Ser Lys Cys Val Thr Ile Pro Arg Ser Leu Asp Gly Arg Leu Gln  
65 70 80

Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr Cys Arg Val Trp  
85 90 95

Arg Trp Pro Asp Leu Gln Ser His His Glu Leu Lys Pro Leu Glu Cys  
100 105 110

Cys Glu Phe Pro Phe Gly Ser Lys Gln Lys Glu Val Cys Ile Asn Pro  
115 120 125

Tyr His Tyr Arg Arg Val Glu Thr Pro Val Leu Pro Pro Val Leu Val  
130 135 140

Pro Arg His Ser Glu Tyr Asn Pro Gln Leu Ser Leu Leu Ala Lys Phe  
145 150 155 160

Arg Ser Ala Ser Leu His Ser Glu Pro Leu Met Pro His Asn Ala Thr  
165 170 175

Tyr Pro Asp Ser Phe Gln Gln Pro Pro Cys Ser Ala Leu Pro Pro Ser  
180 185 190

Pro Ser His Ala Phe Ser Gln Ser Pro Cys Thr Ala Ser Tyr Pro His  
195 200 205

Ser Pro Gly Ser Pro Ser Glu Pro Glu Ser Pro Tyr Gln His Ser Val  
210 215 220

Asp Thr Pro Pro Leu Pro Tyr His Ala Thr Glu Ala Ser Glu Thr Gln  
225 230 235 240

Ser Gly Gln Pro Val Asp Ala Thr Ala Asp Arg His Val Val Leu Ser  
245 250 255

Ile Pro Asn Gly Asp Phe Arg Pro Val Cys Tyr Glu Glu Pro Gln His  
260 265 270

Trp Cys Ser Val Ala Tyr Tyr Glu Leu Asn Asn Arg Val Gly Glu Thr  
275 280 285

Phe Gln Ala Ser Ser Arg Ser Val Leu Ile Asp Gly Phe Thr Asp Pro  
290 295 300

Ser Asn Asn Arg Asn Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn  
305 310 315 320

Arg Asn Ser Thr Ile Glu Asn Thr Arg Arg His Ile Gly Lys Gly Val  
325 330 335

His Leu Tyr Tyr Val Gly Gly Glu Val Tyr Ala Glu Cys Val Ser Asp  
340 345 350

Ser Ser Ile Phe Val Gln Ser Arg Asn Cys Asn Tyr Gln His Gly Phe  
355 360 365

His Pro Ala Thr Val Cys Lys Ile Pro Ser Gly Cys Ser Leu Lys Val  
370 375 380

Phe Asn Asn Gln Leu Phe Ala Gln Leu Leu Ala Gln Ser Val His His  
385 390 395 400

Gly Phe Glu Val Val Tyr Glu Leu Thr Lys Met Cys Thr Ile Arg Met  
405 410 415

Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr His Arg Gln Asp Val Thr  
420 425 430

Ser Thr Pro Cys Trp Ile Glu Ile His Leu His Gly Pro Leu Gln Trp  
435 440 445

Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro His Asn Pro Ile Ser  
450 455 460

Ser Val Ser  
465

<210> 254  
 <211> 5857  
 <212> DNA  
 <213> human organism

<400> 254	
tgcagggttg cagggtctga gattacttgg gctttcctg ccttttctt ttgcttaagg	60
gatggacaag gagctgagat ttatgaccct tattagagaa aaaaatgtgc cttgcttaggg	120
tggggacact tgggtgatgc agtctctc tctcttc ggtgtttata acaaaaacaaa	180
accaaaaatga actgaggggt ttgtaatggt agttgtttg ttgctggaga atgctacttt	240
gcatgctttt tttctcttgc agggtatgtt ctgtcttgc ctttttctt tagaagctac	300
taaagggtgt tggggatgct tctgactatt atgaaggcca aaaggcctgt tgactgggc	360
tgcttttaac ccttccttat ttgctgagaa tgcagccgtg tgacagtaac tgaacattgg	420
tctaaagtct ttccaaaagg tcaaggttca caagaacatc tgctcaaatt aatgaccatg	480
ggggatatga agaccccaga ctttgatgac ctcctggcag catttgacat cccagatatg	540
gtcgatccta aagcagctat tgagtctgga cacgatgacc atgaaagcca catgaagcag	600
aatgctcacg gagaggatga ctccccacgca ccatcatctt ctgatgtggg tgtcagcggtt	660
atcgtcaaga atgttcggaa cattgactct tccgagggcg gggagaaaga cggccacaac	720
cccaactggca atggcttaca taatggttt ctcacagcat cctcccttga cagttacagt	780
aaagatggag caaagtccctt gaaaggagat gtgcctgcct ctgaggtgac actgaaagac	840
tcgacattca gccagtttag cccgatctcc agtgctgaag agtttgatga cgacgagaag	900
attgaggtgg atgacccccc tgacaaggag gacatgcgt caagcttcag gtcgaatgtg	960
ttgacggggt cggctccca gcaggactac gataagctga aggcaactgg aggggaaaac	1020
tccagaaaaa ctggactctc tacgtcaggc aatgtggaga aaaacaaagc tgttaagaga	1080
gaaacagaag ccagttctat aaacctgagt gtttatgaac ctttaaagt cagaaaagca	1140
gaggataaat tgaaggaaag ctctgacaag gtgctggaaa acagagtccct agatggaaag	1200
ctgagctccg agaagaatga caccagcctc cccagcggtt cgccatcaa gacaaagtgc	1260
tcctccaagc tctcgccctg catcgctgcc atcgcggctc tcagcgctaa aaaggcggct	1320
tcagactcct gcaaagaacc agtggccaat tcgagggat cctcccccgtt accaaaagaa	1380
gtaaatgaca gtccgagagc cgctgacaag tctcctgaat cccagaatct catcgacggg	1440
accaaaaaac catccctgaa gcaaccggat agtcccagaa gcatctcaag tgagaacagc	1500
agcaaaggat ccccgctc tcccgaggg tccacaccag caatccccaa agtccgcata	1560

aaaaccatta agacatcttc tggggaaatc aagagaacag tgaccagggt attgccagaa 1620  
gtggatcttg actctggaaa gaaaccttcc gagcagacag cgtccgtat ggcctctgtg 1680  
acatcccttc tgtcgtctcc agcatcagcc gccgtcctt cctctcccc cagggcgccct 1740  
ctccagtctg cggtcgtgac caatgcagtt tcccctgcag agctcacccc caaacaggtc 1800  
acaatcaagc ctgtggctac tgcttcctc ccagtgtctg ctgtgaagac ggcaggatcc 1860  
caagtcatta atttgaagct cgctaacaac accacggtga aagccacggt catatctgct 1920  
gcctctgtcc agagtgccag cagcgccatc attaaagctg ccaacgccc ccagcagcaa 1980  
actgtcgtgg tgccggcatc cagcctggcc aatgccaaac tcgtgccaata gactgtgcac 2040  
cttgccaaacc ttaaccttt gcctcagggt gcccaggcca cctctgaact ccgccaagtg 2100  
ctaacccaaac ctcagcaaca aataaagcag gcaataatca atgcagcagc ctcgcaaccc 2160  
cccaaaaaagg tgtctcgagt ccaggtggtg tcgtccttgc agagttctgt ggtggaaagct 2220  
ttcaacaagg tgctgagcag tgtcaatcca gtccctgttt acatcccaa cctcagtcct 2280  
cccgccaaatg cagggatcac gttaccgacg cgtgggtaca agtgcttgg atgtggggac 2340  
tccttcgcac ttgaaaagag tctgacccag cactacgaca gacggagcgt gcgcatcgaa 2400  
gtaacgtgca accattgtac aaagaacctc gtttttaca acaaatgcag ctcctttcc 2460  
catgcccgtg ggcataagga gaaagggttg gtaatgcaat gctccactt aattttaaag 2520  
ccagtccttccag cagatcaaata gatagttctt ccgtcaagca atacttccac ttcaacttcc 2580  
actcttcaga gccctgtgg agctggcaca cacactgtca caaaaattca gtctggcata 2640  
actgggacag tcatatcgcc tccttcaagc actcccatca cccagccat gccccttagat 2700  
gaagacccct ccaaactgtg tagacatagt ctaaaatgtt tggagtgtaa tgaagtcttc 2760  
caggacgaga catcaactggc tacacatttc cagcaggctg cagatacggag tggacaaaag 2820  
acttgcacta tctgcccagat gctgcttcct aaccagtgc gttatgcac acaccagaga 2880  
atccatcagc acaaatctcc ctacacccgc cctgagtgat gggccatctg caggtcggtg 2940  
cacttccaga cccacgtcac caagaactgt ctgcactaca cgaggagagt tggtttcga 3000  
tgtgtgcatt gcaatgttgcgtat gtactctgtat gtggctgctc tgaagtctca cattcaaggt 3060  
tctcactgtg aagtcttcta caagtgtctt atttgtccaa tggcgttaa gtctgcccc 3120  
agcacacatt cccacgccta cacacagcat cctggcatca agataggaga accaaaaata 3180  
atatataagt gttccatgtg cgacactgtg ttcaccctgc aaaccttgct gtatcgccac 3240

tttgcaccaac acattgaaaa ccagaagggtg tctgtttca agtgtccaga ctgttcttt 3300  
ttatatgcac agaagcaact tatgatggac catatcaagt ctatgcattgg aacattgaaa 3360  
agtattgaag ggcctccaaa cttgggtata aacttgccctt tgagcattaa gcctgcaact 3420  
caaaattcag caaatcagaa caaagaggac accaaatcca tgaatggaa agagaattg 3480  
gaaaagaaaat ctccatctcc tgtgaaaaaa tcaatggaaa ccaagaaaatggcagtcct 3540  
gggtggacgt gttgggagtg tgactgcctg ttcatgcaga gagatgtgtatcatatcccac 3600  
gtgaggaagg agcacggaa gcaaataatggaa aaacacccct gccgcccagtgtgacaagtct 3660  
ttcagctcggtt cccacagcct gtgccggcac aaccggatca agcacaaagg catcaggaaa 3720  
gtgtacgcct gctcgactg cccagactcc agacgtacacctt accaaacg tttgatgctg 3780  
gagaagcactg tccagctgtat gcatggcatc aaggaccctg acctgaaaga aatgacagat 3840  
gccaccaatg aggagggaaac agaaataaaaa gaagacacta aggtccccag tcccaagcgg 3900  
aagttgaaag aaccagttct ggagttcagg cctcccccag gagcaatcac tcaaccactg 3960  
aaaaagctga aaatcaatgt ttttaagggtt cacaagtgtg ccgtgtgtgg ctccaccacc 4020  
gaaaacctgc tgcaattcca cgaacacatc cctcagcaca aatcgatgg ttcttcctac 4080  
cagtgccggg agtgtggcct ctgctacacg tctcacgtct ctctgtccag gcaccccttc 4140  
atcgacaca agttaaaggaa acctcagcca gtgtccaagc aaaatggggc tggggaaat 4200  
aaccaacagg agaacaacc cagccacgag gatgaatccc ctgatggcgc cgtgtcagac 4260  
agaaagtgcg aagtgtgcgc aaaaactttt gaaactgaag ctgccttaaa tactcacatg 4320  
cgacacacag gcatggcctt catcaaatcc aaaaggatga gtcagccga gaaatagcca 4380  
cagatgctcc atgaggaaaa tccctgtcca cattgaaata aaaaagacat ttttggata 4440  
aagtttgcag tataatagag ttaacagtac tgtctaggct gttgcaatataattctttc 4500  
aatgtacctt cttcacctc gtcgtatata tcctcgataa gtattaaaac agtatttgag 4560  
tttaaaagag tttgtatata tttaaatgaa taactttta tactctttgt tacatgtttg 4620  
tatcagtatt tagtgaaaaa ccatttgagt tggtttgggt tagaattttt ctttttgtac 4680  
tgtttctta aaacagagtt cttagtaaca gggcagttc ctgaattcaa ataaaccatt 4740  
ttgtatgttt ggattttgaa tgggttaact aattacaggc taaaataatg ctttttttag 4800  
tgtttttaat ttttagaatt cactacataa attgttaagta attgtgggtc tcaaaaacac 4860  
taggaacttt taagtgtctt agcacttcct cgatgtgcct gcccgtgggg agtgagttca 4920  
catttgagac aactgcactc cagtgtggac gtgcctttgt ctgcaggcca tgccgaagg 4980

tgtttaaagc	agtcttgca	gtcgctcctt	tcccagccgt	ggataaaaac	tgaagctagg	5040
aatctaataa	ggaatgctga	tttcctcagt	tccatttga	ggaatgggga	aggctattct	5100
aaagaaaaaa	atgggattt	tttctcg	agatctgcaa	ggctggctt	aagagcacaa	5160
ggagggaaag	taacgaaagg	gctggactac	tataaaagtt	acaatacgt	agtagacca	5220
atagatttat	atagtcaggt	tttgc	taatttatta	actaactatt	acagaaacac	5280
agctaagaat	atcaagtatt	tctctgg	ttgacagaaa	aaaatcagtt	gacttaaccc	5340
tttgctgtca	aaagagg	tttgc	tctgg	actgcca	ac gttatgg	5400
ttagagtcgg	gatgcacaac	ttcaacc	gactt	tca	tgccg	5460
aattggccgt	taccttaa	actgagccac	ccgggtt	ttcagcc	att tca	5520
tatttaacgt	cggtagt	tttgc	aatgc	aggta	ctgtcc	5580
cgttatagt	tctctgag	agttctat	tttgg	tttgc	tcat	5640
tttgc	tatcc	ctgaacat	tttgc	ttttttt	ttttttt	5700
gaaaaggaat	tctttgt	atata	acttgc	tata	actgt	5760
gttcctcaaa	agg	cttg	gctgt	gtt	actccat	5820
aaacacattt	catatg	aaa	taaacgt	ggg	aa	5857

<210> 255

<211> 1296

<212> PRT

<213> human organism

<400> 255

Met	Lys	Thr	Pro	Asp	Phe	Asp	Asp	Leu	Leu	Ala	Ala	Phe	Asp	Ile	Pro
1					5				10					15	

Asp	Met	Val	Asp	Pro	Lys	Ala	Ala	Ile	Glu	Ser	Gly	His	Asp	Asp	His
					20				25			30			

Glu	Ser	His	Met	Lys	Gln	Asn	Ala	His	Gly	Glu	Asp	Asp	Ser	His	Ala
					35			40		45					

Pro	Ser	Ser	Ser	Asp	Val	Gly	Val	Ser	Val	Ile	Val	Lys	Asn	Val	Arg
					50					55		60			

Asn	Ile	Asp	Ser	Ser	Glu	Gly	Glu	Lys	Asp	Gly	His	Asn	Pro	Thr
					65			70		75		80		

Gly Asn Gly Leu His Asn Gly Phe Leu Thr Ala Ser Ser Leu Asp Ser  
85 90 95

Tyr Ser Lys Asp Gly Ala Lys Ser Leu Lys Gly Asp Val Pro Ala Ser  
100 105 110

Glu Val Thr Leu Lys Asp Ser Thr Phe Ser Gln Phe Ser Pro Ile Ser  
115 120 125

Ser Ala Glu Glu Phe Asp Asp Asp Glu Lys Ile Glu Val Asp Asp Pro  
130 135 140

Pro Asp Lys Glu Asp Met Arg Ser Ser Phe Arg Ser Asn Val Leu Thr  
145 150 155 160

Gly Ser Ala Pro Gln Gln Asp Tyr Asp Lys Leu Lys Ala Leu Gly Gly  
165 170 175

Glu Asn Ser Ser Lys Thr Gly Leu Ser Thr Ser Gly Asn Val Glu Lys  
180 185 190

Asn Lys Ala Val Lys Arg Glu Thr Glu Ala Ser Ser Ile Asn Leu Ser  
195 200 205

Val Tyr Glu Pro Phe Lys Val Arg Lys Ala Glu Asp Lys Leu Lys Glu  
210 215 220

Ser Ser Asp Lys Val Leu Glu Asn Arg Val Leu Asp Gly Lys Leu Ser  
225 230 235 240

Ser Glu Lys Asn Asp Thr Ser Leu Pro Ser Val Ala Pro Ser Lys Thr  
245 250 255

Lys Ser Ser Ser Lys Leu Ser Ser Cys Ile Ala Ala Ile Ala Ala Leu  
260 265 270

Ser Ala Lys Lys Ala Ala Ser Asp Ser Cys Lys Glu Pro Val Ala Asn  
275 280 285

Ser Arg Glu Ser Ser Pro Leu Pro Lys Glu Val Asn Asp Ser Pro Arg  
290 295 300

Ala Ala Asp Lys Ser Pro Glu Ser Gln Asn Leu Ile Asp Gly Thr Lys  
305 310 315 320

Lys Pro Ser Leu Lys Gln Pro Asp Ser Pro Arg Ser Ile Ser Ser Glu  
325 330 335

Asn Ser Ser Lys Gly Ser Pro Ser Ser Pro Ala Gly Ser Thr Pro Ala  
340 345 350

Ile Pro Lys Val Arg Ile Lys Thr Ile Lys Thr Ser Ser Gly Glu Ile  
355 360 365

Lys Arg Thr Val Thr Arg Val Leu Pro Glu Val Asp Leu Asp Ser Gly  
370 375 380

Lys Lys Pro Ser Glu Gln Thr Ala Ser Val Met Ala Ser Val Thr Ser  
385 390 395 400

Leu Leu Ser Ser Pro Ala Ser Ala Ala Val Leu Ser Ser Pro Pro Arg  
405 410 415

Ala Pro Leu Gln Ser Ala Val Val Thr Asn Ala Val Ser Pro Ala Glu  
420 425 430

Leu Thr Pro Lys Gln Val Thr Ile Lys Pro Val Ala Thr Ala Phe Leu  
435 440 445

Pro Val Ser Ala Val Lys Thr Ala Gly Ser Gln Val Ile Asn Leu Lys  
450 455 460

Leu Ala Asn Asn Thr Thr Val Lys Ala Thr Val Ile Ser Ala Ala Ser  
465 470 475 480

Val Gln Ser Ala Ser Ser Ala Ile Ile Lys Ala Ala Asn Ala Ile Gln  
485 490 495

Gln Gln Thr Val Val Pro Ala Ser Ser Leu Ala Asn Ala Lys Leu  
500 505 510

Val Pro Lys Thr Val His Leu Ala Asn Leu Asn Leu Leu Pro Gln Gly  
515 520 525

Ala Gln Ala Thr Ser Glu Leu Arg Gln Val Leu Thr Lys Pro Gln Gln  
530 535 540

Gln Ile Lys Gln Ala Ile Ile Asn Ala Ala Ser Gln Pro Pro Lys  
545 550 555 560

Lys Val Ser Arg Val Gln Val Val Ser Ser Leu Gln Ser Ser Val Val  
565 570 575

Glu Ala Phe Asn Lys Val Leu Ser Ser Val Asn Pro Val Pro Val Tyr  
580 585 590

Ile Pro Asn Leu Ser Pro Pro Ala Asn Ala Gly Ile Thr Leu Pro Thr  
595 600 605

Arg Gly Tyr Lys Cys Leu Glu Cys Gly Asp Ser Phe Ala Leu Glu Lys  
610 615 620

Ser Leu Thr Gln His Tyr Asp Arg Arg Ser Val Arg Ile Glu Val Thr  
625 630 635 640

Cys Asn His Cys Thr Lys Asn Leu Val Phe Tyr Asn Lys Cys Ser Leu  
645 650 655

Leu Ser His Ala Arg Gly His Lys Glu Lys Gly Val Val Met Gln Cys  
660 665 670

Ser His Leu Ile Leu Lys Pro Val Pro Ala Asp Gln Met Ile Val Ser  
675 680 685

Pro Ser Ser Asn Thr Ser Thr Ser Thr Leu Gln Ser Pro Val  
690 695 700

Gly Ala Gly Thr His Thr Val Thr Lys Ile Gln Ser Gly Ile Thr Gly  
705 710 715 720

Thr Val Ile Ser Ala Pro Ser Ser Thr Pro Ile Thr Pro Ala Met Pro  
725 730 735

Leu Asp Glu Asp Pro Ser Lys Leu Cys Arg His Ser Leu Lys Cys Leu  
740 745 750

Glu Cys Asn Glu Val Phe Gln Asp Glu Thr Ser Leu Ala Thr His Phe

755

760

765

Gln Gln Ala Ala Asp Thr Ser Gly Gln Lys Thr Cys Thr Ile Cys Gln  
770 775 780

Met Leu Leu Pro Asn Gln Cys Ser Tyr Ala Ser His Gln Arg Ile His  
785 790 795 800

Gln His Lys Ser Pro Tyr Thr Cys Pro Glu Cys Gly Ala Ile Cys Arg  
805 810 815

Ser Val His Phe Gln Thr His Val Thr Lys Asn Cys Leu His Tyr Thr  
820 825 830

Arg Arg Val Gly Phe Arg Cys Val His Cys Asn Val Val Tyr Ser Asp  
835 840 845

Val Ala Ala Leu Lys Ser His Ile Gln Gly Ser His Cys Glu Val Phe  
850 855 860

Tyr Lys Cys Pro Ile Cys Pro Met Ala Phe Lys Ser Ala Pro Ser Thr  
865 870 875 880

His Ser His Ala Tyr Thr Gln His Pro Gly Ile Lys Ile Gly Glu Pro  
885 890 895

Lys Ile Ile Tyr Lys Cys Ser Met Cys Asp Thr Val Phe Thr Leu Gln  
900 905 910

Thr Leu Leu Tyr Arg His Phe Asp Gln His Ile Glu Asn Gln Lys Val  
915 920 925

Ser Val Phe Lys Cys Pro Asp Cys Ser Leu Leu Tyr Ala Gln Lys Gln  
930 935 940

Leu Met Met Asp His Ile Lys Ser Met His Gly Thr Leu Lys Ser Ile  
945 950 955 960

Glu Gly Pro Pro Asn Leu Gly Ile Asn Leu Pro Leu Ser Ile Lys Pro  
965 970 975

Ala Thr Gln Asn Ser Ala Asn Gln Asn Lys Glu Asp Thr Lys Ser Met  
980 985 990

Asn Gly Lys Glu Lys Leu Glu Lys Lys Ser Pro Ser Pro Val Lys Lys  
995 1000 1005

Ser Met Glu Thr Lys Lys Val Ala Ser Pro Gly Trp Thr Cys Trp  
1010 1015 1020

Glu Cys Asp Cys Leu Phe Met Gln Arg Asp Val Tyr Ile Ser His  
1025 1030 1035

Val Arg Lys Glu His Gly Lys Gln Met Lys Lys His Pro Cys Arg  
1040 1045 1050

Gln Cys Asp Lys Ser Phe Ser Ser Ser His Ser Leu Cys Arg His  
1055 1060 1065

Asn Arg Ile Lys His Lys Gly Ile Arg Lys Val Tyr Ala Cys Ser  
1070 1075 1080

His Cys Pro Asp Ser Arg Arg Thr Phe Thr Lys Arg Leu Met Leu  
1085 1090 1095

Glu Lys His Val Gln Leu Met His Gly Ile Lys Asp Pro Asp Leu  
1100 1105 1110

Lys Glu Met Thr Asp Ala Thr Asn Glu Glu Glu Thr Glu Ile Lys  
1115 1120 1125

Glu Asp Thr Lys Val Pro Ser Pro Lys Arg Lys Leu Glu Glu Pro  
1130 1135 1140

Val Leu Glu Phe Arg Pro Pro Arg Gly Ala Ile Thr Gln Pro Leu  
1145 1150 1155

Lys Lys Leu Lys Ile Asn Val Phe Lys Val His Lys Cys Ala Val  
1160 1165 1170

Cys Gly Phe Thr Thr Glu Asn Leu Leu Gln Phe His Glu His Ile  
1175 1180 1185

Pro Gln His Lys Ser Asp Gly Ser Ser Tyr Gln Cys Arg Glu Cys  
1190 1195 1200

Gly Leu Cys Tyr Thr Ser His Val Ser Leu Ser Arg His Leu Phe  
1205 1210 1215

Ile Val His Lys Leu Lys Glu Pro Gln Pro Val Ser Lys Gln Asn  
1220 1225 1230

Gly Ala Gly Glu Asp Asn Gln Gln Glu Asn Lys Pro Ser His Glu  
1235 1240 1245

Asp Glu Ser Pro Asp Gly Ala Val Ser Asp Arg Lys Cys Lys Val  
1250 1255 1260

Cys Ala Lys Thr Phe Glu Thr Glu Ala Ala Leu Asn Thr His Met  
1265 1270 1275

Arg Thr His Gly Met Ala Phe Ile Lys Ser Lys Arg Met Ser Ser  
1280 1285 1290

Ala Glu Lys  
1295

<210> 256  
<211> 2788  
<212> DNA  
<213> human organism

<400> 256	60
tttcgtcga ctcttaccgg ttggctggc cagctgcgcc gcggctcaca gctgacgatg	60
ggggacccca gcaaggcagga catcttgacc atcttcaagc gcctccgctc ggtgcccact	120
aacaagggtgt gtttgattg tggtgc当地 aatcccagct gggcaagcat aacctatgga	180
gtgttccttt gcattgattg ctcagggtcc caccggcac tgggtttca cttgagttt	240
attcgatcta cagagttgga ttccaactgg tcatggttc agttgcgatg catgcaagtc	300
ggaggaaaacg ctagtgcata ttcctttttt catcaacatg ggtgttccac caatgacacc	360
aatgccaagt acaacagtcg tgctgctcag ctctataggg agaaaaatcaa atcgctcgcc	420
tctcaagcaa cacggaaagca tggcaactgat ctgtggctt atagttgtgt gggtccac	480
ttgtccccctc caccaaagga ggaagatttt tttgcctctc acgtttctcc tgaggtgagt	540
gacacagcgt gggcatcagc aatagcagaa ccatcttctt taacatcaag gcctgtggaa	600
accactttgg aaaataatga aggtggacaa gagcaaggac caagtgtgga aggtcttaat	660

gtaccaacaa aggctacttt agaggtatcc tctatcataa aaaagaaaacc aaatcaagct 720  
aaaaaaggcc ttggggccaa aaaaggaagt ttgggagctc agaaaactggc aaacacatgc 780  
ttaatgaaa ttgaaaaaca agctcaagct gcggataaaa tgaaggagca ggaagacctg 840  
gccaaagggtgg tatctaaaga agaatcaatt gtttcatcat tacgattagc ctataaggat 900  
cttcaaattc aaatgaagaa agacgaaaag atgaacatta gtggcaaaaa aaatgttgac 960  
tcagacagac tcggcatggg atttggaaat tgcagaagtg ttatccaca ttcagtgact 1020  
tcagatatgc agaccataga gcaggaatca cccattatgg caaaaccaag aaaaaagtat 1080  
aatgatgaca gtgacgattc atatttact tccagctaa gttactttga cgagccagtg 1140  
gagttaaagga gcagttctt ctctagctgg gatgacagtt cagattccta ttggaaaaaaaa 1200  
gagaccagca aagatactga aacagttctg aaaaccacag gctattcaga cagacctact 1260  
gctcgccgca agccagatta tgagccagtt gaaaatacag atgaggcccga gaagaagttt 1320  
ggcaatgtca aggccatttc atcagatatg tattttggaa gacaatcccga ggctgattat 1380  
gagaccaggg cccgcctaga gaggctgtcg gcaagttcct ccataagctc ggctgatctg 1440  
ttcgaggagc cgaggaagca gccagcaggg aactacagcc tgtccagtgt gctgccaac 1500  
gcccccgaca tggcgcaagtt caagcaggga gtgagatcggt ttgctggaaa actctccgtc 1560  
tttgctaattg gagtcgtgac ttcaattcag gatcgctacg gttcttaata ctgaagtcat 1620  
gatgtgtatt tcctggagaa attcctcttt aaatgaacaa gtaaccacat ctcaggcggc 1680  
agtgaagtcc agatagttt gcagattgtt ttgctacttt ttcatatggt atatgtttct 1740  
gatttttaat atttctttt agaaattctg agttctgatg taggagctt cctgtgattt 1800  
ctgtttcacg ttcccttcctg tcacaccctc ctttggcgtc tctgtgtata tccttgcttt 1860  
atttcttgg aacctttgat ttcaacactg agggcctgga gacctcggt cctcctgctc 1920  
ctgaaccagg aggcttcattg tgggggagga ggagaggtct ccatgtgaca catggctca 1980  
gggctgccag aatcagcggta tgctggatgg gcctgcagaa acaacactca ccacacacac 2040  
ttcccttcaaa agacaaaag tgactggatgg ctcgtgtgac agattgcttc atttatgttt 2100  
ctacatagta aggtgactgc caaataatat ttgaagtcat ctgtctcttt gtaaattattt 2160  
ttatatgacc tataaattta aaaatgtttt tcagttagtg cttttaaacaa acttaagctt 2220  
ctgcccctgcc aaggaaatta atgttatctt gtgaaagggtg ttgctgtttg aattgatgag 2280  
aaatggaaga tgagaactcc ctaagagttc tcataataaa tcatctcatc acaaataat 2340  
acggatataca gaggtaaagt ggaatgaggt aagaagatac agctacagaa aatagttgcg 2400

tgtatggag aacagtccatt gtaattgggt agttttgtta ataaatatattt ttaaatcttg 2460  
ctttcagaa attaccgaat gtgtataaac aaataaagaa aaataattta gctgtgttt 2520  
agacagcatt agaatatattt gttcagcaca gtaaaatata tttgaaattt gataagccaa 2580  
aaatgtggtt ttgaatgaat attttgtgaa tctttcttaa aagctcaa at ttgttagactt 2640  
ctaaatagaa taaacacttg cagcagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2700  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2760  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2788

<210> 257  
<211> 516  
<212> PRT  
<213> human organism

<400> 257

Met Gly Asp Pro Ser Lys Gln Asp Ile Leu Thr Ile Phe Lys Arg Leu  
1 5 10 15

Arg Ser Val Pro Thr Asn Lys Val Cys Phe Asp Cys Gly Ala Lys Asn  
20 25 30

Pro Ser Trp Ala Ser Ile Thr Tyr Gly Val Phe Leu Cys Ile Asp Cys  
35 40 45

Ser Gly Ser His Arg Ser Leu Gly Val His Leu Ser Phe Ile Arg Ser  
50 55 60

Thr Glu Leu Asp Ser Asn Trp Ser Trp Phe Gln Leu Arg Cys Met Gln  
65 70 75 80

Val Gly Gly Asn Ala Ser Ala Ser Ser Phe Phe His Gln His Gly Cys  
85 90 95

Ser Thr Asn Asp Thr Asn Ala Lys Tyr Asn Ser Arg Ala Ala Gln Leu  
100 105 110

Tyr Arg Glu Lys Ile Lys Ser Leu Ala Ser Gln Ala Thr Arg Lys His  
115 120 125

Gly Thr Asp Leu Trp Leu Asp Ser Cys Val Val Pro Pro Leu Ser Pro  
130 135 140

Pro Pro Lys Glu Glu Asp Phe Phe Ala Ser His Val Ser Pro Glu Val  
145 150 155 160

Ser Asp Thr Ala Trp Ala Ser Ala Ile Ala Glu Pro Ser Ser Leu Thr  
165 170 175

Ser Arg Pro Val Glu Thr Thr Leu Glu Asn Asn Glu Gly Gly Gln Glu  
180 185 190

Gln Gly Pro Ser Val Glu Gly Leu Asn Val Pro Thr Lys Ala Thr Leu  
195 200 205

Glu Val Ser Ser Ile Ile Lys Lys Lys Pro Asn Gln Ala Lys Lys Gly  
210 215 220

Leu Gly Ala Lys Lys Gly Ser Leu Gly Ala Gln Lys Leu Ala Asn Thr  
225 230 235 240

Cys Phe Asn Glu Ile Glu Lys Gln Ala Gln Ala Ala Asp Lys Met Lys  
245 250 255

Glu Gln Glu Asp Leu Ala Lys Val Val Ser Lys Glu Glu Ser Ile Val  
260 265 270

Ser Ser Leu Arg Leu Ala Tyr Lys Asp Leu Glu Ile Gln Met Lys Lys  
275 280 285

Asp Glu Lys Met Asn Ile Ser Gly Lys Lys Asn Val Asp Ser Asp Arg  
290 295 300

Leu Gly Met Gly Phe Gly Asn Cys Arg Ser Val Ile Ser His Ser Val  
305 310 315 320

Thr Ser Asp Met Gln Thr Ile Glu Gln Glu Ser Pro Ile Met Ala Lys  
325 330 335

Pro Arg Lys Lys Tyr Asn Asp Asp Ser Asp Asp Ser Tyr Phe Thr Ser  
340 345 350

Ser Ser Ser Tyr Phe Asp Glu Pro Val Glu Leu Arg Ser Ser Ser Phe  
355 360 365

Ser Ser Trp Asp Asp Ser Ser Asp Ser Tyr Trp Lys Lys Glu Thr Ser  
370 375 380

Lys Asp Thr Glu Thr Val Leu Lys Thr Thr Gly Tyr Ser Asp Arg Pro  
385 390 395 400

Thr Ala Arg Arg Lys Pro Asp Tyr Glu Pro Val Glu Asn Thr Asp Glu  
405 410 415

Ala Gln Lys Lys Phe Gly Asn Val Lys Ala Ile Ser Ser Asp Met Tyr  
420 425 430

Phe Gly Arg Gln Ser Gln Ala Asp Tyr Glu Thr Arg Ala Arg Leu Glu  
435 440 445

Arg Leu Ser Ala Ser Ser Ile Ser Ser Ala Asp Leu Phe Glu Glu  
450 455 460

Pro Arg Lys Gln Pro Ala Gly Asn Tyr Ser Leu Ser Ser Val Leu Pro  
465 470 475 480

Asn Ala Pro Asp Met Ala Gln Phe Lys Gln Gly Val Arg Ser Val Ala  
485 490 495

Gly Lys Leu Ser Val Phe Ala Asn Gly Val Val Thr Ser Ile Gln Asp  
500 505 510

Arg Tyr Gly Ser  
515

<210> 258  
<211> 5571  
<212> DNA  
<213> human organism

<400> 258  
atggatactg tcatgaagca gacacatgct gacacacctg ttgatcattt tctatctggc 60  
ataagaaaagt gtagcagcac cttaagctt aaaagtgaag tcaacaagca tgaaacagcc 120  
cttggaaatgc agaatccaaa tttgaacaat aaagaatgtt gtttcaccctt tacgttgaat 180  
ggaaaactcca gaaaattaga ccgtagtgtt tttacagcat atggtaaacc cagcgagagt 240  
atctactcag ccctgagtgc taatgactat ttcagtgaaa ggataaagaa tcagtttat 300

agaacatttttatgtatggaaatggatccatcaatgc	360
ctcaagtgcc tgccttagtga ttctcatttt aaaattacat ttggtaaaag aaagagtagc	420
aaagaagatg gacacatatt acgccaatgt gaaaatccaa acatggaatg cattctttt	480
catgttggc ctataggaag gacaagaaag aagattgtt agatcaacga acttcatgaa	540
aaaggaagta aactttgtat ttatgccttg aagggtgaga ctattgaagg agccttatgc	600
aaggatggcc gtttcggtc tgacataggt gaatttgaat ggaaactaaa ggaaggatcat	660
aagaaaattt atggaaaaca gtccatggtg gatgaagtat ctggaaaagt cttagaaaatg	720
gacatttcaa aaaaaaaagc attacaacag aaagatatcc ataaaaaaaaat taaacagaat	780
gaaagtgcctt ctgatgaaat taatcaccag agtctgatac agtctaagaa aaaagtccac	840
aaaccaaaga aagatggaga gaccaagat gtagaacaca gcagagagca aattctccca	900
cctcaggatc taagccatta tattaaagat aaaactcgcc agacaattcc caggattaga	960
aattattact tttgtagttt gccccaaaa tataggcaaa taaactcaca agttagacgg	1020
aggccgcattc tgggtaggcg gtatgctatt aatctggatg tccaaaagga ggcaattaat	1080
ctcttaaaga attatcaaac gttgaatgaa gccataatgc atcagtatcc gaattttaaa	1140
gaggaggcac agtgggtaag aaaatatttt cgggaagaac aaaagagaat gaatctttca	1200
ccagctaagc aattcaacat atataaaaag gacttcggaa aaatgactgc aaattctgtt	1260
tcaaggtaaa cctgcgaaca gcttacatat tatagcaagt cagttgggtt catgcaatgg	1320
gacaataatg gaaacacagg taatgctact tgctttgtct tcaatggtgg ttatatttc	1380
acctgtcgac atgttgtaca tcttatggtg ggtaaaaaca cacatccaaag tttgtggcca	1440
gatataatta gcaaattgtgc gaaggtaacc ttcacttata cagagttctg ccctactcct	1500
gacaattggc ttccatttga gccatggctt aaagtgtcca atgaaaatct agattatgcc	1560
attttaaaac taaaagaaaa tggaaatgcg tttcctccag gactatggcg acagattct	1620
cctcaaccat ctactggttt gatttattta attggtcattc ctgaaggcca gatcaagaaa	1680
atagatggtt gtactgtgat tcctctaaac gaacgattga aaaaatatcc aaacgattgt	1740
caagatgggt tggtagatct ctatgatacc accagtaatg tatactgtat gtttacccaa	1800
agaagttcc tatcagaggt ttggaaacaca cacacgctt gttatgatac ttgtttctct	1860
gatgggtcct caggctcccc agtgttaat gcatctggca aattgggtgc tttgcataacc	1920
tttgggtttt tttatcaacg aggatttaat gtgcattcccc ttattgaatt tggttattct	1980
atggattcta ttctttgtga tattaaaaag acaaattgaga gcttgtataa atcattaaat	2040

gatgagaaac ttgagaccta cgatgaagag aaagccggc ccaggccagc ctaccggcga 2100  
ctaggatgct ttcgcattcg ctctcgctt ccaatactcg ggactgggg aaccgggaga 2160  
atagaaggcag gcaaggaccg ccgtggcac ggggtcagtg agacagggtc ctgctcgcg 2220  
cgtcaaggag gagcgctgtg ggtgtccccca gcgcagccaa tcggcttccg aagtagctgg 2280  
agctctggag cctttgccttc ctcaaatacg agcgggaact gcgttgagcg ctggattcca 2340  
ggccgagtgc tggcgaggcg cgcaagtctct aaagagcaac agaataattt cagtacttct 2400  
ctaattgagga tggagtc tag aggagaccca agagccacaa ctaataccca ggctcaaaga 2460  
ttccattcac ctaagaaaaa tccagaagac cagaccatgc cccaaaatag gacaatat 2520  
gttacattga aggctgtcag aaaagagata gaaactcacc aaggccaaga aatgcttgc 2580  
cgtggcacag aaggaatcaa agagtacata aaccttggaa tgccctcag ttgtttccct 2640  
gaagggtggcc aggtggcat tacatttcc caaagtaaaa gtaagcagaa ggaagataac 2700  
cacatatttgcaggcaggcaaaacatcg actgaatgtg tcaaattttt cattcatgca 2760  
atttggatttgcaggcaggcaaaacatcg actgaatgtg tcaaattttt cattcatgca 2820  
cgcaaaactct gtgttatgc ttccaaagga gaaaccatca agatgcact gtcaaggat 2880  
ggcagatttc ttcccttct ggagaatgt gattggaaac tcattgaaaaa caatgacacc 2940  
attttagaaaa gcacccagcc agttgtatgaa tttagaaggca gatactttca ggttgaggat 3000  
gagaaaaagaa tggccccag tgcagcagct tctcagaatc ctgagtcaga gaaaagaaac 3060  
acctgtgtgt tgagagaaca aatcgtggct cagtacccca gtttggaaag agaaagtgaa 3120  
aaaatcatttgcaggcaggcaaaacatcg actgaatgtg tcaaattttt cattcatgca 3180  
ttgcataaaaaa ggttttttgg gaaagtaaca aaaaatttttctt ctgcattaa agtagtggaa 3240  
cttcttgcgtac gtctcagtgc ctgcatttttttttgcattaa ctgcatttttgcattaa agtagtggaa 3300  
tacgccacct gcttttttttgcattaa ctgcatttttgcattaa ctgcatttttgcattaa agtagtggaa 3360  
agcattgtgg gagacggaaat agagccaaat gaaatggccaa ccataattgg tcaatgtgt 3420  
aggggtgacat ttggatgtatgaa agagctaaaaa gacaaggaaaaa caaactactt ttttggatgt 3480  
ccttggtttgcattaa tggatgtatgaa agagctaaaaa gacaaggaaaaa caaactactt ttttggatgt 3540  
ggacaacaag tacctatgga actatataat ggaattactc ctgtgccact tagtgggttg 3600  
atacatatta ttggccatcc atatggagaa aaaaagcaga ttgtatgttgc tgctgtatc 3660  
cctcagggtc agcgagcaaa gaaatgtcag gaacgtgttc agtctaaaaa agcagaaaaat 3720

ccagagtatg tccatatgt tactcaaaga agtttccaga aaatagttca caaccctgat 3780  
gtgattacct atgacactga attttcttt ggggcttccg gctcccctgt gtttGattca 3840  
aaaggttcat tggtgccat gcatgctgct ggcttgctt atacttacca aaatgagact 3900  
cgtatca ttgagttgg ctctaccatg gaatccatcc tccttgatataaagcaaaga 3960  
cataaaccat ggtatgaaga agtatttgc aatcagcagg atgttagaaat gatgagtgtat 4020  
gaggacttgt gagaattcag tctactggat ttaaggaaat ggcttatgga gttgttattt 4080  
cgtaggcatt gaaaatggtt ttctaaactc caaaatggtc atcttataaataat 4140  
attgaccatt tcctatctgc caggcatttt tctaagcaca tgaagaaatt agtcctaaca 4200  
acactatgag atggactata acttgccaa atttttttt ttttgagac tgagtctcac 4260  
tctgtcgctt gggctggagt acagtggtgc gatctcagct cactgcaact tccacccccc 4320  
aggttcaagc gattctttag cctcagtctc ctgagcagct gggattacag gcaaacgcca 4380  
ccacacccag ctaaattttt ttttttttt tgtatTTTA gtagagacag gtttcacca 4440  
tgggttcag gcgggtctcg aactcctgac ctcgtatcc acctgcctcg gccttccaaa 4500  
gtgctggat tacaagttt agccactgca cctggctaac ttgccctatt taaaagtcaa 4560  
gcaatggaa gaataacaag attatatagt aatcagttc atgacactaa aagtcatata 4620  
gtcatagggt ttttcatct ttcatatctt tgcctaaatt catttgcac agtgcaggaa 4680  
ccaaaacttg ttcatctcat gattccctac atctgacata aggaaagtaa gtgctcagaa 4740  
aatgtgcag gtcaataagt tgcaaaagt ggggctgcaa ttaatgctaa cataagagct 4800  
aaatgcttga ttagaaatga tctcaaaacc ttttagaatt tccaaaatct tcataattact 4860  
gaaactgtcg gaatataatgg gtcctgaaat tcagaagatg atagtcactc ttcccatatt 4920  
tataggctat taaggcaagg gatatctaa acatcatatt actttattta gatttctact 4980  
actccaaatta ttaatgttat gtatttctca ttgtttact tcttcatggt attatgaaga 5040  
ctatatacat gattcaacca agcctgcaaa tctccctt gttggattcc actggaccca 5100  
atctgtttc catttccatt gcaatactac taaagccata caatatcaag caccctccct 5160  
ctagggtccag ggactatcac agaagaagca ggcattgtaaat ttttaagga ctgggttcga 5220  
ggggtcgagt gtagaaaaac agcctgttgc attgttaagag tgatgtcacc ttgaagagca 5280  
gctggcatga tgactgctgt ttgactcctg cataccaaga tattctgcag caatgtctt 5340  
aaacagtgcc ggttagtacag ataaccctc ataaagatgc ttatctaacc tccccagtgt 5400  
tcagggtttt cacaagaaag tctgagatataactgctac acgtttgcc aaaaatgctt 5460

gttatataaa gggtaactttt gggagggtga gtgccgcat ttagtggctg ctagaaacat 5520  
tgcttctgtt tgtaagtcc tattaaatgt tctttctgag aaaaaaaaaa a 5571

<210> 259  
<211> 1343  
<212> PRT  
<213> human organism

<400> 259

Met Asp Thr Val Met Lys Gln Thr His Ala Asp Thr Pro Val Asp His  
1 5 10 15

Cys Leu Ser Gly Ile Arg Lys Cys Ser Ser Thr Phe Lys Leu Lys Ser  
20 25 30

Glu Val Asn Lys His Glu Thr Ala Leu Glu Met Gln Asn Pro Asn Leu  
35 40 45

Asn Asn Lys Glu Cys Cys Phe Thr Phe Thr Leu Asn Gly Asn Ser Arg  
50 55 60

Lys Leu Asp Arg Ser Val Phe Thr Ala Tyr Gly Lys Pro Ser Glu Ser  
65 70 75 80

Ile Tyr Ser Ala Leu Ser Ala Asn Asp Tyr Phe Ser Glu Arg Ile Lys  
85 90 95

Asn Gln Phe Asn Lys Asn Ile Ile Val Tyr Glu Glu Lys Thr Ile Asp  
100 105 110

Gly His Ile Asn Leu Gly Met Pro Leu Lys Cys Leu Pro Ser Asp Ser  
115 120 125

His Phe Lys Ile Thr Phe Gly Gln Arg Lys Ser Ser Lys Glu Asp Gly  
130 135 140

His Ile Leu Arg Gln Cys Glu Asn Pro Asn Met Glu Cys Ile Leu Phe  
145 150 155 160

His Val Val Ala Ile Gly Arg Thr Arg Lys Lys Ile Val Lys Ile Asn  
165 170 175

Glu Leu His Glu Lys Gly Ser Lys Leu Cys Ile Tyr Ala Leu Lys Gly  
180 185 190

Glu Thr Ile Glu Gly Ala Leu Cys Lys Asp Gly Arg Phe Arg Ser Asp  
195 200 205

Ile Gly Glu Phe Glu Trp Lys Leu Lys Glu Gly His Lys Lys Ile Tyr  
210 215 220

Gly Lys Gln Ser Met Val Asp Glu Val Ser Gly Lys Val Leu Glu Met  
225 230 235 240

Asp Ile Ser Lys Lys Ala Leu Gln Gln Lys Asp Ile His Lys Lys  
245 250 255

Ile Lys Gln Asn Glu Ser Ala Thr Asp Glu Ile Asn His Gln Ser Leu  
260 265 270

Ile Gln Ser Lys Lys Val His Lys Pro Lys Lys Asp Gly Glu Thr  
275 280 285

Lys Asp Val Glu His Ser Arg Glu Gln Ile Leu Pro Pro Gln Asp Leu  
290 295 300

Ser His Tyr Ile Lys Asp Lys Thr Arg Gln Thr Ile Pro Arg Ile Arg  
305 310 315 320

Asn Tyr Tyr Phe Cys Ser Leu Pro Arg Lys Tyr Arg Gln Ile Asn Ser  
325 330 335

Gln Val Arg Arg Arg Pro His Leu Gly Arg Arg Tyr Ala Ile Asn Leu  
340 345 350

Asp Val Gln Lys Glu Ala Ile Asn Leu Lys Asn Tyr Gln Thr Leu  
355 360 365

Asn Glu Ala Ile Met His Gln Tyr Pro Asn Phe Lys Glu Ala Gln  
370 375 380

Trp Val Arg Lys Tyr Phe Arg Glu Glu Gln Lys Arg Met Asn Leu Ser  
385 390 395 400

Pro Ala Lys Gln Phe Asn Ile Tyr Lys Lys Asp Phe Gly Lys Met Thr

405

410

415

Ala Asn Ser Val Ser Val Ala Thr Cys Glu Gln Leu Thr Tyr Tyr Ser  
420 425 430

Lys Ser Val Gly Phe Met Gln Trp Asp Asn Asn Gly Asn Thr Gly Asn  
435 440 445

Ala Thr Cys Phe Val Phe Asn Gly Gly Tyr Ile Phe Thr Cys Arg His  
450 455 460

Val Val His Leu Met Val Gly Lys Asn Thr His Pro Ser Leu Trp Pro  
465 470 475 480

Asp Ile Ile Ser Lys Cys Ala Lys Val Thr Phe Thr Tyr Thr Glu Phe  
485 490 495

Cys Pro Thr Pro Asp Asn Trp Phe Ser Ile Glu Pro Trp Leu Lys Val  
500 505 510

Ser Asn Glu Asn Leu Asp Tyr Ala Ile Leu Lys Leu Lys Glu Asn Gly  
515 520 525

Asn Ala Phe Pro Pro Gly Leu Trp Arg Gln Ile Ser Pro Gln Pro Ser  
530 535 540

Thr Gly Leu Ile Tyr Leu Ile Gly His Pro Glu Gly Gln Ile Lys Lys  
545 550 555 560

Ile Asp Gly Cys Thr Val Ile Pro Leu Asn Glu Arg Leu Lys Lys Tyr  
565 570 575

Pro Asn Asp Cys Gln Asp Gly Leu Val Asp Leu Tyr Asp Thr Thr Ser  
580 585 590

Asn Val Tyr Cys Met Phe Thr Gln Arg Ser Phe Leu Ser Glu Val Trp  
595 600 605

Asn Thr His Thr Leu Ser Tyr Asp Thr Cys Phe Ser Asp Gly Ser Ser  
610 615 620

Gly Ser Pro Val Phe Asn Ala Ser Gly Lys Leu Val Ala Leu His Thr  
625 630 635 640

Phe Gly Leu Phe Tyr Gln Arg Gly Phe Asn Val His Ala Leu Ile Glu  
645 650 655

Phe Gly Tyr Ser Met Asp Ser Ile Leu Cys Asp Ile Lys Lys Thr Asn  
660 665 670

Glu Ser Leu Tyr Lys Ser Leu Asn Asp Glu Lys Leu Glu Thr Tyr Asp  
675 680 685

Glu Glu Lys Ala Arg Pro Arg Pro Ala Tyr Arg Arg Leu Gly Cys Phe  
690 695 700

Arg Phe Arg Ser Arg Phe Pro Ile Leu Gly Thr Gly Glu Thr Gly Arg  
705 710 715 720

Ile Glu Ala Gly Lys Asp Arg Arg Gly His Gly Val Ser Glu Thr Gly  
725 730 735

Ser Cys Ser Arg Arg Gln Gly Gly Ala Leu Trp Val Ser Pro Ala Gln  
740 745 750

Pro Ile Gly Phe Arg Ser Ser Trp Ser Ser Gly Ala Phe Ala Ser Ser  
755 760 765

Asn Thr Ser Gly Asn Cys Val Glu Arg Trp Ile Pro Gly Arg Val Leu  
770 775 780

Ala Arg Arg Ala Val Ser Lys Glu Gln Gln Asn Asn Cys Ser Thr Ser  
785 790 795 800

Leu Met Arg Met Glu Ser Arg Gly Asp Pro Arg Ala Thr Thr Asn Thr  
805 810 815

Gln Ala Gln Arg Phe His Ser Pro Lys Lys Asn Pro Glu Asp Gln Thr  
820 825 830

Met Pro Gln Asn Arg Thr Ile Tyr Val Thr Leu Lys Ala Val Arg Lys  
835 840 845

Glu Ile Glu Thr His Gln Gly Gln Glu Met Leu Val Arg Gly Thr Glu  
850 855 860

Gly Ile Lys Glu Tyr Ile Asn Leu Gly Met Pro Leu Ser Cys Phe Pro  
865                    870                    875                    880

Glu Gly Gly Gln Val Val Ile Thr Phe Ser Gln Ser Lys Ser Lys Gln  
885                    890                    895

Lys Glu Asp Asn His Ile Phe Gly Arg Gln Asp Lys Ala Ser Thr Glu  
900                    905                    910

Cys Val Lys Phe Tyr Ile His Ala Ile Gly Ile Gly Lys Cys Lys Arg  
915                    920                    925

Arg Ile Val Lys Cys Gly Lys Leu His Lys Lys Gly Arg Lys Leu Cys  
930                    935                    940

Val Tyr Ala Phe Lys Gly Glu Thr Ile Lys Asp Ala Leu Cys Lys Asp  
945                    950                    955                    960

Gly Arg Phe Leu Ser Phe Leu Glu Asn Asp Asp Trp Lys Leu Ile Glu  
965                    970                    975

Asn Asn Asp Thr Ile Leu Glu Ser Thr Gln Pro Val Asp Glu Leu Glu  
980                    985                    990

Gly Arg Tyr Phe Gln Val Glu Val Glu Lys Arg Met Val Pro Ser Ala  
995                    1000                    1005

Ala Ala Ser Gln Asn Pro Glu Ser Glu Lys Arg Asn Thr Cys Val  
1010                    1015                    1020

Leu Arg Glu Gln Ile Val Ala Gln Tyr Pro Ser Leu Lys Arg Glu  
1025                    1030                    1035

Ser Glu Lys Ile Ile Glu Asn Phe Lys Lys Lys Met Lys Val Lys  
1040                    1045                    1050

Asn Gly Glu Thr Leu Phe Glu Leu His Arg Thr Thr Phe Gly Lys  
1055                    1060                    1065

Val Thr Lys Asn Ser Ser Ser Ile Lys Val Val Lys Leu Leu Val  
1070                    1075                    1080

Arg Leu Ser Asp Ser Val Gly Tyr Leu Phe Trp Asp Ser Ala Thr  
1085 1090 1095

Thr Gly Tyr Ala Thr Cys Phe Val Phe Lys Gly Leu Phe Ile Leu  
1100 1105 1110

Thr Cys Arg His Val Ile Asp Ser Ile Val Gly Asp Gly Ile Glu  
1115 1120 1125

Pro Ser Lys Trp Ala Thr Ile Ile Gly Gln Cys Val Arg Val Thr  
1130 1135 1140

Phe Gly Tyr Glu Glu Leu Lys Asp Lys Glu Thr Asn Tyr Phe Phe  
1145 1150 1155

Val Glu Pro Trp Phe Glu Ile His Asn Glu Glu Leu Asp Tyr Ala  
1160 1165 1170

Val Leu Lys Leu Lys Glu Asn Gly Gln Gln Val Pro Met Glu Leu  
1175 1180 1185

Tyr Asn Gly Ile Thr Pro Val Pro Leu Ser Gly Leu Ile His Ile  
1190 1195 1200

Ile Gly His Pro Tyr Gly Glu Lys Lys Gln Ile Asp Ala Cys Ala  
1205 1210 1215

Val Ile Pro Gln Gly Gln Arg Ala Lys Lys Cys Gln Glu Arg Val  
1220 1225 1230

Gln Ser Lys Lys Ala Glu Ser Pro Glu Tyr Val His Met Tyr Thr  
1235 1240 1245

Gln Arg Ser Phe Gln Lys Ile Val His Asn Pro Asp Val Ile Thr  
1250 1255 1260

Tyr Asp Thr Glu Phe Phe Phe Gly Ala Ser Gly Ser Pro Val Phe  
1265 1270 1275

Asp Ser Lys Gly Ser Leu Val Ala Met His Ala Ala Gly Phe Ala  
1280 1285 1290

Tyr Thr Tyr Gln Asn Glu Thr Arg Ser Ile Ile Glu Phe Gly Ser

	1295	1300	1305	
Thr Met Glu Ser Ile Leu Leu Asp Ile Lys Gln Arg His Lys Pro				
1310		1315		1320
Trp Tyr Glu Glu Val Phe Val Asn Gln Gln Asp Val Glu Met Met				
1325		1330		1335
Ser Asp Glu Asp Leu				
1340				
<210> 260				
<211> 2829				
<212> DNA				
<213> human organism				
<400> 260				60
acatttcaaa aaaaatacat agactgatgt ttcagacttg tgcagcataa gcctacaggg				120
tacgaagaat gaaactcttag aatgtttgga gaatgtttca tcattactaa caggatattc				180
ctcatgacat tgctgtctga tcttgacca tcagtctgtg acctgcccct tctctttaca				240
tgcagccgct ctctgctccc tgccccaatg aacatctgca cttaggccccaa gccttggagt				300
aatttacctg aagagtgaca ccattgattt tgaaactact gaagaaaaccc aagacagctg				360
aaaaccagaa ggcacatctgag gagaatgaga ttactcagcc gggtgatcc agcgccaagc				420
cgggccttcc ctgcctgaac tttgaagctg ttttgtctcc agacccagcc ctcatccact				480
caacacattc actgacaaac tctcacgctc acacccggtc atctgattgt gacatcagtt				540
gcaaggggat gaccgagcgc attcacagca tcaaccttca caacttcagc aattccgtgc				600
tcgagaccct caacgagcag cgcaaccgtg gccacttctg tgacgtaacg gtgcgcaccc				660
acgggagcat gctgcgcgc acccgctgctg tgctggcagc cggcagcccc ttcttccagg				720
acaaaactgct gcttggctac agcgacatcg agatcccgtc ggtgggtca gtgcagtcag				780
tgcaaaagct cattgacttc atgtacagcg gcgtgctacg ggtctcgacag tcgaaagctc				840
tgcagatcct cacggccgcc agcatcctgc agatcaaaac agtcatcgac gagtgcacgc				900
gcatcgtgtc acagaacgtg ggcgatgtgt tcccgggat ccaggactcg ggccaggaca				960
cggcgcgggg cactcccgag tcagggcacgt caggccagag cagcgacacg gagtcgggct				1020
acctgcagag ccacccacag cacagcgtgg acaggatcta ctcggcactc tacgcgtgct				1080
ccatgcagaa tggcagcggc gagcgcttt tttacagcgg cgcaagtggc agccaccacg				

agactgcgct cggcctgccc cgcgaccacc acatggaaga ccccagctgg atcacacgca 1140  
tccatgagcg ctcgcagcag atggagcgct acctgtccac cacccccgag accacgcact 1200  
gccgcaagca gccccggcct gtgcgcattcc agaccctagt gggcaacatc cacatcaagc 1260  
aggagatgga ggacgattac gactactacg ggcagcaaag ggtgcagatc ctggaacgca 1320  
acgaatccga ggagtgcacg gaagacacag accaggccga gggcaccgag agtgagccca 1380  
aaggtgaaag cttcgactcg ggcgtcagct cctccatagg caccgagcct gactcggtgg 1440  
agcagcagtt tgggcctggg gcggcgccgg acagccaggc tgaacccacc caaccgagc 1500  
aggctgcaga agcccccgct gaggggtggtc cgccagacaaa ccagctagaa acaggtgctt 1560  
cctctccgga gagaagcaat gaagtggaga tggacagcac ttttatcact gtcagcaaca 1620  
gctccgacaa gagcgtccta caacagcctt cggtaaacac gtccatcggg cagccattgc 1680  
caagtaccca gctctactta cgccagacag aaaccctcac cagcaacctg aggatgcctc 1740  
tgaccttgac cagcaacacg caggtcattt gcacagctgg caacacctac ctgccagccc 1800  
tcttcactac ccagcccgcg ggcagtggcc ccaagcctt cctcttcagc ctgccacagc 1860  
ccctggcagg ccagcagacc cagtttgta cagtgtccca gcccggtctg tcgaccttta 1920  
ctgcacagct gccagcgcca cagccccctgg cctcatccgc aggccacagc acagccagtg 1980  
ggcaaggcga aaaaaaggcct tatgagtgca ctctctgcaa caagactttc accgccaaac 2040  
agaactacgt caagcacatg ttctgtacaca caggtgagaa gccccaccaa tgcagcatct 2100  
gttggcgctc ctttcctta aaggattacc ttatcaagca catggtgaca cacacaggag 2160  
tgagggcata ccagtgttagt atctgcaaca agcgcttcac ccagaagagc tccctcaacg 2220  
tgcacatgct cttccaccgg ggagagaagt cttacgagtg ctacatctgc aaaaagaagt 2280  
tctctcacaa gaccctcctg gagcgacacg tggccctgca cagtgccagc aatgggaccc 2340  
ccccctgcagg cacaccccca ggtgcccccgcttggcccccc aggcgtggcgcctgcacgg 2400  
aggggaccac ttacgtctgc tccgtctgcc cagcaaagtt tgaccaaatc gagcagttca 2460  
acgaccacat gaggatgcat gtgtctgacg gataagttagt atctttctct ctttctttag 2520  
aacaaaaacaa aacaacaaca aaaaacaaac aaacaaaaaa gctatggcac tagaatttaa 2580  
gaaatgtttt gtttcattt ttactttctg tttttgtttt tgtttcgtttt cattttgtac 2640  
tacatgaaga actgtttttt gcctgctggt acattacatt tccggaggct tgggtgaata 2700  
atagtttcc cagtctccct cggatggtgg ccttaaggcc tggtagtgct tcaagaggc 2760  
cactgggtgg atctctagct actggcctct aaatacaacc cttctttaca aaaaaaaaaa 2820



2829

aaaaaaaaaa

<210> 261  
<211> 668  
<212> PRT  
<213> human organism

&lt;400&gt; 261

Met Thr Glu Arg Ile His Ser Ile Asn Leu His Asn Phe Ser Asn Ser  
1 5 10 15

Val Leu Glu Thr Leu Asn Glu Gln Arg Asn Arg Gly His Phe Cys Asp  
20 25 30

Val Thr Val Arg Ile His Gly Ser Met Leu Arg Ala His Arg Cys Val  
35 40 45

Leu Ala Ala Gly Ser Pro Phe Phe Gln Asp Lys Leu Leu Leu Gly Tyr  
50 55 60

Ser Asp Ile Glu Ile Pro Ser Val Val Ser Val Gln Ser Val Gln Lys  
65 70 75 80

Leu Ile Asp Phe Met Tyr Ser Gly Val Leu Arg Val Ser Gln Ser Glu  
85 90 95

Ala Leu Gln Ile Leu Thr Ala Ala Ser Ile Leu Gln Ile Lys Thr Val  
100 105 110

Ile Asp Glu Cys Thr Arg Ile Val Ser Gln Asn Val Gly Asp Val Phe  
115 120 125

Pro Gly Ile Gln Asp Ser Gly Gln Asp Thr Pro Arg Gly Thr Pro Glu  
130 135 140

Ser Gly Thr Ser Gly Gln Ser Ser Asp Thr Glu Ser Gly Tyr Leu Gln  
145 150 155 160

Ser His Pro Gln His Ser Val Asp Arg Ile Tyr Ser Ala Leu Tyr Ala  
165 170 175

Cys Ser Met Gln Asn Gly Ser Gly Glu Arg Ser Phe Tyr Ser Gly Ala  
180 185 190

Val Val Ser His His Glu Thr Ala Leu Gly Leu Pro Arg Asp His His  
195 200 205

Met Glu Asp Pro Ser Trp Ile Thr Arg Ile His Glu Arg Ser Gln Gln  
210 215 220

Met Glu Arg Tyr Leu Ser Thr Thr Pro Glu Thr Thr His Cys Arg Lys  
225 230 235 240

Gln Pro Arg Pro Val Arg Ile Gln Thr Leu Val Gly Asn Ile His Ile  
245 250 255

Lys Gln Glu Met Glu Asp Asp Tyr Asp Tyr Tyr Gly Gln Gln Arg Val  
260 265 270

Gln Ile Leu Glu Arg Asn Glu Ser Glu Glu Cys Thr Glu Asp Thr Asp  
275 280 285

Gln Ala Glu Gly Thr Glu Ser Glu Pro Lys Gly Glu Ser Phe Asp Ser  
290 295 300

Gly Val Ser Ser Ser Ile Gly Thr Glu Pro Asp Ser Val Glu Gln Gln  
305 310 315 320

Phe Gly Pro Gly Ala Ala Arg Asp Ser Gln Ala Glu Pro Thr Gln Pro  
325 330 335

Glu Gln Ala Ala Glu Ala Pro Ala Glu Gly Gly Pro Gln Thr Asn Gln  
340 345 350

Leu Glu Thr Gly Ala Ser Ser Pro Glu Arg Ser Asn Glu Val Glu Met  
355 360 365

Asp Ser Thr Val Ile Thr Val Ser Asn Ser Ser Asp Lys Ser Val Leu  
370 375 380

Gln Gln Pro Ser Val Asn Thr Ser Ile Gly Gln Pro Leu Pro Ser Thr  
385 390 395 400

Gln Leu Tyr Leu Arg Gln Thr Glu Thr Leu Thr Ser Asn Leu Arg Met  
405 410 415

Pro Leu Thr Leu Thr Ser Asn Thr Gln Val Ile Gly Thr Ala Gly Asn  
420 425 430

Thr Tyr Leu Pro Ala Leu Phe Thr Thr Gln Pro Ala Gly Ser Gly Pro  
435 440 445

Lys Pro Phe Leu Phe Ser Leu Pro Gln Pro Leu Ala Gly Gln Gln Thr  
450 455 460

Gln Phe Val Thr Val Ser Gln Pro Gly Leu Ser Thr Phe Thr Ala Gln  
465 470 475 480

Leu Pro Ala Pro Gln Pro Leu Ala Ser Ser Ala Gly His Ser Thr Ala  
485 490 495

Ser Gly Gln Gly Glu Lys Lys Pro Tyr Glu Cys Thr Leu Cys Asn Lys  
500 505 510

Thr Phe Thr Ala Lys Gln Asn Tyr Val Lys His Met Phe Val His Thr  
515 520 525

Gly Glu Lys Pro His Gln Cys Ser Ile Cys Trp Arg Ser Phe Ser Leu  
530 535 540

Lys Asp Tyr Leu Ile Lys His Met Val Thr His Thr Gly Val Arg Ala  
545 550 555 560

Tyr Gln Cys Ser Ile Cys Asn Lys Arg Phe Thr Gln Lys Ser Ser Leu  
565 570 575

Asn Val His Met Arg Leu His Arg Gly Glu Lys Ser Tyr Glu Cys Tyr  
580 585 590

Ile Cys Lys Lys Phe Ser His Lys Thr Leu Leu Glu Arg His Val  
595 600 605

Ala Leu His Ser Ala Ser Asn Gly Thr Pro Pro Ala Gly Thr Pro Pro  
610 615 620

Gly Ala Arg Ala Gly Pro Pro Gly Val Val Ala Cys Thr Glu Gly Thr  
625 630 635 640

Thr Tyr Val Cys Ser Val Cys Pro Ala Lys Phe Asp Gln Ile Glu Gln  
645 650 655

Phe Asn Asp His Met Arg Met His Val Ser Asp Gly  
660 665

<210> 262  
<211> 912  
<212> DNA  
<213> human organism

<400> 262  
atggtggaaag aggaaacagg catatcttac atggtggcag acaagggaca cccttctaca 60  
aactctacca cttctgcgcc gtcgtttcga ccatataaaa acgacacctatg cgaactgcgt 120  
cgaaaaactc cctcacgatg taaaacgaag atcaggagca gatttgaaga attacaaagt 180  
gaatttgtgc cagtcagcat gtcagagaca gaccacatag cctctacttc ctctgataaa 240  
aatgttggga aaacacctga attaaaggaa gactcatgca acttgtttc tggcaatgaa 300  
agcagcaaat tagaaaatga gtccaaacta ttgtcattaa acactgataa aactttatgt 360  
caacctaattg agcataataa tcgaattgaa gcccaggaaa attatattcc agatcatggt 420  
ggaggtgagg attcttgtgc caaaacagac acaggctcag aaaattctga acaaataagct 480  
aattttccta gtggaaattt tgctaaacat atttcaaaaaa caaatgaaac agaacagaaa 540  
gtaacacaaa tatttgtgga attaaggtca tctacatttc cagaatcagc taatgaaaag 600  
acttattcag aaagcccta tgatacagac tgcaccaaga aatttatttc aaaaataaaag 660  
agcgtttcag catcagagga tttgttgaa gaaatagaat ctgagcttt atctacggag 720  
tttgcagaac atcgagtacc aaatggaatg aataagggag aacatgcatt agttctgttt 780  
gaaaagtgtg tgcaagataa atattgcag caggaacata tcataaaaaa ggccagactt 840  
ggctctgtt atttgcacatc aagaacctca attgacacgt taattccgtt tatccaaat 900  
ttatataatgaa 912

<210> 263  
<211> 219  
<212> PRT  
<213> human organism

<400> 263

Met Glu Pro Lys Glu Ala Thr Gly Lys Glu Asn Met Val Thr Lys Lys  
1 5 10 15

Lys Asn Leu Ala Phe Leu Arg Ser Arg Leu Tyr Met Leu Glu Arg Arg  
20 25 30

Lys Thr Asp Thr Val Val Glu Ser Ser Val Ser Gly Asp His Ser Gly  
35 40 45

Thr Leu Arg Arg Ser Gln Ser Asp Arg Thr Glu Tyr Asn Gln Lys Leu  
50 55 60

Gln Glu Lys Met Thr Pro Gln Gly Glu Cys Ser Val Ala Glu Thr Leu  
65 70 75 80

Thr Pro Glu Glu His His Met Lys Arg Met Met Ala Lys Arg Glu  
85 90 95

Lys Ile Ile Lys Glu Leu Ile Gln Thr Glu Lys Asp Tyr Leu Asn Asp  
100 105 110

Leu Glu Leu Cys Val Arg Glu Val Val Gln Pro Leu Arg Asn Lys Lys  
115 120 125

Thr Asp Arg Leu Asp Val Asp Ser Leu Phe Ser Asn Ile Glu Ser Val  
130 135 140

His Gln Ile Ser Ala Lys Leu Leu Ser Leu Leu Glu Glu Ala Thr Thr  
145 150 155 160

Asp Val Glu Pro Ala Met Gln Val Ile Gly Glu Val Phe Leu Gln Ile  
165 170 175

Lys Gly Pro Leu Glu Asp Ile Tyr Lys Ile Tyr Cys Tyr His His Asp  
180 185 190

Glu Ala His Ser Ile Leu Glu Ser Tyr Glu Lys Glu Glu Leu Lys  
195 200 205

Glu His Leu Ser His Cys Ile Gln Ser Leu Lys  
210 215

<210> 264

<211> 3812

<212> DNA

<213> human organism

<400> 264	
gggcctactc tgccgccc gccgccc gcccagcc gccgccc cgcaccgc	60
cctccaggct ccgggacccg gcccgc gcca cggccccgt gcgcgc cccgc	120
cttcgccttc gcctttgtt tcctccgctc cggcgcccc gccccggctc gcgcttgca	180
gggacgcag cgcgcccc cagcggccc gggaaaagcc gcggcgcg cgcgccctg	240
cgcggcggac ccctccttct cctccccgctg tgcgctgccc cttttggct gcgccggc	300
gccgcctggc gggcgagg ggaggtggca ggcgcgttgc caggaggggc gcaccttgc	360
gctcgccac ccccccggaa gtagaccgg gaaggaggagg cggcgccg gagaggag	420
agtggcgcc agtccagcga gggcggggt tggctatgtg ggggtggc cacccttgc	480
tctagacagt ctgatccggg ctggggcgt gtacactcgg cgcacctgctg agactacaga	540
gcctcgggccc ggcacgtgtg gggagtgtgg acacgtctgc tgcccccgc ttctcgctgc	600
tgaggggaag ggagggggcg ggcaggtgca gcccggc tagtggagg ggcggccggc	660
catggagcgg gtgaacgacg cttcgtcgg cccgtctggc tgctacacat accaggtgag	720
cagacacagc acggagatgc tgcacaacct gaaccagcag cgaaaaacg gcggcgctt	780
ctgcgacgtg ctcttgcgg taggcgacga gagcttcca gcgcaccgcg ccgtgctggc	840
cgcctgcaggc gagtaacttgc agtcgggttt cagcggccag ttggcgacg gcggagctgc	900
ggacgggggt ccggctgatg tagggggcgca gacggcagca ccaggcggcg gggccggggg	960
cagccggag ctggagatgc acactatcag ctccaaggta tttgggaca ttctggactt	1020
cgcctacact tcccgcacg tggcgctt ggagagctt cccgaactca tgacggccgc	1080
caagttcctg ctgatgaggt cggttatcga gatctccag gaagtcatca aacagtccaa	1140
cgtacagatc ctggtacccc ctgccccgcg cgtataatg ctcttcgccc cccctggac	1200
ctcgacttg ggctccctt tggacatgac caacggggca gccttggcag ccaacagcaa	1260
tggcatcgcc ggcagcatgc agccagagga ggaggcagct cggcgccgtg gtgcagccat	1320
tgcaaggccaa gcctcttgc ctgtgttacc tgggtggac cgcttgc cttggctgg	1380
accctatcc ccccaactgc tgacttcccc attccccagt gtggcatcca gtgcctcc	1440
cctgactggc aagcgaggcc gggggccccc aaggaaggcc aacctgctgg actcaatgtt	1500
tgggtccccca gggggcctga gggaggcagg catccttcca tgcggtctat gtggtaaggt	1560
gttcactgat gccaaccggc tccggcagca cgaggccag cacgggtgtca ccagcctcca	1620
gctgggctac atcgaccccttc ctccctccgag gctgggtgag aatgggctac ccatctctga	1680

agaccccgac ggccccgaa agaggagccg gaccaggaag caggtggctt gtgagatctg 1740  
cgccaagatc ttccgtatg tgtatcatct taaccggcac aagctgtccc actctgggaa 1800  
gaagccctac tcctgccctg tgtgtggtt gcgggtcaag agaaaagacc gcatgtccta 1860  
ccatgtgcgg tcccatgatg ggtccgtggg caagccttac atctgccaga gctgtggaa 1920  
aggcttctcc aggctgatc acttgaacgg acatatcaag caggtgcaca cttctgagcg 1980  
gcctcacaag tgtcagacct gcaatgcttc ttttgcacc cgagaccgtc tgcgctccca 2040  
cctggcctgt catgaagaca aggtgccctg ccaggtgtgt gggaaagtact tgccggcagc 2100  
atacatggca gaccacctga agaaggcacag cgaggggccc agcaacttct gcagtatctg 2160  
taaccgaggt ttctcctctg ctcctactt aaaggtccat gttaaaaccc accacggtgt 2220  
tcccctccc caggtctcca ggcaccagga gcccatcctg aatgggggag cagcgttcca 2280  
ctgcgccagg acctatggca acaaagaagg ccagaaatgc tcacatcagg atccgattga 2340  
gagctctgac tcctatggtg acctctcaga tgccagcgc ctgaagacgc cagagaagca 2400  
gagtgc当地 ggcgtttct ctcgtccat ggcagtcggg aaaaacaaaa tggagtctga 2460  
tggggagaag aagtacccat gcccgtaatg tggagcttc ttccgctcta agtcctactt 2520  
gaacaaacac atccagaagg tgcatgtccg ggctctcggg ggcccccctgg gggacctggg 2580  
ccctgcctt ggctcacctt tctctcctca gcagaacatg tctctcctcg agtcctttgg 2640  
gttcagatt gttcagtcgg catttgcgtc atcttagta gatcctgagg ttgaccagca 2700  
gcccattggg cctgaaggaa aatgaggcag ctgctgtgtc cccacggaaa caaccatctg 2760  
gggactgctg gaaaaatgctg tgaatgcgg gggaaagtgtat gtttgggttc ttagctgag 2820  
agatTTTAT tcattttaa ctgccttcca accccactcc aactccttct ccaccaccca 2880  
ttctccaaat ggtctttaga aatagatTTT catctgatat tctgcagaaa tatcaatgag 2940  
acttggatg ggacaggggc agaaaacact acataggcct ccaaggcaaa accagtccttca 3000  
gtttctttaa tgggaagaag ctggattcc tgggtgctcaa ttcttagtga ccccaatctt 3060  
atacccaaat ctatgatatt ctggacactc agtggatTTT gtccctccc acttctctag 3120  
ttcgtcatcc tcccttcca tatccttcaa aagaaccaca cttagggtctc cacctactta 3180  
tacaatgcgg atgcccact gtttttaagg aagccagaag catcccatgg accatggggt 3240  
gagtgccctc caagagcccc ctgagctcag ccctctgcct ggagggctcc agacctttct 3300  
gagccctgct tggaggcgag cattttcaact gctaggacaa gctcagctgt tgaggacacc 3360

cccaccccaa attcagttc ttacgtgatt ttaaccattc aacatgctgt tgggtttaa 3420  
ttctctaatt attattatta ttgttattat ttttaggac cagttgtgt gaattgctac 3480  
tgaaagctat cccaggtgat acagagctct ttgtaaaccg cagtcacaca ttagggtag 3540  
tattaaactt tgtagatg taccataatt aacttggcta gttgattgtt tgaagtctat 3600  
ggaagaaata gtttatgca aaattttaaa aaatgcagt ctggtcaggg aagtaggggg 3660  
tttcaatgct gttgggaacc aggaaggtagg gacagccggc agtagggac attgtgtacc 3720  
tcagttgtgt cacatgtgag caagcccagg ttgaccttgt gatgtgaatt gatctgatca 3780  
gactgttatta aaaatgttag tacattactc ta 3812

<210> 265

<211> 641

<212> PRT

<213> human organism

<400> 265

Met Glu Arg Val Asn Asp Ala Ser Cys Gly Pro Ser Gly Cys Tyr Thr  
1 5 10 15

Tyr Gln Val Ser Arg His Ser Thr Glu Met Leu His Asn Leu Asn Gln  
20 25 30

Gln Arg Lys Asn Gly Gly Arg Phe Cys Asp Val Leu Leu Arg Val Gly  
35 40 45

Asp Glu Ser Phe Pro Ala His Arg Ala Val Leu Ala Ala Cys Ser Glu  
50 55 60

Tyr Phe Glu Ser Val Phe Ser Ala Gln Leu Gly Asp Gly Gly Ala Ala  
65 70 75 80

Asp Gly Gly Pro Ala Asp Val Gly Gly Ala Thr Ala Ala Pro Gly Gly  
85 90 95

Gly Ala Gly Gly Ser Arg Glu Leu Glu Met His Thr Ile Ser Ser Lys  
100 105 110

Val Phe Gly Asp Ile Leu Asp Phe Ala Tyr Thr Ser Arg Ile Val Val  
115 120 125

Arg Leu Glu Ser Phe Pro Glu Leu Met Thr Ala Ala Lys Phe Leu Leu

130                    135                    140

Met Arg Ser Val Ile Glu Ile Cys Gln Glu Val Ile Lys Gln Ser Asn  
145    150                            155                            160

Val Gln Ile Leu Val Pro Pro Ala Arg Ala Asp Ile Met Leu Phe Arg  
165    170    175

Pro Pro Gly Thr Ser Asp Leu Gly Phe Pro Leu Asp Met Thr Asn Gly  
180    185    190

Ala Ala Leu Ala Ala Asn Ser Asn Gly Ile Ala Gly Ser Met Gln Pro  
195    200    205

Glu Glu Glu Ala Ala Arg Ala Ala Gly Ala Ala Ile Ala Gly Gln Ala  
210    215    220

Ser Leu Pro Val Leu Pro Gly Val Asp Arg Leu Pro Met Val Ala Gly  
225    230    240

Pro Leu Ser Pro Gln Leu Leu Thr Ser Pro Phe Pro Ser Val Ala Ser  
245    250    255

Ser Ala Pro Pro Leu Thr Gly Lys Arg Gly Arg Gly Arg Pro Arg Lys  
260    265    270

Ala Asn Leu Leu Asp Ser Met Phe Gly Ser Pro Gly Gly Leu Arg Glu  
275    280    285

Ala Gly Ile Leu Pro Cys Gly Leu Cys Gly Lys Val Phe Thr Asp Ala  
290    295    300

Asn Arg Leu Arg Gln His Glu Ala Gln His Gly Val Thr Ser Leu Gln  
305    310    320

Leu Gly Tyr Ile Asp Leu Pro Pro Arg Leu Gly Glu Asn Gly Leu  
325    330    335

Pro Ile Ser Glu Asp Pro Asp Gly Pro Arg Lys Arg Ser Arg Thr Arg  
340    345    350

Lys Gln Val Ala Cys Glu Ile Cys Gly Lys Ile Phe Arg Asp Val Tyr  
355    360    365

His Leu Asn Arg His Lys Leu Ser His Ser Gly Glu Lys Pro Tyr Ser  
370 375 380

Cys Pro Val Cys Gly Leu Arg Phe Lys Arg Lys Asp Arg Met Ser Tyr  
385 390 395 400

His Val Arg Ser His Asp Gly Ser Val Gly Lys Pro Tyr Ile Cys Gln  
405 410 415

Ser Cys Gly Lys Gly Phe Ser Arg Pro Asp His Leu Asn Gly His Ile  
420 425 430

Lys Gln Val His Thr Ser Glu Arg Pro His Lys Cys Gln Thr Cys Asn  
435 440 445

Ala Ser Phe Ala Thr Arg Asp Arg Leu Arg Ser His Leu Ala Cys His  
450 455 460

Glu Asp Lys Val Pro Cys Gln Val Cys Gly Lys Tyr Leu Arg Ala Ala  
465 470 475 480

Tyr Met Ala Asp His Leu Lys Lys His Ser Glu Gly Pro Ser Asn Phe  
485 490 495

Cys Ser Ile Cys Asn Arg Glu Gly Gln Lys Cys Ser His Gln Asp Pro  
500 505 510

Ile Glu Ser Ser Asp Ser Tyr Gly Asp Leu Ser Asp Ala Ser Asp Leu  
515 520 525

Lys Thr Pro Glu Lys Gln Ser Ala Asn Gly Ser Phe Ser Cys Asp Met  
530 535 540

Ala Val Pro Lys Asn Lys Met Glu Ser Asp Gly Glu Lys Lys Tyr Pro  
545 550 555 560

Cys Pro Glu Cys Gly Ser Phe Phe Arg Ser Lys Ser Tyr Leu Asn Lys  
565 570 575

His Ile Gln Lys Val His Val Arg Ala Leu Gly Gly Pro Leu Gly Asp  
580 585 590

Leu Gly Pro Ala Leu Gly Ser Pro Phe Ser Pro Gln Gln Asn Met Ser  
595 600 605

Leu Leu Glu Ser Phe Gly Phe Gln Ile Val Gln Ser Ala Phe Ala Ser  
610 615 620

Ser Leu Val Asp Pro Glu Val Asp Gln Gln Pro Met Gly Pro Glu Gly  
625 630 635 640

Lys

<210> 266  
<211> 2818  
<212> DNA  
<213> human organism

<400> 266  
ccctactccg cctctcgga tccttaaga ggccccctt ggctgccagc tccggggccc 60  
ggcaaaagg ctgggacttt actccgggtg gcggcgagga cgagtctgtg ctccatcagc 120  
tgccgcaccc gccgcctccc gcccccaaac cccatcccg cggtttagcc acgatgagcg 180  
gcagagtcgg cgatctgagc cccaggcaga aggaggcatt ggccaagttt cgggagaatg 240  
tccaggatgt gctgccggcc ctgccaatc cagatgacta ttttctcctg cgttggctcc 300  
gagccagaag cttcgacctg cagaagtcgg aggccatgct ccggaaagcat gtggagttcc 360  
gaaagcaaaa ggacattgac aacatcatta gctggcagcc tccagaggtg atccaacagt 420  
atctgtcagg ggttatgtgt ggctatgacc tggatggctg cccagtctgg tacgacataa 480  
ttggacctct ggatgccaag ggtctgctgt tctcagcctc caaacaggac ctgctgagga 540  
ccaagatgcg ggagtgtgag ctgcttctgc aagagtgtgc ccaccagacc acaaagttgg 600  
ggaggaaggt ggagaccatc accataattt atgactgcga ggggcttggc ctcaagcatc 660  
tctggaagcc tgctgtggag gcctatggag agtttctctg catgtttgag gaaaattatc 720  
ccgaaacact gaagcgtctt tttgttgtt aagccccaa actgtttcct gtggcctata 780  
acctcatcaa acccttcctg agtggggaca ctcgtaagaa gatcatggc ctgggagcaa 840  
atggaaagga ggtttactg aaacatatca gcccgtacca ggtgcctgtg gagtatgggg 900  
gcaccatgac tgaccctgat ggaaacccca agtgcacatc caagatcaac tacgggggtg 960  
acatccccag gaagtattat gtgcgagacc aggtgaaaca gcagtatgaa cacagcgtgc 1020

agattcccc tggctccctcc caccaagtgg agtatgagat cctcttcctt ggctgtgtcc 1080  
tcaggtggca gtttatgtca gatggagcgg atgttggtt tgggatttc ctgaagacca 1140  
agatggaga gaggcagcgg gcaggggaga tgacagaggt gctgcccac cagaggata 1200  
actcccacct ggtccctgaa gatgggaccc tcacctgcag tgatcctggc atctatgtcc 1260  
tgcggttga caacacccatc agttcattc atgccaagaa ggtcaatttc actgtggagg 1320  
tcctgcttcc agacaaagcc tcagaagaga agatgaaaca gctggggca ggcaccccg 1380  
aataacacacct tctcctatag caggcctggc cccctcagtg tctccctgtc aatttctacc 1440  
cctttagca gtcatttcg cacaaccctg aagccaaag aaactgggt ggaggacaga 1500  
cctcaggagc tttcatttca gtttaggcaga ggaagagcga ctgcagtggg tctccgtgtc 1560  
tatcaaatac ctaaggagtc cccaggagct ggctggccat cgtatagga tctgtctgtc 1620  
ctgtaaaactg tgccaaacttc acctgtccag ggacagcgaa gctgggggtg gcggggggca 1680  
tgtaccacag ggtggcagca gggaaaaaaa ttagaaaagg gtgaaagatt gggacttaac 1740  
acttcaggga agtcagctgc cggggagaaaa cttgctccta aatgaacaca taagttaga 1800  
tcgcaatgag gagtagcagg gtagctgggtt gctagagttt cggggggat cagaaactct 1860  
tccaaacatt ttagcactga ggctggggta gctttggct tttccaggt ctcaggaggt 1920  
ggccttagtc agcacacatc ttccactcg gtagacaggc tggcctctcc ctcacttga 1980  
gactttggca actcctggc cacacggcct gcctcttga ttactaatga ttgtcagtga 2040  
ctcagagctt cctggactt cgggtaccca cccgctgttc tccatgcaaa caaagcgcca 2100  
gggaaatgac ccacagggat cgtagctgca gggagggcca gggaggttgg gggtaggt 2160  
gaatgctaaa agcagatcgt ccagtgcctt tttcagtgtct accggcctct caccaagcag 2220  
tcctccatgt gagcaacccc gagacaaaaa tgctaagtgg gatcaagaga gcagcactcg 2280  
gagagggtgt ttgccagttt gagtgtcccg cggtccccgc caacccgctt cctgactgac 2340  
ctgagcaagg tcttactaag cagtccatc tctgtggag gcatgcaacg cgtgcaggga 2400  
gttcaggtgc cggtcggcgt agccaggcct ggaggcccc cagggaggag gccgccccaa 2460  
ggcgcccccg gctgtctcgca gactaggggc tggggcggc cacagacggc ctcgaaacca 2520  
cagcccttac cccaatccca cgagccccgc caacgaacca caggtgctgg gcttttagaga 2580  
acatgggaag gcggccccag acctggcggg aacgccttc cctcagagcc aggccccggc 2640  
cccgcttggg aagctcatct tgctaaagctg agggagctca gggcaaaggc caggctagcg 2700  
cggaccggaa gggcccgagg ctgcacgggc ctctgccaga acgctcagga catccggcc 2760

tgggttaca acgctgttag gaaaattaac caatgaataa agcaacgttc agtgcgca 2818

<210> 267  
<211> 403  
<212> PRT  
<213> human organism

<400> 267

Met Ser Gly Arg Val Gly Asp Leu Ser Pro Arg Gln Lys Glu Ala Leu  
1 5 10 15

Ala Lys Phe Arg Glu Asn Val Gln Asp Val Leu Pro Ala Leu Pro Asn  
20 25 30

Pro Asp Asp Tyr Phe Leu Leu Arg Trp Leu Arg Ala Arg Ser Phe Asp  
35 40 45

Leu Gln Lys Ser Glu Ala Met Leu Arg Lys His Val Glu Phe Arg Lys  
50 55 60

Gln Lys Asp Ile Asp Asn Ile Ile Ser Trp Gln Pro Pro Glu Val Ile  
65 70 75 80

Gln Gln Tyr Leu Ser Gly Gly Met Cys Gly Tyr Asp Leu Asp Gly Cys  
85 90 95

Pro Val Trp Tyr Asp Ile Ile Gly Pro Leu Asp Ala Lys Gly Leu Leu  
100 105 110

Phe Ser Ala Ser Lys Gln Asp Leu Leu Arg Thr Lys Met Arg Glu Cys  
115 120 125

Glu Leu Leu Leu Gln Glu Cys Ala His Gln Thr Thr Lys Leu Gly Arg  
130 135 140

Lys Val Glu Thr Ile Thr Ile Tyr Asp Cys Glu Gly Leu Gly Leu  
145 150 155 160

Lys His Leu Trp Lys Pro Ala Val Glu Ala Tyr Gly Glu Phe Leu Cys  
165 170 175

Met Phe Glu Glu Asn Tyr Pro Glu Thr Leu Lys Arg Leu Phe Val Val  
180 185 190

Lys Ala Pro Lys Leu Phe Pro Val Ala Tyr Asn Leu Ile Lys Pro Phe  
195 200 205

Leu Ser Glu Asp Thr Arg Lys Lys Ile Met Val Leu Gly Ala Asn Trp  
210 215 220

Lys Glu Val Leu Leu Lys His Ile Ser Pro Asp Gln Val Pro Val Glu  
225 230 235 240

Tyr Gly Gly Thr Met Thr Asp Pro Asp Gly Asn Pro Lys Cys Lys Ser  
245 250 255

Lys Ile Asn Tyr Gly Gly Asp Ile Pro Arg Lys Tyr Tyr Val Arg Asp  
260 265 270

Gln Val Lys Gln Gln Tyr Glu His Ser Val Gln Ile Ser Arg Gly Ser  
275 280 285

Ser His Gln Val Glu Tyr Glu Ile Leu Phe Pro Gly Cys Val Leu Arg  
290 295 300

Trp Gln Phe Met Ser Asp Gly Ala Asp Val Gly Phe Gly Ile Phe Leu  
305 310 315 320

Lys Thr Lys Met Gly Glu Arg Gln Arg Ala Gly Glu Met Thr Glu Val  
325 330 335

Leu Pro Asn Gln Arg Tyr Asn Ser His Leu Val Pro Glu Asp Gly Thr  
340 345 350

Leu Thr Cys Ser Asp Pro Gly Ile Tyr Val Leu Arg Phe Asp Asn Thr  
355 360 365

Tyr Ser Phe Ile His Ala Lys Lys Val Asn Phe Thr Val Glu Val Leu  
370 375 380

Leu Pro Asp Lys Ala Ser Glu Glu Lys Met Lys Gln Leu Gly Ala Gly  
385 390 395 400

Thr Pro Lys

<210> 268  
<211> 1464  
<212> DNA  
<213> human organism

<400> 268  
gtggggacag ccgagccgct cggggccccct ggacggcgtc gccaaggagc tgggatcgca 60  
cttgctgcag actttggatg gatttgttt tggtagca tctgatggca aaatcatgta 120  
tatatatccgag accgcttctg tccatttagg cttatcccag gtggagctca cgggcaacag 180  
tatttatgaa tacatccatc cttctgacca cgatgagatg accgctgtcc tcacggccca 240  
ccagccgctg caccaccacc tgctccaagg tatgagatag agaggctgtt ctttcttcga 300  
atgaaatgtg tcttggcgaa aaggaacgctg ggcctgacct gcagcggata caaggtcatc 360  
cactgcagt gctacttgaa gatcaggcag tatatgtgg acatgtccct gtacgactcc 420  
tgctaccaga ttgtggggct ggtggccgtg ggccagtcgc tgccacccag tgccatcacc 480  
gagatcaagc tgtacagtaa catgttcatg ttcagggcca gccttgacct gaagctgata 540  
ttcctggatt ccagggtgac cgaggtgacg ggtacgagc cgcaggacccct gatcgagaag 600  
acccatatacc atcacgtgca cggctgcgac gtgttccacc tccgctacgc acaccaccc 660  
ctgttggta agggccaggt caccaccaag tactaccggc tgctgtccaa gcggggcggc 720  
tgggtgtggg tgcagagcta cgccaccgtg gtgcacaaca gccgctcgtc cggccccac 780  
tgcatcgtga gtgtcaatta tgtactcacg gagattgaat acaaggaact tcagctgtcc 840  
ctggagcagg tgtccactgc caagtccctg gactcctgga ggaccgcctt gtctaccc 900  
caagaaacta ggaaattagt gaaacccaaa aataccaaga tgaagacaaa gctgagaaca 960  
aacccattacc ccccacagca atacagctcg ttccaaatgg acaaactgga atgcggccag 1020  
ctcggaaact ggagagccag tccccctgca agcgctgctg ctcctccaga actgcagccc 1080  
cactcagaaa gcagtgaccc tctgtacacg ccatcctaca gcctgccctt ctccattac 1140  
tacggacact tccctctgga ctctcacgtc ttcagcagca aaaagccaat gttgccggcc 1200  
aagttcgggc agccccaagg atccccttgt gaggtggcac gcttttcct gagcacactg 1260  
ccagccagcg gtgaatgcca gtggcattat gccaacccccc tagtgcctag cagctcgct 1320  
ccagctaaaa atcctccaga gccaccggcg aacactgcta ggcacagcct ggtgccaagc 1380  
tacgaaggca agcagatgtc ctctgcggag ataccgcccag ctccccagga cgcagactga 1440  
ctccctgtttg ctgcgtggac caac 1464

<210> 269  
<211> 667  
<212> PRT  
<213> human organism

<400> 269

Met Lys Glu Lys Ser Lys Asn Ala Ala Lys Thr Arg Arg Glu Lys Glu  
1 5 10 15

Asn Gly Glu Phe Tyr Glu Leu Ala Lys Leu Leu Pro Leu Pro Ser Ala  
20 25 30

Ile Thr Ser Gln Leu Asp Lys Ala Ser Ile Ile Arg Leu Thr Thr Ser  
35 40 45

Tyr Leu Lys Met Arg Ala Val Phe Pro Glu Gly Leu Gly Asp Ala Trp  
50 55 60

Gly Gln Pro Ser Arg Ala Gly Pro Leu Asp Gly Val Ala Lys Glu Leu  
65 70 75 80

Gly Ser His Leu Leu Gln Thr Leu Asp Gly Phe Val Phe Val Val Ala  
85 90 95

Ser Asp Gly Lys Ile Met Tyr Ile Ser Glu Thr Ala Ser Val His Leu  
100 105 110

Gly Leu Ser Gln Val Glu Leu Thr Gly Asn Ser Ile Tyr Glu Tyr Ile  
115 120 125

His Pro Ser Asp His Asp Glu Met Thr Ala Val Leu Thr Ala His Gln  
130 135 140

Pro Leu His His His Leu Leu Gln Glu Tyr Glu Ile Glu Arg Ser Phe  
145 150 155 160

Phe Leu Arg Met Lys Cys Val Leu Ala Lys Arg Asn Ala Gly Leu Thr  
165 170 175

Cys Ser Gly Tyr Lys Val Ile His Cys Ser Gly Tyr Leu Lys Ile Arg  
180 185 190

Gln Tyr Met Leu Asp Met Ser Leu Tyr Asp Ser Cys Tyr Gln Ile Val

195

200

205

Gly Leu Val Ala Val Gly Gln Ser Leu Pro Pro Ser Ala Ile Thr Glu  
210 215 220

Ile Lys Leu Tyr Ser Asn Met Phe Met Phe Arg Ala Ser Leu Asp Leu  
225 230 235 240

Lys Leu Ile Phe Leu Asp Ser Arg Val Thr Glu Val Thr Gly Tyr Glu  
245 250 255

Pro Gln Asp Leu Ile Glu Lys Thr Leu Tyr His His Val His Gly Cys  
260 265 270

Asp Val Phe His Leu Arg Tyr Ala His His Leu Leu Leu Val Lys Gly  
275 280 285

Gln Val Thr Thr Lys Tyr Tyr Arg Leu Leu Ser Lys Arg Gly Gly Trp  
290 295 300

Val Trp Val Gln Ser Tyr Ala Thr Val Val His Asn Ser Arg Ser Ser  
305 310 315 320

Arg Pro His Cys Ile Val Ser Val Asn Tyr Val Leu Thr Glu Ile Glu  
325 330 335

Tyr Lys Glu Leu Gln Leu Ser Leu Glu Gln Val Ser Thr Ala Lys Ser  
340 345 350

Gln Asp Ser Trp Arg Thr Ala Leu Ser Thr Ser Gln Glu Thr Arg Lys  
355 360 365

Leu Val Lys Pro Lys Asn Thr Lys Met Lys Thr Lys Leu Arg Thr Asn  
370 375 380

Pro Tyr Pro Pro Gln Gln Tyr Ser Ser Phe Gln Met Asp Lys Leu Glu  
385 390 395 400

Cys Gly Gln Leu Gly Asn Trp Arg Ala Ser Pro Pro Ala Ser Ala Ala  
405 410 415

Ala Pro Pro Glu Leu Gln Pro His Ser Glu Ser Ser Asp Leu Leu Tyr  
420 425 430

Thr Pro Ser Tyr Ser Leu Pro Phe Ser Tyr His Tyr Gly His Phe Pro  
435 440 445

Leu Asp Ser His Val Phe Ser Ser Lys Lys Pro Met Leu Pro Ala Lys  
450 455 460

Phe Gly Gln Pro Gln Gly Ser Pro Cys Glu Val Ala Arg Phe Phe Leu  
465 470 475 480

Ser Thr Leu Pro Ala Ser Gly Glu Cys Gln Trp His Tyr Ala Asn Pro  
485 490 495

Leu Val Pro Ser Ser Ser Pro Ala Lys Asn Pro Pro Glu Pro Pro  
500 505 510

Ala Asn Thr Ala Arg His Ser Leu Val Pro Ser Tyr Glu Ala Pro Ala  
515 520 525

Ala Ala Val Arg Arg Phe Gly Glu Asp Thr Ala Pro Pro Ser Phe Pro  
530 535 540

Ser Cys Gly His Tyr Arg Glu Glu Pro Ala Leu Gly Pro Ala Lys Ala  
545 550 555 560

Ala Arg Gln Ala Ala Arg Asp Gly Ala Arg Leu Ala Leu Ala Arg Ala  
565 570 575

Ala Pro Glu Cys Cys Ala Pro Pro Thr Pro Glu Ala Pro Gly Ala Pro  
580 585 590

Ala Gln Leu Pro Phe Val Leu Leu Asn Tyr His Arg Val Leu Ala Arg  
595 600 605

Arg Gly Pro Leu Gly Gly Ala Ala Pro Ala Ala Ser Gly Leu Ala Cys  
610 615 620

Ala Pro Gly Gly Pro Glu Ala Ala Thr Gly Ala Leu Arg Leu Arg His  
625 630 635 640

Pro Ser Pro Ala Ala Thr Ser Pro Pro Gly Ala Pro Leu Pro His Tyr  
645 650 655

Leu Gly Ala Ser Val Ile Ile Thr Asn Gly Arg  
660 665

<210> 270  
<211> 1192  
<212> DNA  
<213> human organism

<220>  
<221> misc\_feature  
<222> (1122)..(1122)  
<223> n is a, c, g, or t

<400> 270		
ggcacgagga gaagatgtgg ctgctcatg cttgacttct gccatgggttg tgaggcctcc	60	
ccagccatgt ggaactgttt tcaggtgctg gttccatggc tcttcctgag ccgaaaataaa	120	
ggaaaactcca tagaccttgt ccactggAAC tcgttcccat ctaccctcca ctctatccag	180	
ggtgatggat ctctgcagta agtggaaAGAG ttcttcatgg cccccaaggT tatATCCATC	240	
tagaacttca gcacgtaatt tcatctggaa atagtgcTTT tgtggatata agttaggtAA	300	
aactgaagat gagatcatac tggatttagga tgggatctaa atccaatgaa aatgtcttca	360	
taaaaaacAG gaaAGAACCC atAGAAACAC aAGGAAGAAG gTCATGTGAA gATGGAGGCA	420	
gagattggag ggatgcAGCC accggcccAG gaatGCCAGC agccACCCAG aagCTGGAAAG	480	
gaaatgaggg attctctcCTT agAACCTTTA gagagrACAT ggtcctgtGA acagCTTGT	540	
tttggacttg cccatAGCTT gtataCTCTT actttggATA caATTTATC caAAACTTGGC	600	
taaacAGTTT ctcAGCCTAT ggAAAATTTA aaATGGAGAA gattcaACTC gattCTTACA	660	
gattcaAAAGC aAGAAAATGA tggAACATA ggAGGAGACC aAGAAAGCCT atAAAAAGCA	720	
aaaATATGAA gtGAACATTG tggTAGCTT aAGATGTTA gtgtAGCTGC aggCACCCtA	780	
tacACATGAA AACCCCCAAG gggAAATCCCC ATATCACAGT gtgtGTGAT ATTGACATT	840	
ygtgatCATY tagAGATGTA cAGAAAAGGT gaATCTGTGT TCTGTATATT ctgcctaAGG	900	
caaAGAAAATG tttagCTYTC ttAAAATAG ttCCATAATT ttTTYTAAGA AGCTTGCTT	960	
gAAAACtGTA AGCTTCCAT ATCTGGAGCA ttTCACtTTA AATATTTGGA TAAATATGTT	1020	
atCTTCTTAC ttggACATTt CATGTGTTA gggATTGTYT tytaaATTCT tcctaATTCA	1080	
tatAGCTGCT AACACTTCCC GCAgAGCTAA ACCATTACAG ANTATGAAAT AAAGACCCtA	1140	
ttgatttGAA CTTAAAAAAA AAAAMAMAAA AAAAaaaaAA AAAAaaaaAAAT GA	1192	

<210> 271  
 <211> 1365  
 <212> DNA  
 <213> human organism

<400> 271

atgaaatcaa tctctatgtat gggaaagccctt aagagcctta gtgaaacttg tttaccta	60
ggcataaatg gtatcaaaga tgcaaggaag gtcactgttag gtgtgattgg aagtggagat	120
tttgc当地 cttgaccat tcgacttattt agatgcggct atcatgtggt cataggaagt	180
agaaaatccta agtttgcttc tgaattttt cctcatgtgg tagatgtcac tcatacatgaa	240
gatgctctca caaaaacaaa tataatattt gttgctatac acagagaaca ttatacctcc	300
ctgtgggacc tgagacatct gcttggggt aaaatcctga ttgatgtgag caataacatg	360
aggataaaacc agtacccaga atccaatgct gaatatttgg cttcattattt cccagattct	420
ttgattgtca aaggatttaa tggatgtctca gcttgggcac ttcagttagg acctaaggat	480
gccagccggc aggttatat atgcagcaac aatattcaag cgcgacaaca ggttattgaa	540
cttgc当地 agttgaattt cattcccattt gacttgggat ctttatcatc agccagagag	600
attgaaaattt tacccttacg actctttact ctctggagag ggccagtggg ggttagctata	660
agcttggcca cattttttt ctttattcc tttgtcagag atgtgattca tccatatgct	720
agaaaaccaac agagtgactt ttacaaaattt cctatagaga ttgtgaataa aaccttacct	780
atagttgcca ttactttgct ctccctagta tacctcgca gttttctggc agctgcttat	840
caactttattt acggcaccaaa gtataggaga tttccacctt ggttggaaac ctgggtacag	900
tgtagaaaac agcttggattt actaagttttt ttcttcgcta tggtccatgt tgcctacagc	960
ctctgcttac cgatgagaag gtcagagaga tattttttc tcaacatggc ttatcagcag	1020
gttcatgcaa atattgaaaaa ctcttggaaat gaggaagaag tttggagaat tgaaatgtat	1080
atctccctttt gcataatgag ctttggctta ctttccctcc tggcagtca ttctatccct	1140
tcagtgagca atgctttaaa ctggagagaa ttcaagttta ttcaagtctac acttggat	1200
gtcgctctgc tcataagtac ttccatgtt ttaattttatg gatggaaacg agctttgag	1260
gaagagttactt acagattttt tacaccacca aactttgttc ttgctttgtt tttgc当地	1320
attgtatattc tggatctttt gcagcttgc agataacccag actga	1365

<210> 272  
 <211> 454  
 <212> PRT

<213> human organism

<400> 272

Met Glu Ser Ile Ser Met Met Gly Ser Pro Lys Ser Leu Ser Glu Thr  
1 5 10 15

Cys Leu Pro Asn Gly Ile Asn Gly Ile Lys Asp Ala Arg Lys Val Thr  
20 25 30

Val Gly Val Ile Gly Ser Gly Asp Phe Ala Lys Ser Leu Thr Ile Arg  
35 40 45

Leu Ile Arg Cys Gly Tyr His Val Val Ile Gly Ser Arg Asn Pro Lys  
50 55 60

Phe Ala Ser Glu Phe Phe Pro His Val Val Asp Val Thr His His Glu  
65 70 75 80

Asp Ala Leu Thr Lys Thr Asn Ile Ile Phe Val Ala Ile His Arg Glu  
85 90 95

His Tyr Thr Ser Leu Trp Asp Leu Arg His Leu Leu Val Gly Lys Ile  
100 105 110

Leu Ile Asp Val Ser Asn Asn Met Arg Ile Asn Gln Tyr Pro Glu Ser  
115 120 125

Asn Ala Glu Tyr Leu Ala Ser Leu Phe Pro Asp Ser Leu Ile Val Lys  
130 135 140

Gly Phe Asn Val Val Ser Ala Trp Ala Leu Gln Leu Gly Pro Lys Asp  
145 150 155 160

Ala Ser Arg Gln Val Tyr Ile Cys Ser Asn Asn Ile Gln Ala Arg Gln  
165 170 175

Gln Val Ile Glu Leu Ala Arg Gln Leu Asn Phe Ile Pro Ile Asp Leu  
180 185 190

Gly Ser Leu Ser Ser Ala Arg Glu Ile Glu Asn Leu Pro Leu Arg Leu  
195 200 205

Phe Thr Leu Trp Arg Gly Pro Val Val Ala Ile Ser Leu Ala Thr

210                    215                    220  
Phe Phe Phe Leu Tyr Ser Phe Val Arg Asp Val Ile His Pro Tyr Ala  
225                    230                    235                    240  
Arg Asn Gln Gln Ser Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn  
245                    250                    255  
  
Lys Thr Leu Pro Ile Val Ala Ile Thr Leu Leu Ser Leu Val Tyr Leu  
260                    265                    270  
  
Ala Gly Leu Leu Ala Ala Ala Tyr Gln Leu Tyr Tyr Gly Thr Lys Tyr  
275                    280                    285  
  
Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu Gln Cys Arg Lys Gln  
290                    295                    300  
  
Leu Gly Leu Leu Ser Phe Phe Ala Met Val His Val Ala Tyr Ser  
305                    310                    315                    320  
  
Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn Met  
325                    330                    335  
  
Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu  
340                    345                    350  
  
Glu Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu  
355                    360                    365  
  
Gly Leu Leu Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn  
370                    375                    380  
  
Ala Leu Asn Trp Arg Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr  
385                    390                    395                    400  
  
Val Ala Leu Leu Ile Ser Thr Phe His Val Leu Ile Tyr Gly Trp Lys  
405                    410                    415  
  
Arg Ala Phe Glu Glu Glu Tyr Tyr Arg Phe Tyr Thr Pro Pro Asn Phe  
420                    425                    430  
  
Val Leu Ala Leu Val Leu Pro Ser Ile Val Ile Leu Asp Leu Leu Gln  
435                    440                    445

Leu Cys Arg Tyr Pro Asp  
450

<210> 273  
<211> 1933  
<212> DNA  
<213> human organism

<400> 273  
ccggccgtt ctactccgccc gcgggggtcg cagcggctgc cgccgcgtcc tcgagttcc 60  
agcgtgagga ggaggctgag ggcggagagg cgcatcgtgt tcgaggcgga gaccgagggg 120  
gagccccgcg cgccgcgtcg ctcattgcta tggacagtgc tatcaccctg tggcagttcc 180  
ttcttcagct cctgcagaag cctcagaaca agcacatgat ctgttgacc tctaattatg 240  
ggcagttaa gctttgcag gcagaagagg tggctcgtct ctgggggatt cgcaagaaca 300  
agcctaacat gaattatgac aaactcagcc gagccctcag atactattat gtaaaata 360  
tcatcaaaaa agtgaatggc cagaagtttgc tgtacaagtt tgtctttat ccagagattt 420  
tgaacatggc tccaatgaca gtgggcagga ttgagggtga ctgtgaaagt ttaaacttca 480  
gtgaagtcag cagcagttcc aaagatgtgg agaatggagg gaaagataaa ccaccctcagc 540  
ctgggtccaa gacctcttagc cgcaatgact acatacactc tggcttataat tcttcattta 600  
ctctcaactc tttgaactcc tccaatgtaa agctttcaa attgataaaactgagaatc 660  
cagccgagaa actggcagag aaaaaatctc ctcaggagcc cacaccatct gtcatcaat 720  
ttgtcacgac accttccaaa aagccaccag ttgaacctgt tgctgccacc atttcaattt 780  
gcccaagtttcatct tcagaagaaa ctatccaagc tttggagaca ttgggttccc 840  
caaaactgccc ttccctggaa gccccaccc ctgcctctaa cgtaatgact gctttgcca 900  
ccacaccacc catttcgtcc atacccctt tgcaggaacc tcccagaaca ctttcaccac 960  
caactgatcc tcacccagac atcgacacag acattgattc agtggcttct cagccatgg 1020  
aacttccaga gaatttgcgtct ctggagccta aagaccagga ttcaacttgc ttagaaaagg 1080  
acaaaatgtaaa taattcatca agatccaaga aacccaaagg gtagggactg gcacccaccc 1140  
ttgtgatcac gagcagtgtat ccaagccac tggaaatact gagcccatct ctccctacag 1200  
cttctcttac accagcattt tttcacaga caccatcat actgactcca agcccttgc 1260  
tctccagtat ccacttctgg agtactctca gtcctgttgc tcccctaagt ccagccagac 1320  
tgcaaggtgc taacacactt ttccagttc cttctgtact gaacagtcat gggccattca 1380

ctctgtctgg	gctggatgga	ccttccaccc	ctggcccatt	ttccccagac	ctacagaaga	1440
cataacctat	gcacttgtgg	aatgagagaa	ccgaggaacg	aagaaacaga	cattcaacat	1500
gattgcattt	gaagtgagca	attgatagtt	ctacaatgct	gataatagac	tattgtgatt	1560
tttgccattc	cccattgaaa	acatctttt	aggattctct	ttgaatagga	ctcaagttgg	1620
actatatgta	aaaaaatgcc	ttaattggag	tctaaactcc	acctccctct	gtctttcct	1680
tttcttttc	tttccttcct	tcctttctt	ttctccctta	aaaataatttt	gagctttgtg	1740
ctgaagaagt	ttttgggtgg	ctttagtgac	tgtgcttgc	aaaagcaatt	aagaacaaag	1800
ttactccttc	tggctattgg	gacccttgg	ccagaaaaaa	ttatgcttag	aatctattat	1860
ttaaagaagt	atttgtgaaa	tgaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1920
aaaaaaaaaa	aaa					1933

<210> 274

<211> 431

<212> PRT

<213> human organism

<400> 274

Met	Asp	Ser	Ala	Ile	Thr	Leu	Trp	Gln	Phe	Leu	Leu	Gln	Leu	Leu	Gln
1						5				10			15		

Lys	Pro	Gln	Asn	Lys	His	Met	Ile	Cys	Trp	Thr	Ser	Asn	Asp	Gly	Gln
										25			30		

Phe	Lys	Leu	Leu	Gln	Ala	Glu	Glu	Val	Ala	Arg	Leu	Trp	Gly	Ile	Arg
								40				45			

Lys	Asn	Lys	Pro	Asn	Met	Asn	Tyr	Asp	Lys	Leu	Ser	Arg	Ala	Leu	Arg
						50				55		60			

Tyr	Tyr	Tyr	Val	Lys	Asn	Ile	Ile	Lys	Lys	Val	Asn	Gly	Gln	Lys	Phe
							65			70		75		80	

Val	Tyr	Lys	Phe	Val	Ser	Tyr	Pro	Glu	Ile	Leu	Asn	Met	Asp	Pro	Met
							85			90		95			

Thr	Val	Gly	Arg	Ile	Glu	Gly	Asp	Cys	Glu	Ser	Leu	Asn	Phe	Ser	Glu
								100		105		110			

Val Ser Ser Ser Lys Asp Val Glu Asn Gly Gly Lys Asp Lys Pro  
115 120 125

Pro Gln Pro Gly Ala Lys Thr Ser Ser Arg Asn Asp Tyr Ile His Ser  
130 135 140

Gly Leu Tyr Ser Ser Phe Thr Leu Asn Ser Leu Asn Ser Ser Asn Val  
145 150 155 160

Lys Leu Phe Lys Leu Ile Lys Thr Glu Asn Pro Ala Glu Lys Leu Ala  
165 170 175

Glu Lys Lys Ser Pro Gln Glu Pro Thr Pro Ser Val Ile Lys Phe Val  
180 185 190

Thr Thr Pro Ser Lys Lys Pro Pro Val Glu Pro Val Ala Ala Thr Ile  
195 200 205

Ser Ile Gly Pro Ser Ile Ser Pro Ser Ser Glu Glu Thr Ile Gln Ala  
210 215 220

Leu Glu Thr Leu Val Ser Pro Lys Leu Pro Ser Leu Glu Ala Pro Thr  
225 230 235 240

Ser Ala Ser Asn Val Met Thr Ala Phe Ala Thr Thr Pro Pro Ile Ser  
245 250 255

Ser Ile Pro Pro Leu Gln Glu Pro Pro Arg Thr Pro Ser Pro Pro Leu  
260 265 270

Ser Ser His Pro Asp Ile Asp Thr Asp Ile Asp Ser Val Ala Ser Gln  
275 280 285

Pro Met Glu Leu Pro Glu Asn Leu Ser Leu Glu Pro Lys Asp Gln Asp  
290 295 300 305

Ser Val Leu Leu Glu Lys Asp Lys Val Asn Asn Ser Ser Arg Ser Lys  
305 310 315 320

Lys Pro Lys Gly Leu Gly Leu Ala Pro Thr Leu Val Ile Thr Ser Ser  
325 330 335

Asp Pro Ser Pro Leu Gly Ile Leu Ser Pro Ser Leu Pro Thr Ala Ser

340

345

350

Leu Thr Pro Ala Phe Phe Ser Gln Thr Pro Ile Ile Leu Thr Pro Ser  
355 360 365

Pro Leu Leu Ser Ser Ile His Phe Trp Ser Thr Leu Ser Pro Val Ala  
 370 375 380

Pro	Leu	Ser	Pro	Ala	Arg	Leu	Gln	Gly	Ala	Asn	Thr	Leu	Phe	Gln	Phe
385					390					395					400

Pro Ser Val Leu Asn Ser His Gly Pro Phe Thr Leu Ser Gly Leu Asp  
405 410 415

Gly Pro Ser Thr Pro Gly Pro Phe Ser Pro Asp Leu Gln Lys Thr  
                 420                  425                          430

<210> 275  
<211> 3060  
<212> DNA  
<213> human organism

<400> 275  
aatcaggaac agatcatata ttgaccgaga ttctgagtat ctcttgcaag aaaatgaacc 60  
agatggaact ttagacccaa aattatttgg aagatttacaa aagaaaaaaa atgaccttcg 120  
gtatattgaa atgcagcatt tcagagaaaa gctgccttcg tatggaatgc aaaaggaatt 180  
ggtaaattta attgataacc atcaggtaac agtaataagt ggtgaaactg gttgtggcaa 240  
aaccactcaa gttactcagt tcattttgga taactacatt gaaagaggaa aaggatctgc 300  
ttgcagaata gtttgtactc agccaagaag aatttagtgcc atttcagttg cggaaagagt 360  
agctgcagaa agggcagaat cttgtggcag tgtaatagt actggatatc aaattcgtct 420  
ccagagtcgg ttgccaagga aacagggttc tatcttatac tgtacaacag gaatcatcct 480  
tcagtggctc cagtcagacc cgtatttgc cagtgttagt catatcgtag ttgatgaaat 540  
ccatgaaaga aatctgcagt cagatgttt aatgactgtt gttaaagacc ttctcaattt 600  
tcgatctgac ttgaaagtaa tattgatgag tgcaacattt aatgcagaaa agttttcaga 660  
atatttttgt aactgtccaa tgatacatat acctggttt accttccgg ttgtgaaata 720  
tctttggaa gatgttaattt aaaaaataag gtatgttcca gaacaaaaag aacacagatc 780  
ccagtttaag aggggtttca tgcaaggca tgtaaataga caagaaaaag aagaaaaaga 840

agcaatatat aaagaacgtt ggcagatta tgtaaggaa ctgcgaagaa ggtattctgc 900  
aagtactgta gatgttatag aaatgtatgga ggatgataaa gttgatctga atttgattgt 960  
tgccctcatac cgatacattg ttttggaaaga agaggatggt gcgatactgg tctttctgcc 1020  
aggctggac aatatcagca ctttacatga tctcttgatg tcacaagtaa tgtttaaatac 1080  
agataaaattt ttaattatac ctttacattc actgatgcct acagttaacc agacacaggt 1140  
gtttaaaaga acccctcctg gtgttcggaa aatagtaatt gctaccaaca ttgcggagac 1200  
tagcattacc atagatgatg tcgttatgt gatagatgga ggaaaaataa aagagacgca 1260  
ttttgatact cagaacaata tcagtacaat gtccgctgag tgggttagta aagctaatgc 1320  
caaacagaga aaaggtcgag ctggaagagt tcaacctggt cattgctatc atctgtataa 1380  
tggctttaga gcaagtcttc tagatgacta tcaactgcca gaaattttga gaactccttt 1440  
ggaagaactt tgtttacaaa taaagatttt aaggcttaggt ggaattgctt attttcttag 1500  
tagattaatg gacccaccat caaatgaggc agtgttactc tccataagac acctgatgga 1560  
gctgaacgct ttggataaac aagaagaatt gacaccttgg gtagtccact tggcacgatt 1620  
acccgttgag ccacatattg gaaaaatgat tcttttgga gcactgttct gctgcttaga 1680  
cccagtactc actattgctg ctgtctcag tttcaaagat ccattgtca ttccactggg 1740  
aaaagaaaaag attgcagatg caagaagaaa ggaattggca aaggatacta gaagtgatca 1800  
cttaacagtt gtgaatgcgt ttgagggctg ggaagaggct aggcgacgtg gtttcagata 1860  
cgaaaaggac tattgtggg aatattttct gtcttcaaac acactgcaga tgctgcataa 1920  
catgaaagga cagttgctg agcatcttct tggagctgga tttgtaaagca gtagaaatcc 1980  
taaagatcca gaatctaata taaattcaga taatgagaag ataattaaag ctgtcatctg 2040  
tgctggttta tatcccaaag ttgctaaaat tcgactaaat ttgggtaaaa aaagaaaaat 2100  
ggtaaaaaggtt tacacaaaaaa cogatggcct ggttgctgtt catcctaaat ctgttaatgt 2160  
ggagcaaaca gactttcaact acaactggct tatctatcac ctaaagatga gaacaagcag 2220  
tatataacttg tatgactgca cagaggtttc cccatactgt ctcttggtt ttggaggtga 2280  
catttccatc cagaaggata acgatcagga aactattgct gtagatgagt ggattgtatt 2340  
tcagtctcca gcaagaatttgc cccatcttgc taaggaatta agaaaggaac tagatattct 2400  
tctgcaagag aagattgaaa gtcctcatcc tggactgg aatgacacta aatccagaga 2460  
ctgtgcagta ctgtcagcta ttatagactt gatcaaaaaca cagggaaaagg caactcccag 2520  
gaactttccg ccacgattcc aggtggata ttacagctga cagctttca ggggtggct 2580

<210> 276  
<211> 852  
<212> PRT  
213 human organism

<400> 27

Ile Arg Asn Arg Ser Tyr Ile Asp Arg Asp Ser Glu Tyr Leu Leu Gln  
1 5 10 15

Glu Asn Glu Pro Asp Gly Thr Leu Asp Gln Lys Leu Leu Glu Asp Leu  
20 25 30

Gln Lys Lys Lys Asn Asp Leu Arg Tyr Ile Glu Met Gln His Phe Arg  
35 40 45

Glu Lys Leu Pro Ser Tyr Gly Met Gln Lys Glu Leu Val Asn Leu Ile  
50 55 60

Asp Asn His Gln Val Thr Val Ile Ser Gly Glu Thr Gly Cys Gly Lys  
65 70 75 80

Thr Thr Gln Val Thr Gln Phe Ile Leu Asp Asn Tyr Ile Glu Arg Gly  
85 90 95

Lys Gly Ser Ala Cys Arg Ile Val Cys Thr Gln Pro Arg Arg Ile Ser  
           100                 105                 110

Ala Ile Ser Val Ala Glu Arg Val Ala Ala Glu Arg Ala Glu Ser Cys  
115 120 125

Gly Ser Gly Asn Ser Thr Gly Tyr Gln Ile Arg Leu Gln Ser Arg Leu  
130 135 140

Pro Arg Lys Gln Gly Ser Ile Leu Tyr Cys Thr Thr Gly Ile Ile Leu  
145 150 155 160

Gln Trp Leu Gln Ser Asp Pro Tyr Leu Ser Ser Val Ser His Ile Val  
165 170 175

Leu Asp Glu Ile His Glu Arg Asn Leu Gln Ser Asp Val Leu Met Thr  
180 185 190

Val Val Lys Asp Leu Leu Asn Phe Arg Ser Asp Leu Lys Val Ile Leu  
195 200 205

Met Ser Ala Thr Leu Asn Ala Glu Lys Phe Ser Glu Tyr Phe Gly Asn  
210 215 220

Cys Pro Met Ile His Ile Pro Gly Phe Thr Phe Pro Val Val Glu Tyr  
225 230 235 240

Leu Leu Glu Asp Val Ile Glu Lys Ile Arg Tyr Val Pro Glu Gln Lys  
245 250 255

Glu His Arg Ser Gln Phe Lys Arg Gly Phe Met Gln Gly His Val Asn  
260 265 270

Arg Gln Glu Lys Glu Glu Lys Glu Ala Ile Tyr Lys Glu Arg Trp Pro  
275 280 285

Asp Tyr Val Arg Glu Leu Arg Arg Tyr Ser Ala Ser Thr Val Asp  
290 295 300 320

Val Ile Glu Met Met Glu Asp Asp Lys Val Asp Leu Asn Leu Ile Val  
305 310 315 320

Ala Leu Ile Arg Tyr Ile Val Leu Glu Glu Asp Gly Ala Ile Leu  
325 330 335

Val Phe Leu Pro Gly Trp Asp Asn Ile Ser Thr Leu His Asp Leu Leu  
340 345 350

Met Ser Gln Val Met Phe Lys Ser Asp Lys Phe Leu Ile Ile Pro Leu

355

360

365

His Ser Leu Met Pro Thr Val Asn Gln Thr Gln Val Phe Lys Arg Thr  
370 375 380

Pro Pro Gly Val Arg Lys Ile Val Ile Ala Thr Asn Ile Ala Glu Thr  
385 390 395 400

Ser Ile Thr Ile Asp Asp Val Val Tyr Val Ile Asp Gly Gly Lys Ile  
405 410 415

Lys Glu Thr His Phe Asp Thr Gln Asn Asn Ile Ser Thr Met Ser Ala  
420 425 430

Glu Trp Val Ser Lys Ala Asn Ala Lys Gln Arg Lys Gly Arg Ala Gly  
435 440 445

Arg Val Gln Pro Gly His Cys Tyr His Leu Tyr Asn Gly Leu Arg Ala  
450 455 460

Ser Leu Leu Asp Asp Tyr Gln Leu Pro Glu Ile Leu Arg Thr Pro Leu  
465 470 475 480

Glu Glu Leu Cys Leu Gln Ile Lys Ile Leu Arg Leu Gly Gly Ile Ala  
485 490 495

Tyr Phe Leu Ser Arg Leu Met Asp Pro Pro Ser Asn Glu Ala Val Leu  
500 505 510

Leu Ser Ile Arg His Leu Met Glu Leu Asn Ala Leu Asp Lys Gln Glu  
515 520 525

Glu Leu Thr Pro Leu Gly Val His Leu Ala Arg Leu Pro Val Glu Pro  
530 535 540

His Ile Gly Lys Met Ile Leu Phe Gly Ala Leu Phe Cys Cys Leu Asp  
545 550 555 560

Pro Val Leu Thr Ile Ala Ala Ser Leu Ser Phe Lys Asp Pro Phe Val  
565 570 575

Ile Pro Leu Gly Lys Glu Lys Ile Ala Asp Ala Arg Arg Lys Glu Leu  
580 585 590

Ala Lys Asp Thr Arg Ser Asp His Leu Thr Val Val Asn Ala Phe Glu  
595 600 605

Gly Trp Glu Glu Ala Arg Arg Arg Gly Phe Arg Tyr Glu Lys Asp Tyr  
610 615 620

Cys Trp Glu Tyr Phe Leu Ser Ser Asn Thr Leu Gln Met Leu His Asn  
625 630 635 640

Met Lys Gly Gln Phe Ala Glu His Leu Leu Gly Ala Gly Phe Val Ser  
645 650 655

Ser Arg Asn Pro Lys Asp Pro Glu Ser Asn Ile Asn Ser Asp Asn Glu  
660 665 670

Lys Ile Ile Lys Ala Val Ile Cys Ala Gly Leu Tyr Pro Lys Val Ala  
675 680 685

Lys Ile Arg Leu Asn Leu Gly Lys Arg Lys Met Val Lys Val Tyr  
690 695 700

Thr Lys Thr Asp Gly Leu Val Ala Val His Pro Lys Ser Val Asn Val  
705 710 715 720

Glu Gln Thr Asp Phe His Tyr Asn Trp Leu Ile Tyr His Leu Lys Met  
725 730 735

Arg Thr Ser Ser Ile Tyr Leu Tyr Asp Cys Thr Glu Val Ser Pro Tyr  
740 745 750

Cys Leu Leu Phe Phe Gly Gly Asp Ile Ser Ile Gln Lys Asp Asn Asp  
755 760 765

Gln Glu Thr Ile Ala Val Asp Glu Trp Ile Val Phe Gln Ser Pro Ala  
770 775 780

Arg Ile Ala His Leu Val Lys Glu Leu Arg Lys Glu Leu Asp Ile Leu  
785 790 795 800

Leu Gln Glu Lys Ile Glu Ser Pro His Pro Val Asp Trp Asn Asp Thr  
805 810 815

Lys Ser Arg Asp Cys Ala Val Leu Ser Ala Ile Ile Asp Leu Ile Lys  
820 825 830

Thr Gln Glu Lys Ala Thr Pro Arg Asn Phe Pro Pro Arg Phe Gln Asp  
835 840 845

Gly Tyr Tyr Ser  
850

<210> 277  
<211> 1671  
<212> DNA  
<213> human organism

<400> 277	
gattttatcc tggaacatta cagtgaagat ggctatttat atgaagatga aattgcagat	60
cttatggatc tgagacaagc ttgtcgacg cctagccgg atgaggccgg ggtgaaactg	120
ctgatgacat acttcatcca gctggcctt gtcgagagtc gattcttccc gcccacacgg	180
cagatggac tcctgttcac ctggtatgac tctctcaccg gggttccggc cagccagcag	240
aacctgctgc tggagaaggc cagtgtcctg ttcaacactg gggccctcta caccagatt	300
gggaccggcgt gtgatcgca gacgcaggct gggctggaga gtgccataga tgccttcag	360
agagccgcag gggtttaaa ttacctgaaa gacacattt cccatactcc aagttacgac	420
atgagccctg ccatgctcag cgtgctcgac aaaatgatgc ttgcacaagc ccaagaaagc	480
gtgtttgaga aaatcagcct tcctgggatc cggaatgaat tcttcatgct ggtgaaggtg	540
gctcaggagg ctgctaaggt gggagaggtc taccaacagc tacacgcagc catgagccag	600
gcgcgggtga aagagaacat cccctactcc tggccagct tagcctgcgt gaaggcccac	660
cactacgcgg ccctggccca ctacttcaact gccatcctcc tcatacgacca ccaggtgaag	720
ccaggcacgg atctggacca ccaggagaag tgcctgtccc agctctacga ccacatgcca	780
gaggggctga cacccttggc cacactgaag aatgatcagc agcgccgaca gctggggaaag	840
tcccacttgc gcagagccat ggctcatcac gaggagtcgg tgcggggaggc cagcctctgc	900
aagaagctgc ggagcattga ggtgctacag aaggtgctgt gtgccgcaca ggaacgctcc	960
cggctcacgt acgcccagca ccaggaggag gatgacctgc tgaacctgat cgacgcccc	1020
agtgttggc ctaaaaactga gcaagaggtt gacattatat tgccccagtt ctccaagctg	1080
acagtcacgg acttcttcca gaagctggc cccttatctg tgtttcggc taacaagcgg	1140

tggacgcctc	ctcgaagcat	ccgcttact	gcagaagaag	gggacttggg	gttcaccttg	1200
agaggaaacg	cccccggtca	ggttcaacttc	ctggatcctt	actgctctgc	ctcggtggca	1260
ggagcccgaa	aaggagatta	tattgtctcc	attcagcttg	tgattgtaa	gtggctgacg	1320
ctgagtgagg	ttatgaagct	gctgaagago	tttggcgagg	acgagatcga	gatgaaagtc	1380
gtgagcctcc	tggactccac	atcatccatg	cataataaga	gtgccacata	ctccgtggga	1440
atgcagaaaa	cgtactccat	gatctgctta	gccattgatg	atgacgacaa	aactgataaa	1500
accaagaaaa	tctccaagaa	gctttccttc	ctgagttggg	gcaccaacaa	gaacagacag	1560
aagtcaagcca	gcacccctgtg	cctccatcg	gtcggggctg	cacggcctca	ggtcaagaag	1620
aagctgcctc	ccccttcag	cttctcaac	tcagacagtt	cttggacta	a	1671

<210> 278

<211> 556

<212> PRT

<213> human organism

<400> 278

Asp	Phe	Ile	Leu	Glu	His	Tyr	Ser	Glu	Asp	Gly	Tyr	Leu	Tyr	Glu	Asp
1								5				10			15

Glu	Ile	Ala	Asp	Leu	Met	Asp	Leu	Arg	Gln	Ala	Cys	Arg	Thr	Pro	Ser
						20						25			30

Arg	Asp	Glu	Ala	Gly	Val	Glu	Leu	Leu	Met	Thr	Tyr	Phe	Ile	Gln	Leu
								35				40			45

Gly	Phe	Val	Glu	Ser	Arg	Phe	Phe	Pro	Pro	Thr	Arg	Gln	Met	Gly	Leu
								50				55			60

Leu	Phe	Thr	Trp	Tyr	Asp	Ser	Leu	Thr	Gly	Val	Pro	Val	Ser	Gln	Gln
								65				70			80

Asn	Leu	Leu	Leu	Glu	Lys	Ala	Ser	Val	Leu	Phe	Asn	Thr	Gly	Ala	Leu
								85				90			95

Tyr	Thr	Gln	Ile	Gly	Thr	Arg	Cys	Asp	Arg	Gln	Thr	Gln	Ala	Gly	Leu
								100				105			110

Glu	Ser	Ala	Ile	Asp	Ala	Phe	Gln	Arg	Ala	Ala	Gly	Val	Leu	Asn	Tyr
												115			125

Leu Lys Asp Thr Phe Thr His Thr Pro Ser Tyr Asp Met Ser Pro Ala  
130 135 140

Met Leu Ser Val Leu Val Lys Met Met Leu Ala Gln Ala Gln Glu Ser  
145 150 155 160

Val Phe Glu Lys Ile Ser Leu Pro Gly Ile Arg Asn Glu Phe Phe Met  
165 170 175

Leu Val Lys Val Ala Gln Glu Ala Ala Lys Val Gly Glu Val Tyr Gln  
180 185 190

Gln Leu His Ala Ala Met Ser Gln Ala Pro Val Lys Glu Asn Ile Pro  
195 200 205

Tyr Ser Trp Ala Ser Leu Ala Cys Val Lys Ala His His Tyr Ala Ala  
210 215 220

Leu Ala His Tyr Phe Thr Ala Ile Leu Leu Ile Asp His Gln Val Lys  
225 230 235 240

Pro Gly Thr Asp Leu Asp His Gln Glu Lys Cys Leu Ser Gln Leu Tyr  
245 250 255

Asp His Met Pro Glu Gly Leu Thr Pro Leu Ala Thr Leu Lys Asn Asp  
260 265 270

Gln Gln Arg Arg Gln Leu Gly Lys Ser His Leu Arg Arg Ala Met Ala  
275 280 285

His His Glu Glu Ser Val Arg Glu Ala Ser Leu Cys Lys Lys Leu Arg  
290 295 300

Ser Ile Glu Val Leu Gln Lys Val Leu Cys Ala Ala Gln Glu Arg Ser  
305 310 315 320

Arg Leu Thr Tyr Ala Gln His Gln Glu Glu Asp Asp Leu Leu Asn Leu  
325 330 335

Ile Asp Ala Pro Ser Val Val Ala Lys Thr Glu Gln Glu Val Asp Ile  
340 345 350

Ile Leu Pro Gln Phe Ser Lys Leu Thr Val Thr Asp Phe Phe Gln Lys  
355 360 365

Leu Gly Pro Leu Ser Val Phe Ser Ala Asn Lys Arg Trp Thr Pro Pro  
370 375 380

Arg Ser Ile Arg Phe Thr Ala Glu Glu Gly Asp Leu Gly Phe Thr Leu  
385 390 395 400

Arg Gly Asn Ala Pro Val Gln Val His Phe Leu Asp Pro Tyr Cys Ser  
405 410 415

Ala Ser Val Ala Gly Ala Arg Glu Gly Asp Tyr Ile Val Ser Ile Gln  
420 425 430

Leu Val Asp Cys Lys Trp Leu Thr Leu Ser Glu Val Met Lys Leu Leu  
435 440 445

Lys Ser Phe Gly Glu Asp Glu Ile Glu Met Lys Val Val Ser Leu Leu  
450 455 460

Asp Ser Thr Ser Ser Met His Asn Lys Ser Ala Thr Tyr Ser Val Gly  
465 470 475 480

Met Gln Lys Thr Tyr Ser Met Ile Cys Leu Ala Ile Asp Asp Asp Asp  
485 490 495

Lys Thr Asp Lys Thr Lys Lys Ile Ser Lys Lys Leu Ser Phe Leu Ser  
500 505 510

Trp Gly Thr Asn Lys Asn Arg Gln Lys Ser Ala Ser Thr Leu Cys Leu  
515 520 525

Pro Ser Val Gly Ala Ala Arg Pro Gln Val Lys Lys Lys Leu Pro Ser  
530 535 540

Pro Phe Ser Leu Leu Asn Ser Asp Ser Ser Trp Tyr  
545 550 555

<210> 279  
<211> 2674  
<212> DNA  
<213> human organism

<400> 279  
gaattcggca cgagccttgt tggaggttct gggggcgcaga accgctactg ctgccttcgg  
ctctccttgg gaaaaaaataa aatttgaacc ttttgagct gtgtgtctaaa tcttcagtgg  
gacaatgggt tcagacaaaa gagtgagtag aacagagcgt agtggaaagat acgggttccat  
catagacagg gatgaccgtg atgagcgtga atccccaaaggc aggccggaggg actcagatta  
caaaagatct agtgtatgtc ggaggggtga tagatatgtat gactaccgag actatgacag  
tccagagaga gagcgtgaaa gaaggaacag tgaccgatcc gaagatggct accattcaga  
tggtgactat ggtgagcacg actataggca tgacatcagt gacgagaggg agagcaagac  
catcatgctg cgcggccttc ccatcaccat cacagagagc gatattcgag aaatgtatgg  
gtccttcgaa ggcctcagc ctgcggatgt gaggctgatg aagagaaaaa caggtgagag  
cttgcttagt tcctgatatt attgttctct tccccattcc cacctcagtc cctaaagaac  
atcctgattc ccccagtctt caagcacatg aattcagaat gaaaggtttgc ccatggctaa  
ggaatgtgac tcttgaaaaa ccatgttagc atctgaggaa ctttttaaa ctttgggg  
gggacttttt ttcccttagg taagtaatga ttataaaact ctttttttt tttgactata  
gtcggttgca tggttacttt aagcgtggaa tcaaattggag tggcatttag ttcaggcggc  
ttgttccttgc ccatggcaaa gtatcaagaa gatccccaaag tcaagtacata tttgtaaagc  
tgcttccaa ttggcttgc cacgcagtgt tgaagcagtgg ggagagagat tcacctgtta  
taaaggaact gactaacaca agtatccccgt ctatatctga atgctgtctc taggtgtaa  
ccgtggtttc gccttcgtgg agtttatca cttgcaagat gctaccagct ggatggaaagc  
caatcaggtt gcttcactca ccaagtcttag atattcatga aatggaaaca agtctgtaca  
atttaaaaaa aaggttgaag gagtggtttg ttccaaagga gtgacttttt tttaaaaaaaa  
aagctttgtatattaaaaaa ttgatgttac tagaataagt acagtaccaa ggacttcatt  
atagaattttgc ttctgcctt aaacatggct acctacccgtt cagggcttttgc ttaactactg  
aatacctgtc tgtaatcactca taaaacatct ttatgtttcc cttttttcttgc gtttggata  
ttcctattat gtccatttgag agtaagcttgc gtatatcaaa ctctccattt gacagtgtaa  
agaacatagt gaaagtctgtt ggcggcattt ttataagtaa ttcccttattt ctgcctgtaa  
accacaaagc ctcctggagg cgtaactgct cagaccggtc ttcaggaaat attaaggac  
tttagtggaaat ttatgaacaa taagtctgtat gagattagcc tgggagtggtt gtcctgcagg  
tgtctaatct agagtggcat taacattcttgc gaatgcctt tatagtctgtt

<210> 280  
<211> 143  
<212> PRT  
<213> human organism

<400> 280

Met Gly Ser Asp Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr  
1 5 10 15

Gly Ser Ile Ile Asp Arg Asp Asp Arg Asp Glu Arg Glu Ser Arg Ser  
20 25 30

Arg Arg Arg Asp Ser Asp Tyr Lys Arg Ser Ser Asp Asp Arg Arg Gly  
35 40 45

Asp Arg Tyr Asp Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg  
50 55 60

Glu Arg Arg Asn Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly  
65 70 75 80

Asp Tyr Gly Glu His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Glu  
85 90 95

Ser Lys Thr Ile Met Leu Arg Gly Leu Pro Ile Thr Ile Thr Glu Ser  
100 105 110

Asp Ile Arg Glu Met Met Glu Ser Phe Glu Gly Pro Gln Pro Ala Asp  
115 120 125

Val Arg Leu Met Lys Arg Lys Thr Gly Glu Ser Leu Leu Ser Ser  
130 135 140

<210> 281  
<211> 4000  
<212> DNA  
<213> human organism

<400> 281  
cggccgctt tttctcaaga tggcagattc ccactgaggc tgagggggcc gagctcgcc 60  
gccgcgttcc cttctccgtt gccatgaacc gcggacaccc cggcccccgtat ggccccccgtg 120  
tacgaaggta tggcctcaca tgtgcaagtt ttctcccctc acacccttca atcaagtgcc 180  
ttctgttagtg tgaagaaact aaaagtagag ccaagttcca actgggacat gactgggtac 240  
ggctcccaca gcaaagtgtt cagccagagc aagaacatac caccttctca gccagcctcc 300  
acaaccgtca gcacccctt gccggtccca aacccaagcc taccttacga gcagaccatc 360  
gtcttcccag gaagcaccgg gcacatcggt gtcacccatcg caagcagcac ttctgtcacc 420  
gggcaagtcc tcggcggacc acacaaccta atgcgtcgaa gcactgtgag cctccttgc 480  
acctacaaa aatgtggact caagcgtaag agcgaggaga tcgagaacac aagcagcgtg 540  
cagatcatcg aggagcatcc acccatgatt cagaataatg caagcggggc cactgtcgcc 600  
actgccacca cgtctactgc cacctccaaa aacagcggct ccaacagcga gggcgactat 660  
cagctggtgc agcatgaggt gctgtgctcc atgaccaaca cctacgaggt cttagagttc 720  
ttggggccgag ggacgtttgg acaagtggtc aagtgctgga aacggggcac caatgagatc 780  
gtagccatca agatcctgaa gaaccgccc tcctatgccc gacaaggta gattgaagtg 840  
agcatcctgg cccgggtttagt cacggagagt gccgatgact ataacttcgt ccgggcctac 900

gaatgcttcc agcacaagaa ccacacgtgc ttggcttcg agatgttgg a cagaacctc 960  
tatgactttc tgaagcaaaa caagtttagc cccttgc ccc tcaaatacat tcgcccagtt 1020  
ctccagcagg tagccacagc cctgatgaaa ctcaaaagcc taggtcttat ccacgctgac 1080  
ctcaaaccag aaaacatcat gctggtgat ccattctagac aaccatacag agtcaaggc 1140  
atcgactttg gtccagccag ccacgtctcc aaggctgtgt gctccaccta cttgcagtcc 1200  
agatattaca gggccctga gatcatcctt ggtttaccat tttgtgaggc aattgacatg 1260  
tggccctgg gctgtgttat tgcagaattt ttcctgggtt ggccgttata tccaggagct 1320  
tcggagtatg atcagattcg gtatattca caaacacagg gtttgcctgc tgaatattta 1380  
ttaagcgccg ggacaaagac aactaggtt ttcaaccgtg acacggactc accatatcct 1440  
ttgtggagac tgaagacacc agatgaccat gaagcagaga cagggattaa gtcaaaagaa 1500  
gcaagaaagt acatttcaa ctgttagat gatatggccc aggtgaacat gacgacagat 1560  
ttggaaggga gcgacatgtt ggttagaaag gctgaccggc gggagttcat tgacctgtt 1620  
aagaagatgc tgaccattga tgctgacaag agaatcactc caatcgaaac cctgaaccat 1680  
cccttgtca ccatgacaca cttactcgat tttccccaca gcacacacgt caaatcatgt 1740  
ttccagaaca tggagatctg caagcgtcg gtgaatatgt atgacacggc gaaccagagc 1800  
aaaacccctt tcacacgca cgtggccccc agcacgtcca ccaacacgtc catgacctt 1860  
aacaaccagc tgaccactgt ccacaaccag gctccctcct ctaccagtgc cactattcc 1920  
ttagccaatc ccgaagtctc catabaaac tacccatcta cactctacca gccctcagcg 1980  
gcatccatgg ctgcagtggc ccagcggagc atgcccctgc agacaggaac agcccagatt 2040  
tgtgcccggc ctgaccgtt ccagcaagct ctcatgtgt gtccccccgg cttccaaggc 2100  
ttgcaggcct ctccctctaa gcacgctggc tactcggtgc gaatggaaaa tgcagttccc 2160  
atcgtaactc aagccccagg agctcagcct cttcagatcc aaccaggtct gcttgcggc 2220  
caggcttggc caagtggac ccagcagatc ctgctcccc cagcatggca gcaactgact 2280  
ggagtgccca cccacacatc agtgcagcat gccaccgtga ttcccggagac catggcaggc 2340  
acccagcagc tggcggactg gagaatacg catgctcactg gaagccatta taatccatc 2400  
atgcagcagc ctgcactatt gaccggcat gtgacccttc cagcagcaca gcccttaat 2460  
gtgggtgtgg cccacgtat gccccggcag ccaaccagca ccacccctc ccggaaagagt 2520  
aagcagcacc agtcatctgt gagaatgtc tccaccgtgt aggtgtcctc ctctcaggcc 2580  
atcagctccc cacagcgtatc caagcgtgtc aaggagaaca cacctccccg ctgtgccatg 2640

gtgcacagta	gcccggcctg	cagcacctcg	gtcacctgtg	ggtggggcga	cgtggcctcc	2700
agcaccaccc	gggaacggca	gcggcagaca	attgtcattc	ccgacactcc	cagccccacg	2760
gtcagcgtca	tcaccatcg	cagtgacacg	gacgaggagg	aggaacagaa	acacgcccc	2820
accagcactg	tctccaagca	aagaaaaaac	gtcatcagct	gtgtcacagt	ccacgactcc	2880
ccctactccg	actcctccag	caacaccagc	ccctactccg	tgcagcagcg	tgctggcac	2940
aacaatgcca	atgccttga	caccaagggg	agcctggaga	atcactgcac	gggaaacccc	3000
cgaaccatca	tcgtgccacc	cctgaaaacc	caggccagcg	aagtatttgt	ggagtgtgat	3060
agcctggtgc	cagtcaacac	cagtcaccac	tcgtccctcct	acaagtccaa	gtcctccagc	3120
aacgtgacct	ccaccagcgg	tcactttca	gggagctcat	ctggagccat	cacctaccgg	3180
cagcagcggc	cgggccccca	cttccagcag	cagcagccac	tcaatctcag	ccaggctcag	3240
cagcacatca	ccacggaccg	cactggagc	caccgaaggc	agcaggccta	catcactccc	3300
accatggccc	aggctccgta	ctccttcccc	cacaacagcc	ccagccacgg	cactgtgcac	3360
ccgcatctgg	ctgcagccgc	tgccgctgcc	cacccccc	cccagcccc	cctctacacc	3420
tacactgcgc	cggcggccct	gggctccacc	ggcacccgtgg	cccacctgg	ggcctcgcaa	3480
ggctctgcgc	gccacaccgt	gcagcacact	gcctacccag	ccagcatcgt	ccaccaggc	3540
cccgtagca	tgggcccccg	ggtcctgccc	tgcaccacca	tccacccgag	tcagtatcca	3600
gcccaatttgc	cccaccagac	ctacatcagc	gcctcgccag	cctccaccgt	ctacactgga	3660
tacccactga	gccccgccaa	ggtcaaccag	tacccttaca	tataaacact	ggaggggagg	3720
gagggaggga	gggagggaga	aatggcccg	agggaggagg	gagagaagga	gggaggcgct	3780
cctgggaccg	tgggcgctgg	ccttttatac	tgaagatgcc	gcacacaaac	aatgcaaacg	3840
ggcaggggc	gggggggggg	ggggcagagg	gcagggggac	gggtcgggac	accagtgaaa	3900
cttgaaccgg	gaagtgggag	gacgttagagc	agagaagaga	acattttaa	aaggaaggga	3960
ttaaagaggg	tggaaatct	atggtttta	ttttaaaaaaa			4000

<210> 282  
 <211> 1198  
 <212> PRT  
 <213> human organism

<400> 282

Met	Ala	Pro	Val	Tyr	Glu	Gly	Met	Ala	Ser	His	Val	Gln	Val	Phe	Ser
1					5				10					15	

Pro His Thr Leu Gln Ser Ser Ala Phe Cys Ser Val Lys Lys Leu Lys  
20 25 30

Val Glu Pro Ser Ser Asn Trp Asp Met Thr Gly Tyr Gly Ser His Ser  
35 40 45

Lys Val Tyr Ser Gln Ser Lys Asn Ile Pro Pro Ser Gln Pro Ala Ser  
50 55 60

Thr Thr Val Ser Thr Ser Leu Pro Val Pro Asn Pro Ser Leu Pro Tyr  
65 70 75 80

Glu Gln Thr Ile Val Phe Pro Gly Ser Thr Gly His Ile Val Val Thr  
85 90 95

Ser Ala Ser Ser Thr Ser Val Thr Gly Gln Val Leu Gly Gly Pro His  
100 105 110

Asn Leu Met Arg Arg Ser Thr Val Ser Leu Leu Asp Thr Tyr Gln Lys  
115 120 125

Cys Gly Leu Lys Arg Lys Ser Glu Glu Ile Glu Asn Thr Ser Ser Val  
130 135 140

Gln Ile Ile Glu Glu His Pro Pro Met Ile Gln Asn Asn Ala Ser Gly  
145 150 155 160

Ala Thr Val Ala Thr Ala Thr Ser Thr Ala Thr Ser Lys Asn Ser  
165 170 175

Gly Ser Asn Ser Glu Gly Asp Tyr Gln Leu Val Gln His Glu Val Leu  
180 185 190

Cys Ser Met Thr Asn Thr Tyr Glu Val Leu Glu Phe Leu Gly Arg Gly  
195 200 205

Thr Phe Gly Gln Val Val Lys Cys Trp Lys Arg Gly Thr Asn Glu Ile  
210 215 220

Val Ala Ile Lys Ile Leu Lys Asn Arg Pro Ser Tyr Ala Arg Gln Gly  
225 230 235 240

Gln Ile Glu Val Ser Ile Leu Ala Arg Leu Ser Thr Glu Ser Ala Asp  
245 250 255

Asp Tyr Asn Phe Val Arg Ala Tyr Glu Cys Phe Gln His Lys Asn His  
260 265 270

Thr Cys Leu Val Phe Glu Met Leu Glu Gln Asn Leu Tyr Asp Phe Leu  
275 280 285

Lys Gln Asn Lys Phe Ser Pro Leu Pro Leu Lys Tyr Ile Arg Pro Val  
290 295 300

Leu Gln Gln Val Ala Thr Ala Leu Met Lys Leu Lys Ser Leu Gly Leu  
305 310 315 320

Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu Val Asp Pro Ser  
325 330 335

Arg Gln Pro Tyr Arg Val Lys Val Ile Asp Phe Gly Ser Ala Ser His  
340 345 350

Val Ser Lys Ala Val Cys Ser Thr Tyr Leu Gln Ser Arg Tyr Tyr Arg  
355 360 365

Ala Pro Glu Ile Ile Leu Gly Leu Pro Phe Cys Glu Ala Ile Asp Met  
370 375 380

Trp Ser Leu Gly Cys Val Ile Ala Glu Leu Phe Leu Gly Trp Pro Leu  
385 390 395 400

Tyr Pro Gly Ala Ser Glu Tyr Asp Gln Ile Arg Tyr Ile Ser Gln Thr  
405 410 415

Gln Gly Leu Pro Ala Glu Tyr Leu Leu Ser Ala Gly Thr Lys Thr Thr  
420 425 430

Arg Phe Phe Asn Arg Asp Thr Asp Ser Pro Tyr Pro Leu Trp Arg Leu  
435 440 445

Lys Thr Pro Asp Asp His Glu Ala Glu Thr Gly Ile Lys Ser Lys Glu  
450 455 460

Ala Arg Lys Tyr Ile Phe Asn Cys Leu Asp Asp Met Ala Gln Val Asn  
465 470 475 480

Met Thr Thr Asp Leu Glu Gly Ser Asp Met Leu Val Glu Lys Ala Asp  
485 490 495

Arg Arg Glu Phe Ile Asp Leu Leu Lys Lys Met Leu Thr Ile Asp Ala  
500 505 510

Asp Lys Arg Ile Thr Pro Ile Glu Thr Leu Asn His Pro Phe Val Thr  
515 520 525

Met Thr His Leu Leu Asp Phe Pro His Ser Thr His Val Lys Ser Cys  
530 535 540

Phe Gln Asn Met Glu Ile Cys Lys Arg Arg Val Asn Met Tyr Asp Thr  
545 550 555 560

Val Asn Gln Ser Lys Thr Pro Phe Ile Thr His Val Ala Pro Ser Thr  
565 570 575

Ser Thr Asn Leu Thr Met Thr Phe Asn Asn Gln Leu Thr Thr Val His  
580 585 590

Asn Gln Ala Pro Ser Ser Thr Ser Ala Thr Ile Ser Leu Ala Asn Pro  
595 600 605

Glu Val Ser Ile Leu Asn Tyr Pro Ser Thr Leu Tyr Gln Pro Ser Ala  
610 615 620

Ala Ser Met Ala Ala Val Ala Gln Arg Ser Met Pro Leu Gln Thr Gly  
625 630 635 640

Thr Ala Gln Ile Cys Ala Arg Pro Asp Pro Phe Gln Gln Ala Leu Ile  
645 650 655

Val Cys Pro Pro Gly Phe Gln Gly Leu Gln Ala Ser Pro Ser Lys His  
660 665 670

Ala Gly Tyr Ser Val Arg Met Glu Asn Ala Val Pro Ile Val Thr Gln  
675 680 685

Ala Pro Gly Ala Gln Pro Leu Gln Ile Gln Pro Gly Leu Leu Ala Gln

690

695

700

Gln Ala Trp Pro Ser Gly Thr Gln Gln Ile Leu Leu Pro Pro Ala Trp  
705 710 715 720

Gln Gln Leu Thr Gly Val Ala Thr His Thr Ser Val Gln His Ala Thr  
725 730 735

Val Ile Pro Glu Thr Met Ala Gly Thr Gln Gln Leu Ala Asp Trp Arg  
740 745 750

Asn Thr His Ala His Gly Ser His Tyr Asn Pro Ile Met Gln Gln Pro  
755 760 765

Ala Leu Leu Thr Gly His Val Thr Leu Pro Ala Ala Gln Pro Leu Asn  
770 775 780

Val Gly Val Ala His Val Met Arg Gln Gln Pro Thr Ser Thr Thr Ser  
785 790 795 800

Ser Arg Lys Ser Lys Gln His Gln Ser Ser Val Arg Asn Val Ser Thr  
805 810 815

Cys Glu Val Ser Ser Ser Gln Ala Ile Ser Ser Pro Gln Arg Ser Lys  
820 825 830

Arg Val Lys Glu Asn Thr Pro Pro Arg Cys Ala Met Val His Ser Ser  
835 840 845

Pro Ala Cys Ser Thr Ser Val Thr Cys Gly Trp Gly Asp Val Ala Ser  
850 855 860

Ser Thr Thr Arg Glu Arg Gln Arg Gln Thr Ile Val Ile Pro Asp Thr  
865 870 875 880

Pro Ser Pro Thr Val Ser Val Ile Thr Ile Ser Ser Asp Thr Asp Glu  
885 890 895

Glu Glu Glu Gln Lys His Ala Pro Thr Ser Thr Val Ser Lys Gln Arg  
900 905 910

Lys Asn Val Ile Ser Cys Val Thr Val His Asp Ser Pro Tyr Ser Asp  
915 920 925

Ser Ser Ser Asn Thr Ser Pro Tyr Ser Val Gln Gln Arg Ala Gly His  
930 935 940

Asn Asn Ala Asn Ala Phe Asp Thr Lys Gly Ser Leu Glu Asn His Cys  
945 950 955 960

Thr Gly Asn Pro Arg Thr Ile Ile Val Pro Pro Leu Lys Thr Gln Ala  
965 970 975

Ser Glu Val Leu Val Glu Cys Asp Ser Leu Val Pro Val Asn Thr Ser  
980 985 990

His His Ser Ser Ser Tyr Lys Ser Lys Ser Ser Ser Asn Val Thr Ser  
995 1000 1005

Thr Ser Gly His Ser Ser Gly Ser Ser Ser Gly Ala Ile Thr Tyr  
1010 1015 1020

Arg Gln Gln Arg Pro Gly Pro His Phe Gln Gln Gln Pro Leu  
1025 1030 1035

Asn Leu Ser Gln Ala Gln Gln His Ile Thr Thr Asp Arg Thr Gly  
1040 1045 1050

Ser His Arg Arg Gln Gln Ala Tyr Ile Thr Pro Thr Met Ala Gln  
1055 1060 1065

Ala Pro Tyr Ser Phe Pro His Asn Ser Pro Ser His Gly Thr Val  
1070 1075 1080

His Pro His Leu Ala Ala Ala Ala Ala Ala His Leu Pro Thr  
1085 1090 1095

Gln Pro His Leu Tyr Thr Tyr Thr Ala Pro Ala Ala Leu Gly Ser  
1100 1105 1110

Thr Gly Thr Val Ala His Leu Val Ala Ser Gln Gly Ser Ala Arg  
1115 1120 1125

His Thr Val Gln His Thr Ala Tyr Pro Ala Ser Ile Val His Gln  
1130 1135 1140

Val Pro Val Ser Met Gly Pro Arg Val Leu Pro Ser Pro Thr Ile  
1145 1150 1155

His Pro Ser Gln Tyr Pro Ala Gln Phe Ala His Gln Thr Tyr Ile  
1160 1165 1170

Ser Ala Ser Pro Ala Ser Thr Val Tyr Thr Gly Tyr Pro Leu Ser  
1175 1180 1185

Pro Ala Lys Val Asn Gln Tyr Pro Tyr Ile  
1190 1195

<210> 283

<211> 1464

<212> DNA

<213> human organism

<400> 283	
agtacagacc aggttaaccct ggagtgaagc ggtttagtta gaagggagca gataaactcg	60
tcactctagt agctttaacc ctcaccctga ggcaccccttag caatcagcca ttgcctgcaa	120
gcctccaaag cttgtcttg cctaataatgg agcccaaaga agccactggg aaagaaaaca	180
tggtcaccaa gaaaaagaat ctggccttct tgaggtctag actctatatg ctggagagaa	240
ggaagactga cactgtggtt gagagcagtg tttctgggga ccactctggc accttgagga	300
ggagccaatc tgacaggacc gaataacaacc agaaattaca agaaaagatg actccacagg	360
gtgagtgttc tgttagctgag accttaaccc cagaggaaga gcatcatatg aagaggatga	420
tggcaaagcg ggaaaagatc attaaggagc tgatacagac agaaaaggat tatctcaatg	480
atctagagct gtgtgttagg gaagtggttc agcccctgag aaataaaaag actgataggc	540
tggatgtgga tagcttgttt agcaacattt agtccgtgca tcagatatca gccaaagctgc	600
tgtcattgtt ggaagaggcc acaacagacg tggAACCGGC catgcaagta attggagaag	660
tattcttgca gattaaaggg ccactggaag atatttataa aatctactgc tatcaccatg	720
atgaagcaca tagtatactg gagtcctatg aaaaggaaga agagctgaag gaacatttg	780
gccactgtat ccagtccctta aagtaaggcc ttttcaaatg atgattccca tctccctctca	840
gttgccttagc agggAACATT ttaaatggat gtagatgaaa ggtctcacat aaatcctatg	900
tttatgaga cttgctggga gctctgcttt gcattccctt tataaaaaagc tgacatgcca	960
gaagccctga ttgactttt ttccccctgc gagaatgact aaaaataaca tggaagaaga	1020

tttagagctc	tgca	gcatt	aaaaatgca	atatcaaaat	ataaaatgtg	gaagaaaagc	1080
ctcttcttaa	agctattgt	a	c	tgcctgg	ccccacgt	ttcaaggatt	1140
acacgtggcc	ccatgaccac	tggagcacat	gggttaatgg	agttagggg	atggc	1200	
actctgc	atg	ccgtcttct	ttccccaaac	tcactgt	gagatgggt	aagacaagtc	1260
aggccttgtt	aaagttagtt	tcagaacaat	tactcat	gcc	ttc	atccctaaaa	1320
cattggtggg	ggagctacac	aatgtacttt	ttctttcta	gaggaagtat	ctattcactg	1380	
tgaaaatctg	aaaaatataa	caaagtatgt	gtaagataaa	aacc	cc	tgc	1440
aaaaaaaaaa	aaaaaaaaaa	aaaa					1464

<210> 284

<211> 219

<212> PRT

<213> human organism

<400> 284

Met	Glu	Pro	Lys	Glu	Ala	Thr	Gly	Lys	Glu	Asn	Met	Val	Thr	Lys	Lys
1				5				10					15		

Lys	Asn	Leu	Ala	Phe	Leu	Arg	Ser	Arg	Leu	Tyr	Met	Leu	Glu	Arg	Arg
				20			25					30			

Lys	Thr	Asp	Thr	Val	Val	Glu	Ser	Ser	Val	Ser	Gly	Asp	His	Ser	Gly
	35					40					45				

Thr	Leu	Arg	Arg	Ser	Gln	Ser	Asp	Arg	Thr	Glu	Tyr	Asn	Gln	Lys	Leu
	50				55				60						

Gln	Glu	Lys	Met	Thr	Pro	Gln	Gly	Glu	Cys	Ser	Val	Ala	Glu	Thr	Leu
65				70		75						80			

Thr	Pro	Glu	Glu	Glu	His	His	Met	Lys	Arg	Met	Met	Ala	Lys	Arg	Glu
					85			90				95			

Lys	Ile	Ile	Lys	Glu	Leu	Ile	Gln	Thr	Glu	Lys	Asp	Tyr	Leu	Asn	Asp
			100					105				110			

Leu	Glu	Leu	Cys	Val	Arg	Glu	Val	Val	Gln	Pro	Leu	Arg	Asn	Lys	Lys
			115				120				125				

Thr	Asp	Arg	Leu	Asp	Val	Asp	Ser	Leu	Phe	Ser	Asn	Ile	Glu	Ser	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130

135

140

His Gln Ile Ser Ala Lys Leu Leu Ser Leu Leu Glu Glu Ala Thr Thr  
145 150 155 160

Asp Val Glu Pro Ala Met Gln Val Ile Gly Glu Val Phe Leu Gln Ile  
165 170 175

Lys Gly Pro Leu Glu Asp Ile Tyr Lys Ile Tyr Cys Tyr His His Asp  
180 185 190

Glu Ala His Ser Ile Leu Glu Ser Tyr Glu Lys Glu Glu Leu Lys  
195 200 205

Glu His Leu Ser His Cys Ile Gln Ser Leu Lys  
210 215

<210> 285

<211> 3004

<212> DNA

<213> human organism

<400> 285

cccttatggc gattgggcgg ctgcagagac caggactcag ttcccctgcc ctagtctgag 60

cctagtgggt gggactcagc tcagagtcaag ttttcagaag caggttcag ttgcagagtt 120

ttcctacact tttcctgcgc tagagcagcg agcagcctgg aacagaccca ggcggaggac 180

acctgtgggg gagggagcgc ctggaggagc ttagagaccc cagccggcgc tgatctcacc 240

atgtgcggat ttgcgaggcg cgccctggag ctgctagaga tccggaagca cagccccgag 300

gtgtgcgaag ccaccaagac tgcggcttt ggagaaagcg tgagcagggg gccaccgcgg 360

tctccggcct gtctgcaccc tgtgcctga gctgcctgac agtgacaatg acatcccagt 420

taccagtgtc cttgaattga tagtggcttc tgtttgcag tctcatataa gaactacagc 480

tcatcaggag gagatcgcag cagggtaaga gacaccaaca ccatgttctg cacgaagctc 540

aaggatctca agatcacagg agagtgtcct ttctccttac tggcaccagg tcaagttcct 600

aacgagtctt cagaggaggc agcaggaagc tcagagagct gcaaagcaac cgtccccatc 660

tgtcaagaca ttcctgagaa gaacatacaa gaaagtcttc ctcaaagaaa aaccagtcgg 720

agccgagtct atcttcacac tttggcagag agtatttgca aactgatttt cccagagttt 780

gaacggctga atgttgcaact tcagagaaca ttggcaaagc aaaaaataaa agaaagcagg 840

aaatcttgg aaagagaaga cttgaaaaa acaattgcag agcaagcagt gcagcagagt 900  
ccagtggagt tatcaaagaa tctcttggtg aagaggttt taaaatatgt tacgaggaag 960  
atgaaaacat cttgggggtg gttggaggca cccttaaaga ttttaaaca gcttcagtac 1020  
ccttctgaaa cagagcagcc attgccaaga agcagaaaa agggcagct tgaggacgcc 1080  
tccattctat gcctggataa ggaggatgtat tttctacatg tttactactt cttccctaag 1140  
agaaccacct ccctgattct tcccggcatc ataaaggcag ctgctcacgt attatatgaa 1200  
acggaagtgg aagtgtcggtt aatgcctccc tgcttcata atgattgcag cgagtttgt 1260  
aatcagccct acttgttgcata ctccggtcac atgaaaagca ccaagccatc cctgtcccc 1320  
agcaaaccctt agtcctcgct ggtgattccc acatcgctat tctgcaagac atttccattc 1380  
catttcatgt ttgacaaaaga tatgacaatt ctgcaatttg gcaatggcat cagaaggctg 1440  
atgaacagga gagactttca aggaaagcct aattttgaat actttgaaat tctgactcca 1500  
aaaatcaacc agacctttag cgggatcatg actatgttga atatgcagtt tggttacga 1560  
gtgaggagat gggacaactc tgtgaagaaa tcttcaaggg ttatggacct caaaggccaa 1620  
atgatctaca ttgttgaatc cagtgcatac ttgttttgg ggtcaccctg tgtggacaga 1680  
ttagaagatt ttacaggacg agggctctac ctctcagaca tcccaattca caatgcactg 1740  
aggatgtgg tcttaatagg ggaacaagcc cgagctcaag atggcctgaa gaagaggctg 1800  
gggaagctga aggctaccct tgagcaagcc caccaagccc tggaggagga gaagaaaaag 1860  
acagtagacc ttctgtgctc catatttccc tgtgaggttg ctcagcagct gtggcaaggg 1920  
caagttgtgc aagccaagaa gttcagtaat gtcaccatgc tcttctcaga catcgttggg 1980  
ttcactgcca tctgctccca gtgctcaccc ctgcaggta tcaccatgtc caatgcactg 2040  
tacactcgct tcgaccagca gtgtggagag ctggatgtct acaaggtgga gaccattgcg 2100  
atgcctattt tgtggcttgg gggattacac aaagagagtg atactcatgc tgttcagata 2160  
gcgcgtatgg ccctgaagat gatggagctc tctgatgaag ttatgtctcc ccatggagaa 2220  
cctatcaaga tgcgaattgg actgcactct ggatcagttt ttgctggcgt cggtggagtt 2280  
aaaatgcaccctt gttactgtct ttttggaaac aatgtcactc tggctaaca atttgagtcc 2340  
tgcagtgtac cacgaaaaat caatgtcagc ccaacaactt acagattact caaagactgt 2400  
cctggtttcg ttttacccc tcgatcaagg gaggaacttc caccaaaactt ccctagtgaa 2460  
atccccggaa tctgccattt tctggatgtc taccaacaag gaacaaactc aaaaccatgc 2520  
ttccaaaaga aagatgtgga agatgcagc caattttta ggcaaagcat caggaataga 2580

ttagcaacct atataacctat ttataagtct ttggggttt actcattgaa gatgtgtaga 2640  
gcctctgaaa gcactttagg gattgttagat ggctaacaag cagtattaaa atttcaggag 2700  
ccaagtcaca atcttctcc tggtaacat gacaaaatgt actcacttca gtacttcagc 2760  
tcttcaagaa aaaaaaaaaa acctaaaaaa gctactttt gggagtatt tctattat 2820  
aaccagcact tactacctgt actcaaaatt cagcaccttg tacatatatc agataattgt 2880  
agtcaattgt acaaactgat ggagtcacct gcaatctcat atcctggtgg aatgccatgg 2940  
ttattaaagt gtgttgtga tagttgtcgt caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3000  
aaaaa 3004

<210> 286  
<211> 690  
<212> PRT  
<213> human organism

<400> 286

Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro  
1 5 10 15

Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu  
20 25 30

Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln  
35 40 45

Asp Ile Pro Glu Lys Asn Ile Gln Glu Ser Leu Pro Gln Arg Lys Thr  
50 55 60

Ser Arg Ser Arg Val Tyr Leu His Thr Leu Ala Glu Ser Ile Cys Lys  
65 70 75 80

Leu Ile Phe Pro Glu Phe Glu Arg Leu Asn Val Ala Leu Gln Arg Thr  
85 90 95

Leu Ala Lys His Lys Ile Lys Glu Ser Arg Lys Ser Leu Glu Arg Glu  
100 105 110

Asp Phe Glu Lys Thr Ile Ala Glu Gln Ala Val Ala Ala Gly Val Pro  
115 120 125

Val Glu Val Ile Lys Glu Ser Leu Gly Glu Glu Val Phe Lys Ile Cys  
130 135 140

Tyr Glu Glu Asp Glu Asn Ile Leu Gly Val Val Gly Gly Thr Leu Lys  
145 150 155 160

Asp Phe Leu Asn Ser Phe Ser Thr Leu Leu Lys Gln Ser Ser His Cys  
165 170 175

Gln Glu Ala Gly Lys Arg Gly Arg Leu Glu Asp Ala Ser Ile Leu Cys  
180 185 190

Leu Asp Lys Glu Asp Asp Phe Leu His Val Tyr Tyr Phe Phe Pro Lys  
195 200 205

Arg Thr Thr Ser Leu Ile Leu Pro Gly Ile Ile Lys Ala Ala Ala His  
210 215 220

Val Leu Tyr Glu Thr Glu Val Glu Val Ser Leu Met Pro Pro Cys Phe  
225 230 235 240

His Asn Asp Cys Ser Glu Phe Val Asn Gln Pro Tyr Leu Leu Tyr Ser  
245 250 255

Val His Met Lys Ser Thr Lys Pro Ser Leu Ser Pro Ser Lys Pro Gln  
260 265 270

Ser Ser Leu Val Ile Pro Thr Ser Leu Phe Cys Lys Thr Phe Pro Phe  
275 280 285

His Phe Met Phe Asp Lys Asp Met Thr Ile Leu Gln Phe Gly Asn Gly  
290 295 300

Ile Arg Arg Leu Met Asn Arg Arg Asp Phe Gln Gly Lys Pro Asn Phe  
305 310 315 320

Glu Glu Tyr Phe Glu Ile Leu Thr Pro Lys Ile Asn Gln Thr Phe Ser  
325 330 335

Gly Ile Met Thr Met Leu Asn Met Gln Phe Val Val Arg Val Arg Arg  
340 345 350

Trp Asp Asn Ser Val Lys Lys Ser Ser Arg Val Met Asp Leu Lys Gly

355

360

365

Gln Met Ile Tyr Ile Val Glu Ser Ser Ala Ile Leu Phe Leu Gly Ser  
370 375 380

Pro Cys Val Asp Arg Leu Glu Asp Phe Thr Gly Arg Gly Leu Tyr Leu  
385 390 395 400

Ser Asp Ile Pro Ile His Asn Ala Leu Arg Asp Val Val Leu Ile Gly  
405 410 415

Glu Gln Ala Arg Ala Gln Asp Gly Leu Lys Lys Arg Leu Gly Lys Leu  
420 425 430

Lys Ala Thr Leu Glu Gln Ala His Gln Ala Leu Glu Glu Glu Lys Lys  
435 440 445

Lys Thr Val Asp Leu Leu Cys Ser Ile Phe Pro Cys Glu Val Ala Gln  
450 455 460

Gln Leu Trp Gln Gly Gln Val Val Gln Ala Lys Lys Phe Ser Asn Val  
465 470 475 480

Thr Met Leu Phe Ser Asp Ile Val Gly Phe Thr Ala Ile Cys Ser Gln  
485 490 495

Cys Ser Pro Leu Gln Val Ile Thr Met Leu Asn Ala Leu Tyr Thr Arg  
500 505 510

Phe Asp Gln Gln Cys Gly Glu Leu Asp Val Tyr Lys Val Glu Thr Ile  
515 520 525

Gly Asp Ala Tyr Cys Val Ala Gly Gly Leu His Lys Glu Ser Asp Thr  
530 535 540

His Ala Val Gln Ile Ala Leu Met Ala Leu Lys Met Met Glu Leu Ser  
545 550 555 560

Asp Glu Val Met Ser Pro His Gly Glu Pro Ile Lys Met Arg Ile Gly  
565 570 575

Leu His Ser Gly Ser Val Phe Ala Gly Val Val Gly Val Lys Met Pro  
580 585 590

Arg Tyr Cys Leu Phe Gly Asn Asn Val Thr Leu Ala Asn Lys Phe Glu  
595 600 605

Ser Cys Ser Val Pro Arg Lys Ile Asn Val Ser Pro Thr Thr Tyr Arg  
610 615 620

Leu Leu Lys Asp Cys Pro Gly Phe Val Phe Thr Pro Arg Ser Arg Glu  
625 630 635 640

Glu Leu Pro Pro Asn Phe Pro Ser Glu Ile Pro Gly Ile Cys His Phe  
645 650 655

Leu Asp Ala Tyr Gln Gln Gly Thr Asn Ser Lys Pro Cys Phe Gln Lys  
660 665 670

Lys Asp Val Glu Asp Gly Asn Ala Asn Phe Leu Gly Lys Ala Ser Gly  
675 680 685

Ile Asp  
690

<210> 287  
<211> 7193  
<212> DNA  
<213> human organism

<400> 287  
agaataagggg cagggaccgc ggctcctatc tcttggtgat ccccttcccc attccgcccc 60  
cgccctcaacg cccagcacag tgccctgcac acagtagtcg ctcaataaat gttcgtggat 120  
gatgatgatg atgatgatga aaaaaatgca gcataacgg cagcagcaag cgaccacgc 180  
gaacgaggca aactatgcaa gaggcaccag acttccttct tctggtaag gaccaacttc 240  
tcagccgaat agctccaagc aaactgtcct gtcttggcaa gctgcaatcg atgctgctag 300  
acaggccaaag gctgccaaa ctatgacac ctctgcaccc ccacctgttag gatctctc 360  
ccaaagaaaa cgtcagcaat acgccaagag caaaaaacag ggttaactcgt ccaacagccg 420  
acctgcccgc gccctttct gtttatcact caataacccc atccgaagag cctgcattag 480  
tatagtggaa tggaaaccat ttgacatatt tatattattg gctatTTTg ccaattgtgt 540  
ggccttagct atttacatcc cattccctga agatgattct aattcaacaa atcataactt 600  
ggaaaaagta gaatatgcct tcctgattat ttttacagtc gagacattt tgaagattat 660

agcgatggta ttattgtac atcctaatac ttatgttagg aatggatggaa atttactggaa 720  
tttgttata gtaatagtag gattgttag tgtaatttg gaacaattaa ccaaagaaac 780  
agaaggcggg aaccactcaa gcggcaaatc tggaggctt gatgtcaaag ccctccgtgc 840  
cttcgagtg ttgcgaccac ttgcactagt gtcaggggtg cccagttac aagttgtcct 900  
gaactccatt ataaaagcca tggttcccct cttcacata gccctttgg tattattgt 960  
aatcataatc tatgttattt taggattggaa actttttattt ggaaaaatgc aaaaaacatg 1020  
ttttttgct gactcagata tcgttagctga agaggaccca gctccatgtg cggtctcagg 1080  
gaatggacgc cagtgtactg ccaatggcac ggaatgttagg agtggctggg ttggccgaa 1140  
cgaggcatc accaactttg ataacttgc ctttgcattt ctactgtgt ttcagtgcatt 1200  
caccatggag ggctggacag acgtgctcta ctggtaaat gatgcgatag gatggaaatg 1260  
gccatgggtg tattttgtta gtctgatcat cttggctca ttttcgtcc ttaacctgg 1320  
tcttgggtc cttagtgag aattctcaa ggaaagagag aaggcaaaag cacggggaga 1380  
tttccagaag ctccggaga agcagcagct ggaggaggat ctaaagggtc acttggattg 1440  
gatcacccaa gctgaggaca tcgatccgga gaatgaggaa gaaggaggag aggaaggcaa 1500  
acgaaatact agcatgccc ccagcgagac tgagtctgtg aacacagaga acgtcagcgg 1560  
tgaaggcgag aaccgaggct gctgtggaaag tctctgggtc tggtggagac ggagaggcgc 1620  
ggccaaggcg gggccctctg ggtgtcggcg gtggggtcaa gccatctcaa aatccaaact 1680  
cagccgacgc tggcgctcgct ggaaccgatt caatcgaga agatgttaggg ccggcgtgaa 1740  
gtctgtcacg ttttactggc tggttatcgt cttgggttt ctgaacaccc taaccatttc 1800  
ctctgagcac tacaatcagc cagattgggt gacacagatt caagatattt ccaacaaatg 1860  
cctctggct ctgttcaccc gcgagatgct ggtaaaaatg tacagcttgg gcctccaagc 1920  
atatttcgtc tctctttca accgggttga ttgcttcgtg gtgtgtgggtg gaatcactga 1980  
gacgatcctg gtggaaactgg aaatcatgtc tccccctgggg atctctgtgt ttcgggtgt 2040  
gcccctctta agaatcttca aagtgaccag gcactggact tccctgagca acttagtggc 2100  
atccttattt aactccatga agtccatcgc ttgcgtgtt cttctgttt ttctcttcatt 2160  
tatcatcttt tccttgcttgg ggtatgcagct gtttggcggc aagtttaatt ttgatgaaac 2220  
gcaaaccaag cggagcacct ttgacaattt ccctcaagca cttctcacag tgttccagat 2280  
cctgacaggc gaagactgga atgctgtgat gtacgatggc atcatggcattt acggggggcccc 2340

atcctttca ggaatgatcg tctgcata cttcatcata ctcttcattt gtggtaacta 2400  
tattctactg aatgtcttct tggccatcgc tgtagacaat ttggctgatg ctgaaagtct 2460  
gaacactgct cagaaagaag aagcggaga aaaggagagg aaaaagattg ccagaaaaga 2520  
gaggcttagaa aataaaaaga acaacaaacc agaagtcaac cagatagcca acagtgacaa 2580  
caaggttaca attgatgact atagagaaga ggtatgaagac aaggaccctt atccgccttg 2640  
cgatgtgccca gtaggggaag aggaagagga agaggaggag gatgaacctg aggttcctgc 2700  
cgaggccccgt cctcgaagga tctcgagtt gaacatgaag gaaaaaattt ccccccattttc 2760  
tgaaggagc gctttttca ttcttagcaa gaccaacccg atccgcgttag gctgccacaa 2820  
gctcatcaac caccacatct tcaccaacct catcctgtc ttcatcatgc tgagcagcgc 2880  
tgccctggcc gcagaggacc ccatccgcag ccactccttc cgaaacacga tactgggta 2940  
ctttgactat gccttcacag ccatcttac tggttagatc ctgttgaaga tgacaacttt 3000  
tggagcttcc tcaccaaaag gggccttctg caggaactac ttcaatttgc tggatatgct 3060  
ggtggttggg gtgtctctgg tgtcatttgg gattcaatcc agtgcacatct ccgttgtgaa 3120  
gattctgagg gtcttaaggg tcctgcgtcc cctcaggggcc atcaacagag caaaaggact 3180  
taagcacgtg gtccagtgcg tcttcgtggc catccggacc atcggcaaca tcatgatcgt 3240  
cactaccctc ctgcagttca tggttgcctg tatcggggtc cagttgtca agggaaagtt 3300  
ctatcgctgt acggatgaag ccaaaagtaa ccctgaagaa tgcaggggac ttttcatcct 3360  
ctacaaggat gggatgttgc acagtccctgt ggtccgtgaa cggatctggc aaaacagtga 3420  
tttcaacttc gacaacgtcc tctctgctat gatggcgctc ttcacagtct ccacgttga 3480  
gggctggcct gcgttgctgt ataaagccat cgactcgaat ggagagaaca tcggccaaat 3540  
ctacaaccac cgcgtggaga tctccatctt cttcatcatc tacatcatca ttgttagctt 3600  
cttcatgatg aacatcttgc tggcatttgc catcgttaca tttcaggaac aaggagaaaa 3660  
agagtataag aactgtgagc tggacaaaaaa tcagcgtcag tggatgttgc acgccttgc 3720  
agcacgtccc ttgcggagat acatccccaa aaaccctac cagtcataatgt tctggatcgt 3780  
ggtaactct tcgccttcg aatacatgat gtttgcctc atcatgctca acacactctg 3840  
cttggccatg cagcactacg agcagtccaa gatgttcaat gatggccatgg acattctgaa 3900  
catggcttc accgggggtgt tcaccgtcga gatggtttg aaagtcatcg catttaagcc 3960  
taaggggtat tttagtgacg cctgaaacac gtttgcactcc cttcatcgtaa tcggcagcat 4020  
tatagacgtg gccctcagcg aagcggaccc aactgaaagt gaaaatgtcc ctgtccaaac 4080

tgctacacct gggactctg aagagagcaa tagaatctcc atcaccttt tccgtcttt 4140  
ccgagtatcg cgattggtga agcttctcag cagggggaa ggcattccgga cattgctgtg 4200  
gactttatt aagtccatttc aggcgctccc gtatgtggcc ctccatcatag ccatgctgtt 4260  
cttcatctat gcggtcattt gcatgcagat gtttggaaa gttgccatga gagataacaa 4320  
ccagatcaat aggaacaata acttccagac gttccccag gccgtgctgc tgctcttcag 4380  
gtgtgcaaca ggtgaggcct ggcaggagat catgctggcc tgtctccag ggaagctctg 4440  
tgacccttag tcagattaca accccgggaa ggagtataca tgtggagca actttgccat 4500  
tgtctatttc atcagtttt acatgctctg tgcatttctg atcatcaatc ttttgcgc 4560  
tgtcatcatg gataatttcg actatctgac ccggactgg tctattttgg ggcctcacca 4620  
tttagatgaa ttcaaaagaa tatggtcaga atatgaccct gaggcaaagg gaaggataaa 4680  
acacccgtat gtggtcactc tgcttcgacg catccagcct cccctgggtt ttggaaagtt 4740  
atgtccacac agggtagcgt gcaagagatt agttgccatg aacatgcctc tcaacagtga 4800  
cgggacagtc atgttaatg caaccctgtt tgctttgggtt cgaacggctc ttaagatcaa 4860  
gaccgaaggg aacctggagc aagctaatac agaacttcgg gctgtataa agaaaatttg 4920  
gaagaaaacc agcatgaaat tacttgacca agttgtccct ccagctggtg atgatgaggt 4980  
aacccgtgggg aagttctatg ccactttcct gatacaggac tacttttagga aattcaagaa 5040  
acggaaagaa caaggactgg tggaaagta ccctgcgaag aacaccacaa ttgccttaca 5100  
ggcgggatta aggacactgc atgacattgg gccagaaatc cggcgtgcta tatcgtgtga 5160  
tttgcaagat gacgagcctg aggaaacaaa acgagaagaa gaagatgatg tttcaaaaag 5220  
aaatggtgcc ctgcttggaa accatgtcaa tcatgttaat agttagatggagatccct 5280  
tcagcagacc aataccaccc accgtccct gcatgtccaa aggcccttcaa ttccacactc 5340  
aagtgatact gagaaaccgc ttttcctcc agcaggaaat tcggtgtgtc ataaccatca 5400  
taaccataat tccataggaa agcaagttcc cacctcaaca aatgccaatc tcaataatgc 5460  
caatatgtcc aaagctgccc atggaaagcg gcccagcattt gggAACCTTG agcatgtgtc 5520  
tgaaaatggg catcatttctt cccacaagca tgaccggag cctcagagaa ggtccagtgt 5580  
gaaaagaacc cgctattatg aaacttacat taggtccgac tcaggagatg aacagctccc 5640  
aactatgtc cgggaaagacc cagagataca tggctatttc agggacccccc actgcttggg 5700  
ggagcaggag tatttcagta gtgaggaatg ctacgaggat gacagctcgc ccacctggag 5760

caggcaaaac tatggctact acagcagata cccaggcaga aacatcgact ctgagaggcc	5820
ccgaggctac catcatcccc aaggattttt ggaggacgt gactcgccc tttgctatga	5880
ttcacggaga tctccaagga gacgcctact acctcccacc ccagcatccc accggagatc	5940
ctccttcaac tttgagtgcc tgcgccggca gagcagccag gaagaggccc cgtcgtctcc	6000
catttcccc catcgacgg ccctgcctct gcatctaattt cagcaacaga tcatggcagt	6060
tgcggcccta gattcaagta aagcccagaa gtactcaccg agtcaactcga cccggcgt	6120
ggccacccct ccagcaaccc ctccctaccg ggactggaca ccgtgctaca ccccccgtat	6180
ccaagtggag cagtcagagg ccctggacca ggtgaacggc agcctgcccgt ccctgcacccg	6240
cagtcctgg tacacagacg agcccgacat ctccctaccgg actttcacac cagccagcct	6300
gactgtcccc agcagcttcc ggaacaaaaaa cagcgacaaag cagaggagtg cggacagctt	6360
ggtggaggca gtcctgatat ccgaaggctt gggacgctat gcaaggggacc caaaaatttgt	6420
gtcagcaaca aaacacgaaa tcgctgatgc ctgtgacctc accatcgacg agatggagag	6480
tgccagccago accctgctta atgggaacgt gcgtccccga gccaacgggg atgtggggcc	6540
cctctcacac cggcaggact atgagctaca ggacttttgt cctggctaca gcgacgaaga	6600
gccagaccct gggagggatg aggaggacct ggcggatgaa atgatatgca tcaccacctt	6660
gtagccccca gcgagggggca gactggctct ggcctcaggt ggggcgcagg agagccaggg	6720
aaaaagtgcc tcatagttag gaaagttag gcactagttt ggagtaatat tcaattaatt	6780
agacttttgt ataagagatg tcatgcctca agaaagccat aaacctggta ggaacaggc	6840
ccaagcgggtt gagcctggca gagtaccatg cgctcgcccc cagctgcagg aaacagcagg	6900
ccccggccctc tcacagagga tgggtgagga ggccagacct gccctgcccc attgtccaga	6960
tgggcactgc tgtggagtct gcttctccca tgtaccaggg caccaggccc acccaactga	7020
aggcatggcg gcgggggtgca ggggaaagt aaaggtgatg acgatcatca cacctcggt	7080
cgttacctca gccatcggtc tagcatatca gtcactgggc ccaacatatc cattttaaa	7140
cccttcccc caaatacact gcgtcctggt tcctgttttag ctgttctgaa ata	7193

<210> 288  
 <211> 2181  
 <212> PRT  
 <213> human organism

<400> 288

Met Met Met Met Met Lys Lys Met Gln His Gln Arg Gln Gln

1 5 10 15

Gln Ala Asp His Ala Asn Glu Ala Asn Tyr Ala Arg Gly Thr Arg Leu  
20 25 30

Pro Leu Ser Gly Glu Gly Pro Thr Ser Gln Pro Asn Ser Ser Lys Gln  
35 40 45

Thr Val Leu Ser Trp Gln Ala Ala Ile Asp Ala Ala Arg Gln Ala Lys  
50 55 60

Ala Ala Gln Thr Met Ser Thr Ser Ala Pro Pro Pro Val Gly Ser Leu  
65 70 75 80

Ser Gln Arg Lys Arg Gln Gln Tyr Ala Lys Ser Lys Lys Gln Gly Asn  
85 90 95

Ser Ser Asn Ser Arg Pro Ala Arg Ala Leu Phe Cys Leu Ser Leu Asn  
100 105 110

Asn Pro Ile Arg Arg Ala Cys Ile Ser Ile Val Glu Trp Lys Pro Phe  
115 120 125

Asp Ile Phe Ile Leu Leu Ala Ile Phe Ala Asn Cys Val Ala Leu Ala  
130 135 140

Ile Tyr Ile Pro Phe Pro Glu Asp Asp Ser Asn Ser Thr Asn His Asn  
145 150 155 160

Leu Glu Lys Val Glu Tyr Ala Phe Leu Ile Ile Phe Thr Val Glu Thr  
165 170 175

Phe Leu Lys Ile Ile Ala Tyr Gly Leu Leu Leu His Pro Asn Ala Tyr  
180 185 190

Val Arg Asn Gly Trp Asn Leu Leu Asp Phe Val Ile Val Ile Val Gly  
195 200 205

Leu Phe Ser Val Ile Leu Glu Gln Leu Thr Lys Glu Thr Glu Gly Gly  
210 215 220

Asn His Ser Ser Gly Lys Ser Gly Gly Phe Asp Val Lys Ala Leu Arg  
225 230 235 240

Ala Phe Arg Val Leu Arg Pro Leu Arg Leu Val Ser Gly Val Pro Ser  
245 250 255

Leu Gln Val Val Leu Asn Ser Ile Ile Lys Ala Met Val Pro Leu Leu  
260 265 270

His Ile Ala Leu Leu Val Leu Phe Val Ile Ile Ile Tyr Ala Ile Ile  
275 280 285

Gly Leu Glu Leu Phe Ile Gly Lys Met His Lys Thr Cys Phe Phe Ala  
290 295 300

Asp Ser Asp Ile Val Ala Glu Glu Asp Pro Ala Pro Cys Ala Phe Ser  
305 310 315 320

Gly Asn Gly Arg Gln Cys Thr Ala Asn Gly Thr Glu Cys Arg Ser Gly  
325 330 335

Trp Val Gly Pro Asn Gly Gly Ile Thr Asn Phe Asp Asn Phe Ala Phe  
340 345 350

Ala Met Leu Thr Val Phe Gln Cys Ile Thr Met Glu Gly Trp Thr Asp  
355 360 365

Val Leu Tyr Trp Val Asn Asp Ala Ile Gly Trp Glu Trp Pro Trp Val  
370 375 380

Tyr Phe Val Ser Leu Ile Ile Leu Gly Ser Phe Phe Val Leu Asn Leu  
385 390 395 400

Val Leu Gly Val Leu Ser Gly Glu Phe Ser Lys Glu Arg Glu Lys Ala  
405 410 415

Lys Ala Arg Gly Asp Phe Gln Lys Leu Arg Glu Lys Gln Gln Leu Glu  
420 425 430

Glu Asp Leu Lys Gly Tyr Leu Asp Trp Ile Thr Gln Ala Glu Asp Ile  
435 440 445

Asp Pro Glu Asn Glu Glu Gly Glu Glu Gly Lys Arg Asn Thr  
450 455 460

Ser Met Pro Thr Ser Glu Thr Glu Ser Val Asn Thr Glu Asn Val Ser  
465                    470                    475                    480

Gly Glu Gly Glu Asn Arg Gly Cys Cys Gly Ser Leu Trp Cys Trp Trp  
485 490 495

Arg Arg Arg Gly Ala Ala Lys Ala Gly Pro Ser Gly Cys Arg Arg Trp  
500 505 510

Gly Gln Ala Ile Ser Lys Ser Lys Leu Ser Arg Arg Trp Arg Arg Arg Trp  
515 520 525

Asn Arg Phe Asn Arg Arg Arg Cys Arg Ala Ala Val Lys Ser Val Thr  
530 535 540

Phe Tyr Trp Leu Val Ile Val Leu Val Phe Leu Asn Thr Leu Thr Ile  
 545 550 555 560

Ser Ser Glu His Tyr Asn Gln Pro Asp Trp Leu Thr Gln Ile Gln Asp  
565 570 575

Ile Ala Asn Lys Val Leu Leu Ala Leu Phe Thr Cys Glu Met Leu Val  
580 585 590

Lys Met Tyr Ser Leu Gly Leu Gln Ala Tyr Phe Val Ser Leu Phe Asn  
595 600 605

Arg Phe Asp Cys Phe Val Val Cys Gly Gly Ile Thr Glu Thr Ile Leu  
610 615 620

Val Glu Leu Glu Ile Met Ser Pro Leu Gly Ile Ser Val Phe Arg Cys  
625 630 635 640

Val Arg Leu Leu Arg Ile Phe Lys Val Thr Arg His Trp Thr Ser Leu  
645 650 655

Ser Asn Leu Val Ala Ser Leu Leu Asn Ser Met Lys Ser Ile Ala Ser  
660 665 670

Leu Leu Leu Leu Phe Leu Phe Ile Ile Ile Phe Ser Leu Leu Gly  
675 680 685

Met Gln Leu Phe Gly Gly Lys Phe Asn Phe Asp Glu Thr Gln Thr Lys  
690 695 700

Arg Ser Thr Phe Asp Asn Phe Pro Gln Ala Leu Leu Thr Val Phe Gln  
705 710 715 720

Ile Leu Thr Gly Glu Asp Trp Asn Ala Val Met Tyr Asp Gly Ile Met  
725 730 735

Ala Tyr Gly Gly Pro Ser Ser Ser Gly Met Ile Val Cys Ile Tyr Phe  
740 745 750

Ile Ile Leu Phe Ile Cys Gly Asn Tyr Ile Leu Leu Asn Val Phe Leu  
755 760 765

Ala Ile Ala Val Asp Asn Leu Ala Asp Ala Glu Ser Leu Asn Thr Ala  
770 775 780

Gln Lys Glu Glu Ala Glu Glu Lys Glu Arg Lys Lys Ile Ala Arg Lys  
785 790 795 800

Glu Ser Leu Glu Asn Lys Lys Asn Asn Lys Pro Glu Val Asn Gln Ile  
805 810 815

Ala Asn Ser Asp Asn Lys Val Thr Ile Asp Asp Tyr Arg Glu Glu Asp  
820 825 830

Glu Asp Lys Asp Pro Tyr Pro Pro Cys Asp Val Pro Val Gly Glu Glu  
835 840 845

Glu Glu Glu Glu Glu Asp Glu Pro Glu Val Pro Ala Gly Pro Arg  
850 855 860

Pro Arg Arg Ile Ser Glu Leu Asn Met Lys Glu Lys Ile Ala Pro Ile  
865 870 875 880

Pro Glu Gly Ser Ala Phe Phe Ile Leu Ser Lys Thr Asn Pro Ile Arg  
885 890 895

Val Gly Cys His Lys Leu Ile Asn His His Ile Phe Thr Asn Leu Ile  
900 905 910

Leu Val Phe Ile Met Leu Ser Ser Ala Ala Leu Ala Ala Glu Asp Pro

915

920

925

Ile Arg Ser His Ser Phe Arg Asn Thr Ile Leu Gly Tyr Phe Asp Tyr  
930 935 940

Ala Phe Thr Ala Ile Phe Thr Val Glu Ile Leu Leu Lys Met Thr Thr  
945 950 955 960

Phe Gly Ala Phe Leu His Lys Gly Ala Phe Cys Arg Asn Tyr Phe Asn  
965 970 975

Leu Leu Asp Met Leu Val Val Gly Val Ser Leu Val Ser Phe Gly Ile  
980 985 990

Gln Ser Ser Ala Ile Ser Val Val Lys Ile Leu Arg Val Leu Arg Val  
995 1000 1005

Leu Arg Pro Leu Arg Ala Ile Asn Arg Ala Lys Gly Leu Lys His  
1010 1015 1020

Val Val Gln Cys Val Phe Val Ala Ile Arg Thr Ile Gly Asn Ile  
1025 1030 1035

Met Ile Val Thr Thr Leu Leu Gln Phe Met Phe Ala Cys Ile Gly  
1040 1045 1050

Val Gln Leu Phe Lys Gly Lys Phe Tyr Arg Cys Thr Asp Glu Ala  
1055 1060 1065

Lys Ser Asn Pro Glu Glu Cys Arg Gly Leu Phe Ile Leu Tyr Lys  
1070 1075 1080

Asp Gly Asp Val Asp Ser Pro Val Val Arg Glu Arg Ile Trp Gln  
1085 1090 1095

Asn Ser Asp Phe Asn Phe Asp Asn Val Leu Ser Ala Met Met Ala  
1100 1105 1110

Leu Phe Thr Val Ser Thr Phe Glu Gly Trp Pro Ala Leu Leu Tyr  
1115 1120 1125

Lys Ala Ile Asp Ser Asn Gly Glu Asn Ile Gly Pro Ile Tyr Asn  
1130 1135 1140

His Arg Val Glu Ile Ser Ile Phe Phe Ile Ile Tyr Ile Ile Ile  
1145 1150 1155

Val Ala Phe Phe Met Met Asn Ile Phe Val Gly Phe Val Ile Val  
1160 1165 1170

Thr Phe Gln Glu Gln Gly Glu Lys Glu Tyr Lys Asn Cys Glu Leu  
1175 1180 1185

Asp Lys Asn Gln Arg Gln Cys Val Glu Tyr Ala Leu Lys Ala Arg  
1190 1195 1200

Pro Leu Arg Arg Tyr Ile Pro Lys Asn Pro Tyr Gln Tyr Lys Phe  
1205 1210 1215

Trp Tyr Val Val Asn Ser Ser Pro Phe Glu Tyr Met Met Phe Val  
1220 1225 1230

Leu Ile Met Leu Asn Thr Leu Cys Leu Ala Met Gln His Tyr Glu  
1235 1240 1245

Gln Ser Lys Met Phe Asn Asp Ala Met Asp Ile Leu Asn Met Val  
1250 1255 1260

Phe Thr Gly Val Phe Thr Val Glu Met Val Leu Lys Val Ile Ala  
1265 1270 1275

Phe Lys Pro Lys Gly Tyr Phe Ser Asp Ala Trp Asn Thr Phe Asp  
1280 1285 1290

Ser Leu Ile Val Ile Gly Ser Ile Ile Asp Val Ala Leu Ser Glu  
1295 1300 1305

Ala Asp Pro Thr Glu Ser Glu Asn Val Pro Val Pro Thr Ala Thr  
1310 1315 1320

Pro Gly Asn Ser Glu Glu Ser Asn Arg Ile Ser Ile Thr Phe Phe  
1325 1330 1335

Arg Leu Phe Arg Val Met Arg Leu Val Lys Leu Leu Ser Arg Gly  
1340 1345 1350

Glu Gly Ile Arg Thr Leu Leu Trp Thr Phe Ile Lys Ser Phe Gln  
1355 1360 1365

Ala Leu Pro Tyr Val Ala Leu Leu Ile Ala Met Leu Phe Phe Ile  
1370 1375 1380

Tyr Ala Val Ile Gly Met Gln Met Phe Gly Lys Val Ala Met Arg  
1385 1390 1395

Asp Asn Asn Gln Ile Asn Arg Asn Asn Asn Phe Gln Thr Phe Pro  
1400 1405 1410

Gln Ala Val Leu Leu Leu Phe Arg Cys Ala Thr Gly Glu Ala Trp  
1415 1420 1425

Gln Glu Ile Met Leu Ala Cys Leu Pro Gly Lys Leu Cys Asp Pro  
1430 1435 1440

Glu Ser' Asp Tyr Asn Pro Gly Glu Glu Tyr Thr Cys Gly Ser Asn  
1445 1450 1455

Phe Ala Ile Val Tyr Phe Ile Ser Phe Tyr Met Leu Cys Ala Phe  
1460 1465 1470

Leu Ile Ile Asn Leu Phe Val Ala Val Ile Met Asp Asn Phe Asp  
1475 1480 1485

Tyr Leu Thr Arg Asp Trp Ser Ile Leu Gly Pro His His Leu Asp  
1490 1495 1500

Glu Phe Lys Arg Ile Trp Ser Glu Tyr Asp Pro Glu Ala Lys Gly  
1505 1510 1515

Arg Ile Lys His Leu Asp Val Val Thr Leu Leu Arg Arg Ile Gln  
1520 1525 1530

Pro Pro Leu Gly Phe Gly Lys Leu Cys Pro His Arg Val Ala Cys  
1535 1540 1545

Lys Arg Leu Val Ala Met Asn Met Pro Leu Asn Ser Asp Gly Thr  
1550 1555 1560

Val Met Phe Asn Ala Thr Leu Phe Ala Leu Val Arg Thr Ala Leu  
1565 1570 1575

Lys Ile Lys Thr Glu Gly Asn Leu Glu Gln Ala Asn Glu Glu Leu  
1580 1585 1590

Arg Ala Val Ile Lys Lys Ile Trp Lys Lys Thr Ser Met Lys Leu  
1595 1600 1605

Leu Asp Gln Val Val Pro Pro Ala Gly Asp Asp Glu Val Thr Val  
1610 1615 1620

Gly Lys Phe Tyr Ala Thr Phe Leu Ile Gln Asp Tyr Phe Arg Lys  
1625 1630 1635

Phe Lys Lys Arg Lys Glu Gln Gly Leu Val Gly Lys Tyr Pro Ala  
1640 1645 1650

Lys Asn Thr Thr Ile Ala Leu Gln Ala Gly Leu Arg Thr Leu His  
1655 1660 1665

Asp Ile Gly Pro Glu Ile Arg Arg Ala Ile Ser Cys Asp Leu Gln  
1670 1675 1680

Asp Asp Glu Pro Glu Glu Thr Lys Arg Glu Glu Glu Asp Asp Val  
1685 1690 1695

Phe Lys Arg Asn Gly Ala Leu Leu Gly Asn His Val Asn His Val  
1700 1705 1710

Asn Ser Asp Arg Arg Asp Ser Leu Gln Gln Thr Asn Thr Thr His  
1715 1720 1725

Arg Pro Leu His Val Gln Arg Pro Ser Ile Pro Pro Ala Ser Asp  
1730 1735 1740

Thr Glu Lys Pro Leu Phe Pro Pro Ala Gly Asn Ser Val Cys His  
1745 1750 1755

Asn His His Asn His Asn Ser Ile Gly Lys Gln Val Pro Thr Ser  
1760 1765 1770

Thr Asn Ala Asn Leu Asn Asn Ala Asn Met Ser Lys Ala Ala His

1775                    1780                    1785

Gly Lys Arg Pro Ser Ile Gly Asn Leu Glu His Val Ser Glu Asn  
1790                    1795                    1800

Gly His His Ser Ser His Lys His Asp Arg Glu Pro Gln Arg Arg  
1805                    1810                    1815

Ser Ser Val Lys Arg Thr Arg Tyr Tyr Glu Thr Tyr Ile Arg Ser  
1820                    1825                    1830

Asp Ser Gly Asp Glu Gln Leu Pro Thr Ile Cys Arg Glu Asp Pro  
1835                    1840                    1845

Glu Ile His Gly Tyr Phe Arg Asp Pro His Cys Leu Gly Glu Gln  
1850                    1855                    1860

Glu Tyr Phe Ser Ser Glu Glu Cys Tyr Glu Asp Asp Ser Ser Pro  
1865                    1870                    1875

Thr Trp Ser Arg Gln Asn Tyr Gly Tyr Tyr Ser Arg Tyr Pro Gly  
1880                    1885                    1890

Arg Asn Ile Asp Ser Glu Arg Pro Arg Gly Tyr His His Pro Gln  
1895                    1900                    1905

Gly Phe Leu Glu Asp Asp Ser Pro Val Cys Tyr Asp Ser Arg  
1910                    1915                    1920

Arg Ser Pro Arg Arg Arg Leu Leu Pro Pro Thr Pro Ala Ser His  
1925                    1930                    1935

Arg Arg Ser Ser Phe Asn Phe Glu Cys Leu Arg Arg Gln Ser Ser  
1940                    1945                    1950

Gln Glu Glu Val Pro Ser Ser Pro Ile Phe Pro His Arg Thr Ala  
1955                    1960                    1965

Leu Pro Leu His Leu Met Gln Gln Gln Ile Met Ala Val Ala Gly  
1970                    1975                    1980

Leu Asp Ser Ser Lys Ala Gln Lys Tyr Ser Pro Ser His Ser Thr  
1985                    1990                    1995

Arg Ser Trp Ala Thr Pro Pro Ala Thr Pro Pro Tyr Arg Asp Trp  
2000 2005 2010

Thr Pro Cys Tyr Thr Pro Leu Ile Gln Val Glu Gln Ser Glu Ala  
2015 2020 2025

Leu Asp Gln Val Asn Gly Ser Leu Pro Ser Leu His Arg Ser Ser  
2030 2035 2040

Trp Tyr Thr Asp Glu Pro Asp Ile Ser Tyr Arg Thr Phe Thr Pro  
2045 2050 2055

Ala Ser Leu Thr Val Pro Ser Ser Phe Arg Asn Lys Asn Ser Asp  
2060 2065 2070

Lys Gln Arg Ser Ala Asp Ser Leu Val Glu Ala Val Leu Ile Ser  
2075 2080 2085

Glu Gly Leu Gly Arg Tyr Ala Arg Asp Pro Lys Phe Val Ser Ala  
2090 2095 2100

Thr Lys His Glu Ile Ala Asp Ala Cys Asp Leu Thr Ile Asp Glu  
2105 2110 2115

Met Glu Ser Ala Ala Ser Thr Leu Leu Asn Gly Asn Val Arg Pro  
2120 2125 2130

Arg Ala Asn Gly Asp Val Gly Pro Leu Ser His Arg Gln Asp Tyr  
2135 2140 2145

Glu Leu Gln Asp Phe Gly Pro Gly Tyr Ser Asp Glu Glu Pro Asp  
2150 2155 2160

Pro Gly Arg Asp Glu Glu Asp Leu Ala Asp Glu Met Ile Cys Ile  
2165 2170 2175

Thr Thr Leu  
2180

<210> 289  
<211> 4187  
<212> DNA

<213> human organism

<400> 289  
aactcccgcc tcgggacgcc tcgggtcgg gctccggctg cggctgctgc tgccgcgcc 60  
gcgctccggc gcgtccgcct cctgtgcgg ccgcggagca gtctgcggcc cgccgtgcgc 120  
cctcagctcc ttttcctgag cccgcgcga tggagctgc gcggggatcc cccggccagac 180  
ccgcgggtt gcctctgctc agcgtcctgc tgctgcgcgt gctggcggc acccagacag 240  
ccattgtctt catcaaggcag cgcgcctccc aggatgcact gcaggggcgc cggcgctgc 300  
ttcgctgtga gggtgaggct cccggcccg tacatgtgta ctggctgctc gatggggccc 360  
ctgtccagga cacggagcgg cgtttcgcggc agggcagcag cctgagcttt gcagctgtgg 420  
accggctgca ggactctggc accttcagggt gtgtggctcg ggatgatgtc actggagaag 480  
aagccgcag tgccaacgcc tccttcaaca tcaaattggat tgaggcagggt cctgtggcc 540  
tgaagcatcc agcctcgaa gctgagatcc agccacagac ccaggtcaca cttcggtgcc 600  
acattgatgg gcaccctcgg cccacacctacc aatggttccg agatgggacc cccctttctg 660  
atggtcagag caaccacaca gtcagcagca aggagcggaa cctgacgctc cggccagctg 720  
gtcctgagca tagtggctg tattcctgct gcgcacacag tgctttggc caggcttgca 780  
gcagccagaa ctaccccttg agcattgctg atgaaagctt tgccagggtg gtgctggcac 840  
cccaggacgt ggttagtagcg aggtatgagg aggccatgtt ccattgccag ttctcagccc 900  
agccacccccc gagcctgcag tggcttttg aggtgagac tcccatcaact aaccgcagtc 960  
gccccccaca cctccgcaga gccacagtgt ttgccaacgg gtctctgctg ctgacccagg 1020  
tcggccacg caatgcaggg atctaccgct gcattggcca gggcagagg ggcccaccca 1080  
tcatcctgga agccacactt cacctagcag agattgaaga catgccgcta tttgagccac 1140  
gggtgtttac agctggcagc gaggagcgtg tgacctgcct tcccccaag ggtctgccag 1200  
agcccagcgt gtgggtggag cacgcggag tccggctgcc caccatggc agggtctacc 1260  
agaaggccca cgagctggtg ttggccaata ttgctgaaag tgatgctggt gtctacacct 1320  
gccacgcggc caacctggct ggtcagcggc gacaggatgt caacatcaact gtggccactg 1380  
tgccctcctg gctgaagaag ccccaagaca gccagctgga ggagggcaaa cccggctact 1440  
tggattgcct gacccaggcc acacaaaaac ctacagttgt ctggcacaga aaccagatgc 1500  
tcatctcaga ggactcacgg ttcgagggtct tcaagaatgg gaccttgcgc atcaacagcg 1560  
tggaggtgta tgatggaca tggtaaccgtt gtatgagcag caccggcagcc ggcagcatcg 1620

aggcgcaagc ccgtgtccaa gtgctggaaa agctcaagtt cacaccacca ccccagccac 1680  
agcagtgcac ggagtttgcac aaggaggcca cggtgccttg ttcagccaca ggccgagaga 1740  
agcccaactat taagtggaa cgggcagatg ggagcagcct cccagagtgg gtgacagaca 1800  
acgctgggac cctgcatttt gcccgggtga ctcgagatga cgctggcaac tacacttgca 1860  
ttgcctccaa cgggcccgcag ggccagattc gtgcccattgt ccagctcact gtggcagttt 1920  
ttatcacctt caaagtggaa ccagagcgta cgactgtgta ccagggccac acagccctac 1980  
tgcaagtgcga ggcccagggg gaccccaagc cgctgattca gtggaaaggc aaggaccgca 2040  
tcctggaccc caccaagctg ggacccagga tgcacatctt ccagaatggc tccctgggtga 2100  
tccatgacgt ggccccctgag gactcaggcc gctacacctg cattgcaggc aacagctgca 2160  
acatcaagca cacggaggcc cccctctatg tcgtggacaa gcctgtgccg gaggagtcgg 2220  
agggccctgg cagccctccc ccctacaaga tgatccagac cattgggttg tcgggtgggtg 2280  
ccgctgtggc ctacatcatt gccgtgctgg gcctcatgtt ctactgcaag aagcgctgca 2340  
aagccaagcg gctgcagaag cagcccgagg gcgaggagcc agagatggaa tgcctcaacg 2400  
gagggccctt gcagaacggg cagccctcag cagagatcca agaagaagtg gccttgcacca 2460  
gcttgggctc cggcccccgcg gccaccaaca aacgccacag cacaagtgt aagatgcact 2520  
tcccacggtc tagcctgcag cccatcacca cgctggggaa gagtgagttt ggggagggtgt 2580  
tcctggcaaa ggctcagggc ttggaggagg gagtggcaga gaccctggta cttgtgaaga 2640  
gcctgcagac gaaggatgag cagcagcagc tggacttccg gagggagttt gagatgtttt 2700  
ggaagctgaa ccacgccaac gtggtgccgc tcctggggct gtgcccggag gctgagcccc 2760  
actacatggt gctggaatat gtggatctgg gagacctcaa gcagttcctg aggatttcca 2820  
agagcaagga taaaaattt aagtcacagc ccctcagcac caagcagaag gtggccctat 2880  
gcacccaggt agccctggc atggagcacc tgtccaacaa ccgttttgt cataaggact 2940  
tggctgcgcg taactgcctg gtcagtgcac agagacaagt gaaggtgtct gcctgggccc 3000  
tcagcaagga tgtgtacaac agtgagttt accacttccg ccaggcctgg gtgccgctgc 3060  
gctggatgtc ccccgaggcc atcctggagg gtgacttctc taccaagtct gatgtctggg 3120  
ccttcggtgt gctgatgtgg gaagtgttta cacatggaga gatgccccat ggtggcagg 3180  
cagatgtga agtactggca gatttgcagg ctgggaaggc tagacttcct cagcccgagg 3240  
gctgcccttc caaactctat cggctgatgc agcgctgctg gcgcctcagc cccaaggacc 3300  
ggccctcctt cagttagatt gccagcgccc tgggagacag caccgtggac agcaagccgt 3360

gaggagggag cccgctcagg atggcctggg caggggagga catctctaga ggaaagctca	3420
cacatgtatg ggcaagatcc ctgtcctcct gggccctgag gtgccttagt gcaacaggca	3480
ttgctgaggt ctgagcaggg cctggccttt ctcctcttc ctcaccctca tccttggga	3540
ggctgacttg gacccaaact gggcgactag ggcttgagc tggcagttt cccctgccac	3600
ctcttcctct atcagggaca gtgtgggtgc cacagtaac cccaatttct ggcttcaac	3660
ttctccctt gaccgggtcc aactctgcca ctcatctgcc aactttgcct ggggagggct	3720
aggcttggga tgagctgggt ttgtgggag ttcctaata ttctcaagtt ctgggcacac	3780
agggttaatg agtctcttgc ccactggtcc acttgggggt ctagaccagg attatagagg	3840
acacagcaag tgagtccctcc ccactctggg cttgtgcaca ctgaccaga cccacgtctt	3900
ccccaccctt ctctccttcc ctcatcctaa gtgcctggca gatgaaggag tttcaggag	3960
cttttgcacac tatataaacc gcccttttg tatgcaccac gggcggcttt tatatgtaat	4020
tgcagcgtgg ggtgggtggg catgggaggt aggggtgggc cctggagatg aggaggggtgg	4080
gccatcctta ccccacactt ttattgttgt cgtttttgtt ttgtttgtt ttttgttt	4140
tgttttgtt tttacactcg ctgctctcaa taaataagcc tttttta	4187

<210> 290  
 <211> 1070  
 <212> PRT  
 <213> human organism

<400> 290

Met Gly Ala Ala Arg Gly Ser Pro Ala Arg Pro Arg Arg Leu Pro Leu			
1	5	10	15

Leu Ser Val Leu Leu Pro Leu Leu Gly Gly Thr Gln Thr Ala Ile			
20	25	30	

Val Phe Ile Lys Gln Pro Ser Ser Gln Asp Ala Leu Gln Gly Arg Arg			
35	40	45	

Ala Leu Leu Arg Cys Glu Val Glu Ala Pro Gly Pro Val His Val Tyr			
50	55	60	

Trp Leu Leu Asp Gly Ala Pro Val Gln Asp Thr Glu Arg Arg Phe Ala			
65	70	75	80

Gln Gly Ser Ser Leu Ser Phe Ala Ala Val Asp Arg Leu Gln Asp Ser  
85 90 95

Gly Thr Phe Gln Cys Val Ala Arg Asp Asp Val Thr Gly Glu Glu Ala  
100 105 110

Arg Ser Ala Asn Ala Ser Phe Asn Ile Lys Trp Ile Glu Ala Gly Pro  
115 120 125

Val Val Leu Lys His Pro Ala Ser Glu Ala Glu Ile Gln Pro Gln Thr  
130 135 140

Gln Val Thr Leu Arg Cys His Ile Asp Gly His Pro Arg Pro Thr Tyr  
145 150 155 160

Gln Trp Phe Arg Asp Gly Thr Pro Leu Ser Asp Gly Gln Ser Asn His  
165 170 175

Thr Val Ser Ser Lys Glu Arg Asn Leu Thr Leu Arg Pro Ala Gly Pro  
180 185 190

Glu His Ser Gly Leu Tyr Ser Cys Cys Ala His Ser Ala Phe Gly Gln  
195 200 205

Ala Cys Ser Ser Gln Asn Phe Thr Leu Ser Ile Ala Asp Glu Ser Phe  
210 215 220

Ala Arg Val Val Leu Ala Pro Gln Asp Val Val Val Ala Arg Tyr Glu  
225 230 235 240

Glu Ala Met Phe His Cys Gln Phe Ser Ala Gln Pro Pro Pro Ser Leu  
245 250 255

Gln Trp Leu Phe Glu Asp Glu Thr Pro Ile Thr Asn Arg Ser Arg Pro  
260 265 270

Pro His Leu Arg Arg Ala Thr Val Phe Ala Asn Gly Ser Leu Leu Leu  
275 280 285

Thr Gln Val Arg Pro Arg Asn Ala Gly Ile Tyr Arg Cys Ile Gly Gln  
290 295 300

Gly Gln Arg Gly Pro Pro Ile Ile Leu Glu Ala Thr Leu His Leu Ala

305	310	315	320	
Glu Ile Glu Asp Met Pro Leu Phe Glu Pro Arg Val Phe Thr Ala Gly				
	325	330	335	
Ser Glu Glu Arg Val Thr Cys Leu Pro Pro Lys Gly Leu Pro Glu Pro				
	340	345	350	
Ser Val Trp Trp Glu His Ala Gly Val Arg Leu Pro Thr His Gly Arg				
	355	360	365	
Val Tyr Gln Lys Gly His Glu Leu Val Leu Ala Asn Ile Ala Glu Ser				
	370	375	380	
Asp Ala Gly Val Tyr Thr Cys His Ala Ala Asn Leu Ala Gly Gln Arg				
	385	390	395	400
Arg Gln Asp Val Asn Ile Thr Val Ala Thr Val Pro Ser Trp Leu Lys				
	405	410	415	
Lys Pro Gln Asp Ser Gln Leu Glu Glu Gly Lys Pro Gly Tyr Leu Asp				
	420	425	430	
Cys Leu Thr Gln Ala Thr Pro Lys Pro Thr Val Val Trp Tyr Arg Asn				
	435	440	445	
Gln Met Leu Ile Ser Glu Asp Ser Arg Phe Glu Val Phe Lys Asn Gly				
	450	455	460	
Thr Leu Arg Ile Asn Ser Val Glu Val Tyr Asp Gly Thr Trp Tyr Arg				
	465	470	475	480
Cys Met Ser Ser Thr Pro Ala Gly Ser Ile Glu Ala Gln Ala Arg Val				
	485	490	495	
Gln Val Leu Glu Lys Leu Lys Phe Thr Pro Pro Pro Gln Pro Gln Gln				
	500	505	510	
Cys Met Glu Phe Asp Lys Glu Ala Thr Val Pro Cys Ser Ala Thr Gly				
	515	520	525	
Arg Glu Lys Pro Thr Ile Lys Trp Glu Arg Ala Asp Gly Ser Ser Leu				
	530	535	540	

Pro Glu Trp Val Thr Asp Asn Ala Gly Thr Leu His Phe Ala Arg Val  
545 550 555 560

Thr Arg Asp Asp Ala Gly Asn Tyr Thr Cys Ile Ala Ser Asn Gly Pro  
565 570 575

Gln Gly Gln Ile Arg Ala His Val Gln Leu Thr Val Ala Val Phe Ile  
580 585 590

Thr Phe Lys Val Glu Pro Glu Arg Thr Thr Val Tyr Gln Gly His Thr  
595 600 605

Ala Leu Leu Gln Cys Glu Ala Gln Gly Asp Pro Lys Pro Leu Ile Gln  
610 615 620

Trp Lys Gly Lys Asp Arg Ile Leu Asp Pro Thr Lys Leu Gly Pro Arg  
625 630 635 640

Met His Ile Phe Gln Asn Gly Ser Leu Val Ile His Asp Val Ala Pro  
645 650 655

Glu Asp Ser Gly Arg Tyr Thr Cys Ile Ala Gly Asn Ser Cys Asn Ile  
660 665 670

Lys His Thr Glu Ala Pro Leu Tyr Val Val Asp Lys Pro Val Pro Glu  
675 680 685

Glu Ser Glu Gly Pro Gly Ser Pro Pro Pro Tyr Lys Met Ile Gln Thr  
690 695 700

Ile Gly Leu Ser Val Gly Ala Ala Val Ala Tyr Ile Ile Ala Val Leu  
705 710 715 720

Gly Leu Met Phe Tyr Cys Lys Lys Arg Cys Lys Ala Lys Arg Leu Gln  
725 730 735

Lys Gln Pro Glu Gly Glu Pro Glu Met Glu Cys Leu Asn Gly Gly  
740 745 750

Pro Leu Gln Asn Gly Gln Pro Ser Ala Glu Ile Gln Glu Glu Val Ala  
755 760 765

Leu Thr Ser Leu Gly Ser Gly Pro Ala Ala Thr Asn Lys Arg His Ser  
770                    775                    780

Thr Ser Asp Lys Met His Phe Pro Arg Ser Ser Leu Gln Pro Ile Thr  
785                    790                    795                    800

Thr Leu Gly Lys Ser Glu Phe Gly Glu Val Phe Leu Ala Lys Ala Gln  
805                    810                    815

Gly Leu Glu Glu Gly Val Ala Glu Thr Leu Val Leu Val Lys Ser Leu  
820                    825                    830

Gln Thr Lys Asp Glu Gln Gln Leu Asp Phe Arg Arg Glu Leu Glu  
835                    840                    845

Met Phe Gly Lys Leu Asn His Ala Asn Val Val Arg Leu Leu Gly Leu  
850                    855                    860

Cys Arg Glu Ala Glu Pro His Tyr Met Val Leu Glu Tyr Val Asp Leu  
865                    870                    875                    880

Gly Asp Leu Lys Gln Phe Leu Arg Ile Ser Lys Ser Lys Asp Glu Lys  
885                    890                    895

Leu Lys Ser Gln Pro Leu Ser Thr Lys Gln Lys Val Ala Leu Cys Thr  
900                    905                    910

Gln Val Ala Leu Gly Met Glu His Leu Ser Asn Asn Arg Phe Val His  
915                    920                    925

Lys Asp Leu Ala Ala Arg Asn Cys Leu Val Ser Ala Gln Arg Gln Val  
930                    935                    940

Lys Val Ser Ala Leu Gly Leu Ser Lys Asp Val Tyr Asn Ser Glu Tyr  
945                    950                    955                    960

Tyr His Phe Arg Gln Ala Trp Val Pro Leu Arg Trp Met Ser Pro Glu  
965                    970                    975

Ala Ile Leu Glu Gly Asp Phe Ser Thr Lys Ser Asp Val Trp Ala Phe  
980                    985                    990

Gly Val Leu Met Trp Glu Val Phe Thr His Gly Glu Met Pro His Gly  
995 1000 1005

Gly Gln Ala Asp Asp Glu Val Leu Ala Asp Leu Gln Ala Gly Lys  
1010 1015 1020

Ala Arg Leu Pro Gln Pro Glu Gly Cys Pro Ser Lys Leu Tyr Arg  
1025 1030 1035

Leu Met Gln Arg Cys Trp Ala Leu Ser Pro Lys Asp Arg Pro Ser  
1040 1045 1050

Phe Ser Glu Ile Ala Ser Ala Leu Gly Asp Ser Thr Val Asp Ser  
1055 1060 1065

Lys Pro  
1070

<210> 291  
<211> 3150  
<212> DNA  
<213> human organism

<400> 291  
atggggagcc ggacgccaga gtcccccttc cacgccgtgc agctgcgctg gggcccccgg 60  
cgccgaccggc cgctssgtcc gctgctgttg ctgctssgtc cgccgccacc cagggtcggg 120  
ggcttcaact tagacgcgga ggccccagca gtactctcggt ggccccccggg ctccttcttc 180  
ggattctcag tggagttta ccggccggga acagacgggg tcagtgtgct ggtgggagca 240  
cccaaggcta ataccagcca gccaggagtg ctgcagggtg gtgctgtcta cctctgtcct 300  
tgggtgcca gccccacaca gtgcacccccc attgaatttg acagcaaagg ctctcggctc 360  
ctggagtcct cactgtccag ctcagaggga gaggagcctg tggagtacaa gtccttgcag 420  
tggttcgggg caacagttcg agcccatggc tcctccatct tggcatgcgc tccactgtac 480  
agctggcgca cagagaagga gccactgagc gaccccggtgg gcacctgcta cctctccaca 540  
gataacttca cccgaattct ggagtatgca ccctggcgct cagatttcag ctgggcagca 600  
ggacagggtt actgccaagg aggcttcagt gccgagttca ccaagactgg ccgtgtggtt 660  
ttaggtggac caggaagcta tttctggcaa ggccagatcc tgtctgccac tcaggagcag 720  
attgcagaat cttattaccc cgagtacctg atcaacctgg ttcaggggca gctgcagact 780  
cgccaggcca gttccatcta tcatgacagc tacctaggat actctgtggc tggtggtaa 840

ttcagtggtg atgacacaga agactttgtt gctggtgtgc ccaaaggaa cctcacttac	900
ggctatgtca ccatacctaa tggctcagac attcgatccc tctacaactt ctcagggaa	960
cagatggcct cctactttgg ctatgcagtg gccgccacag acgtcaatgg ggacgggctg	1020
gatgacttgc tgggtggggc acccctgctc atggatcgga cccctgacgg gcggcctcag	1080
gaggtgggca gggctacgt ctacctgcag cacccagccg gcatagagcc cacgcccacc	1140
cttaccctca ctggccatga tgagttggc cgatttggca gtccttgcac cccccctgggg	1200
gacctggacc aggatggcta caatgatgtg gccatcgggg ctcccttgg tggggagacc	1260
cagcagggag tagtgtttgtt atttcctggg ggcccaggag ggctgggctc taagccttcc	1320
caggttctgc agcccctgtg ggcagccagc cacacccag acttctttgg ctctgccctt	1380
cgaggaggcc gagacctgga tggcaatggc tatcctgatc tgatttggg gtccttgggt	1440
gtggacaagg ctgtggtata cagggccgc cccatcgtgt ccgctagtgc ctccctcacc	1500
atcttccccg ccatgttcaa cccagaggag cggagctgca gcttagaggg gaaccctgtg	1560
gcctgcatca accttagctt ctgcctcaat gcttctggaa aacacgttgc tgactccatt	1620
ggttcacag tggaacttca gctggactgg cagaagcaga agggaggggt acggcggca	1680
ctgttcctgg cctccaggca ggcaaccctg acccagaccc tgctcatcca gaatggggct	1740
cgagaggatt gcagagagat gaagatctac ctcaggaacg agtcagaatt tcgagacaaa	1800
ctctcgccga ttcacatcgc tctcaacttc tccttggacc cccaagcccc agtggacagc	1860
cacggcctca ggccagccct acattatcag agcaagagcc ggatagagga caaggctcag	1920
atcttgctgg actgtggaga agacaacatc tgtgtgcctg acctgcagct ggaagtgttt	1980
ggggagcaga accatgtgta cctgggtgac aagaatgccc tgaacctcac tttccatgcc	2040
cagaatgtgg gtgaggggtgg cgcctatgag gctgagcttc gggtcaccgc ccctccagag	2100
gctgagtaact caggactcgt cagacaccca gggaaacttct ccagcctgag ctgtgactac	2160
tttgcgtga accagagccg cctgctggtg tgtgacctgg gcaacccat gaaggcagga	2220
gccagtctgt ggggtggcct tcggtttaca gtcctcatac tccgggacac taagaaaacc	2280
atccagtttgc acttccagat cctcagcaag aatctcaaca actcgcaaag cgacgtggtt	2340
tcctttcggc tctccgtgga ggctcaggcc caggtcacccc tgaacgggtt ctccaagcct	2400
gaggcagtgc tattcccaagt aagcgactgg catccccgag accagcctca gaaggaggag	2460
gacctgggac ctgctgtcca ccatgtctat gagctcatca accaaggccc cagctccatt	2520

agccagggtg tgctggaact cagctgtccc caggctctgg aaggtcagca gctcctatat	2580
gtgaccagag ttacgggact caactgcacc accaatcacc ccattaaccc aaagggcctg	2640
gagttggatc ccgagggttc cctgcaccac cagcaaaaac gggaaagctcc aagccgcagc	2700
tctgcttcct cgggacctca gatcctgaaa tgcccgagg ctgagtgtt caggctgcgc	2760
tgtgagctcg ggccccgtca ccaacaagag agccaaagtc tgcagttgca tttccgagtc	2820
tggccaaga ctttcttgca gcgggagcac cagccattta gcctgcagtg tgaggctgtg	2880
tacaaagccc tgaagatgcc ctaccgaatc ctgcctcgcc agctgccccaaaagagcgt	2940
caggtggcca cagctgtgca atggaccaag gcagaaggca gctatggcgt cccactgtgg	3000
atcatcatcc tagccatcct gttggcctc ctgctcctag gtctactcat ctacatcctc	3060
tacaagcttg gattctcaa acgctccctc ccataatggca ccgccatggaa aaaagctcag	3120
ctcaaggcctc cagccaccc tcgtgcctga	3150

<210> 292

<211> 1049

<212> PRT

<213> human organism

<400> 292

Met	Gly	Ser	Arg	Thr	Pro	Glu	Ser	Pro	Leu	His	Ala	Val	Gln	Leu	Arg
1															15

Trp	Gly	Pro	Arg	Arg	Arg	Pro	Pro	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu
20															30

Leu	Pro	Pro	Pro	Arg	Val	Gly	Gly	Phe	Asn	Leu	Asp	Ala	Glu	Ala
35														
					40					45				

Pro	Ala	Val	Leu	Ser	Gly	Pro	Pro	Gly	Ser	Phe	Phe	Gly	Phe	Ser	Val
50															60

Glu	Phe	Tyr	Arg	Pro	Gly	Thr	Asp	Gly	Val	Ser	Val	Leu	Val	Gly	Ala
65															80
					70				75						

Pro	Lys	Ala	Asn	Thr	Ser	Gln	Pro	Gly	Val	Leu	Gln	Gly	Gly	Ala	Val
															95
									85		90				

Tyr	Leu	Cys	Pro	Trp	Gly	Ala	Ser	Pro	Thr	Gln	Cys	Thr	Pro	Ile	Glu
															110
									100		105				

Phe Asp Ser Lys Gly Ser Arg Leu Leu Glu Ser Ser Leu Ser Ser Ser  
115 120 125

Glu Gly Glu Glu Pro Val Glu Tyr Lys Ser Leu Gln Trp Phe Gly Ala  
130 135 140

Thr Val Arg Ala His Gly Ser Ser Ile Leu Ala Cys Ala Pro Leu Tyr  
145 150 155 160

Ser Trp Arg Thr Glu Lys Glu Pro Leu Ser Asp Pro Val Gly Thr Cys  
165 170 175

Tyr Leu Ser Thr Asp Asn Phe Thr Arg Ile Leu Glu Tyr Ala Pro Cys  
180 185 190

Arg Ser Asp Phe Ser Trp Ala Ala Gly Gln Gly Tyr Cys Gln Gly Gly  
195 200 205

Phe Ser Ala Glu Phe Thr Lys Thr Gly Arg Val Val Leu Gly Gly Pro  
210 215 220

Gly Ser Tyr Phe Trp Gln Gly Gln Ile Leu Ser Ala Thr Gln Glu Gln  
225 230 235 240

Ile Ala Glu Ser Tyr Tyr Pro Glu Tyr Leu Ile Asn Leu Val Gln Gly  
245 250 255

Gln Leu Gln Thr Arg Gln Ala Ser Ser Ile Tyr Asp Asp Ser Tyr Leu  
260 265 270

Gly Tyr Ser Val Ala Val Gly Glu Phe Ser Gly Asp Asp Thr Glu Asp  
275 280 285

Phe Val Ala Gly Val Pro Lys Gly Asn Leu Thr Tyr Gly Tyr Val Thr  
290 295 300

Ile Leu Asn Gly Ser Asp Ile Arg Ser Leu Tyr Asn Phe Ser Gly Glu  
305 310 315 320

Gln Met Ala Ser Tyr Phe Gly Tyr Ala Val Ala Ala Thr Asp Val Asn  
325 330 335

Gly Asp Gly Leu Asp Asp Leu Leu Val Gly Ala Pro Leu Leu Met Asp  
340 345 350

Arg Thr Pro Asp Gly Arg Pro Gln Glu Val Gly Arg Val Tyr Val Tyr  
355 360 365

Leu Gln His Pro Ala Gly Ile Glu Pro Thr Pro Thr Leu Thr Leu Thr  
370 375 380

Gly His Asp Glu Phe Gly Arg Phe Gly Ser Ser Leu Thr Pro Leu Gly  
385 390 395 400

Asp Leu Asp Gln Asp Gly Tyr Asn Asp Val Ala Ile Gly Ala Pro Phe  
405 410 415

Gly Gly Glu Thr Gln Gln Gly Val Val Phe Val Phe Pro Gly Gly Pro  
420 425 430

Gly Gly Leu Gly Ser Lys Pro Ser Gln Val Leu Gln Pro Leu Trp Ala  
435 440 445

Ala Ser His Thr Pro Asp Phe Phe Gly Ser Ala Leu Arg Gly Gly Arg  
450 455 460

Asp Leu Asp Gly Asn Gly Tyr Pro Asp Leu Ile Val Gly Ser Phe Gly  
465 470 475 480

Val Asp Lys Ala Val Val Tyr Arg Gly Arg Pro Ile Val Ser Ala Ser  
485 490 495

Ala Ser Leu Thr Ile Phe Pro Ala Met Phe Asn Pro Glu Glu Arg Ser  
500 505 510

Cys Ser Leu Glu Gly Asn Pro Val Ala Cys Ile Asn Leu Ser Phe Cys  
515 520 525

Leu Asn Ala Ser Gly Lys His Val Ala Asp Ser Ile Gly Phe Thr Val  
530 535 540

Glu Leu Gln Leu Asp Trp Gln Lys Gln Lys Gly Gly Val Arg Arg Ala  
545 550 555 560

Leu Phe Leu Ala Ser Arg Gln Ala Thr Leu Thr Gln Thr Leu Leu Ile

565

570

575

Gln Asn Gly Ala Arg Glu Asp Cys Arg Glu Met Lys Ile Tyr Leu Arg  
580 585 590

Asn Glu Ser Glu Phe Arg Asp Lys Leu Ser Pro Ile His Ile Ala Leu  
595 600 605

Asn Phe Ser Leu Asp Pro Gln Ala Pro Val Asp Ser His Gly Leu Arg  
610 615 620

Pro Ala Leu His Tyr Gln Ser Lys Ser Arg Ile Glu Asp Lys Ala Gln  
625 630 635 640

Ile Leu Leu Asp Cys Gly Glu Asp Asn Ile Cys Val Pro Asp Leu Gln  
645 650 655

Leu Glu Val Phe Gly Glu Gln Asn His Val Tyr Leu Gly Asp Lys Asn  
660 665 670

Ala Leu Asn Leu Thr Phe His Ala Gln Asn Val Gly Glu Gly Gly Ala  
675 680 685

Tyr Glu Ala Glu Leu Arg Val Thr Ala Pro Pro Glu Ala Glu Tyr Ser  
690 695 700

Gly Leu Val Arg His Pro Gly Asn Phe Ser Ser Leu Ser Cys Asp Tyr  
705 710 715 720

Phe Ala Val Asn Gln Ser Arg Leu Leu Val Cys Asp Leu Gly Asn Pro  
725 730 735

Met Lys Ala Gly Ala Ser Leu Trp Gly Gly Leu Arg Phe Thr Val Pro  
740 745 750

His Leu Arg Asp Thr Lys Lys Thr Ile Gln Phe Asp Phe Gln Ile Leu  
755 760 765

Ser Lys Asn Leu Asn Asn Ser Gln Ser Asp Val Val Ser Phe Arg Leu  
770 775 780

Ser Val Glu Ala Gln Ala Gln Val Thr Leu Asn Gly Val Ser Lys Pro  
785 790 795 800

Glu Ala Val Leu Phe Pro Val Ser Asp Trp His Pro Arg Asp Gln Pro  
805 810 815

Gln Lys Glu Glu Asp Leu Gly Pro Ala Val His His Val Tyr Glu Leu  
820 825 830

Ile Asn Gln Gly Pro Ser Ser Ile Ser Gln Gly Val Leu Glu Leu Ser  
835 840 845

Cys Pro Gln Ala Leu Glu Gly Gln Gln Leu Leu Tyr Val Thr Arg Val  
850 855 860

Thr Gly Leu Asn Cys Thr Thr Asn His Pro Ile Asn Pro Lys Gly Leu  
865 870 875 880

Glu Leu Asp Pro Glu Gly Ser Leu His His Gln Gln Lys Arg Glu Ala  
885 890 895

Pro Ser Arg Ser Ser Ala Ser Ser Gly Pro Gln Ile Leu Lys Cys Pro  
900 905 910

Glu Ala Glu Cys Phe Arg Leu Arg Cys Glu Leu Gly Pro Leu His Gln  
915 920 925

Gln Glu Ser Gln Ser Leu Gln Leu His Phe Arg Val Trp Ala Lys Thr  
930 935 940

Phe Leu Gln Arg Glu His Gln Pro Phe Ser Leu Gln Cys Glu Ala Val  
945 950 955 960

Tyr Lys Ala Leu Lys Met Pro Tyr Arg Ile Leu Pro Arg Gln Leu Pro  
965 970 975

Gln Lys Glu Arg Gln Val Ala Thr Ala Val Gln Trp Thr Lys Ala Glu  
980 985 990

Gly Ser Tyr Gly Val Pro Leu Trp Ile Ile Ile Leu Ala Ile Leu Phe  
995 1000 1005

Gly Leu Leu Leu Leu Gly Leu Leu Ile Tyr Ile Leu Tyr Lys Leu  
1010 1015 1020

Gly Phe Phe Lys Arg Ser Leu Pro Tyr Gly Thr Ala Met Glu Lys  
1025 1030 1035

Ala Gln Leu Lys Pro Pro Ala Thr Ser Asp Ala  
1040 1045

<210> 293  
<211> 1373  
<212> DNA  
<213> human organism

<400> 293  
gggggcgccc cgcgctgacc ctccctgggc accgctgggg acgatggcgc tgctgcctt 60  
gctgctggtc gtggccctac cgccgggtgtg gacagacgcc aacctgactg cgagacaacg 120  
agatccagag gactcccagc gaacggacga gggtgacaat agagtgtggt gtcatgtttg 180  
tgagagagaa aacactttcg agtgcagaa cccaaggagg tgcaaattgga cagagccata 240  
ctgcgttata gcggccgtga aaatatttcc acgtttttc atggttgcga agcagtgctc 300  
cgctgggtgt gcagcgatgg agagacccaa gccagaggag aagcggttcc tcctggaaga 360  
gcccatgccc ttcttttacc tcaagtgttg taaaattcgc tactgcaatt tagaggggcc 420  
acctatcaac tcatcagtgt tcaaagaata tgctggagc atgggtgaga gctgtggtgg 480  
gctgtggctg gccatcctcc tgctgctggc ctccattgca gccggcctca gcctgtcttg 540  
agccacggga ctgccacaga ctgagccttc cggagcatgg actcgctcca gaccgttgc 600  
acctgttgca ttaaacttgt tttctgttga ttaccttttgc gtttgacttc ccagggtctt 660  
gggatgggag agtggggatc aggtgcagtt ggctcttaac cctcaagggt tctttaactc 720  
acattcagag gaagtccaga tctcctgagt agtgattttg gtgacaagtt tttcttttg 780  
aaatcaaacc ttgttaactca tttattgctg atggcoactc tttcccttga ctcccccttg 840  
cctctgaggg cttcagtttattt gatggggagg gaggcctaag taccactcat ggagagtatg 900  
tgctgagatg cttccgaccc ttcaagggtgac gcaggaacac tgggggagtc tgaatgattt 960  
gggtgaagac atccctggag tgaaggactc ctcagcatgg ggggcagtgg ggcacacgtt 1020  
agggctgccc ccattccagt ggtggaggcg ctgtggatgg ctgctttcc tcaaccccttc 1080  
ctaccagatt ccaggaggca gaagataact aattgtgttg aagaaaactta gacttcaccc 1140  
accagctggc acaggtgcac agattcataa attcccacac gtgtgtgttc aacatctgaa 1200  
acttaggcca agtagagagc atcagggtaa atggcggtca tttctctgtt aagatgcagc 1260

catccatggg gagctgagaa atcagactca aagttccacc aaaaacaaat acaaggggac 1320  
ttcaaaagtt cacgaaaaaaaaaaaaaaaaaaaaaaa aaa 1373

<210> 294  
<211> 165  
<212> PRT  
<213> human organism  
  
<400> 294

Met Ala Leu Leu Ala Leu Leu Val Val Ala Leu Pro Arg Val Trp  
1 5 10 15

Thr Asp Ala Asn Leu Thr Ala Arg Gln Arg Asp Pro Glu Asp Ser Gln  
20 25 30

Arg Thr Asp Glu Gly Asp Asn Arg Val Trp Cys His Val Cys Glu Arg  
35 40 45

Glu Asn Thr Phe Glu Cys Gln Asn Pro Arg Arg Cys Lys Trp Thr Glu  
50 55 60

Pro Tyr Cys Val Ile Ala Ala Val Lys Ile Phe Pro Arg Phe Phe Met  
65 70 75 80

Val Ala Lys Gln Cys Ser Ala Gly Cys Ala Ala Met Glu Arg Pro Lys  
85 90 95

Pro Glu Glu Lys Arg Phe Leu Leu Glu Glu Pro Met Pro Phe Phe Tyr  
100 105 110

Leu Lys Cys Cys Lys Ile Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile  
115 120 125

Asn Ser Ser Val Phe Lys Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys  
130 135 140

Gly Gly Leu Trp Leu Ala Ile Leu Leu Leu Ala Ser Ile Ala Ala  
145 150 155 160

Gly Leu Ser Leu Ser  
165